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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:39:42 / Search time 3691.2 Seconds
(without alignments)
16303.117 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	621.4	42.2	1856	8	AF005096 Ricinus c
2	559.4	38.0	1684	6	AR076814 Sequence
3	559.4	38.0	1684	6	AR084177 Sequence
4	559.4	38.0	1684	6	BD062571 An sunflow
5	559.4	38.0	1684	6	BD070919 An oleoel
6	559.4	38.0	1685	6	AR020904 Sequence
7	559.4	38.0	1685	6	AR200408 Sequence
8	559.4	38.0	1685	6	138430 Sequence 4
9	559.4	38.0	1685	6	AF007561 Borago of
10	556.2	37.8	1687	8	BD079010 Echium pl
11	553	37.6	1450	8	AY055118 Echium ge
12	551.4	37.5	1478	8	AY055117 Echium ge
13	538.2	36.6	1347	8	AY131238 Argania s
14	529.4	36.0	1341	8	AP406816 Argilegia
15	460.8	31.3	1591	8	HACTB5RN
16	460.8	31.3	1606	6	AX007273 Sequence
17	459.8	31.3	1869	8	AF133728 Borago of
18	459.4	31.2	1594	6	AX007239 Sequence
19	459.4	31.2	1610	8	BNMJ4160 Brasica
20	449.6	30.6	110149	8	AC005397 Arabidops
21	443.2	30.1	1385	8	AY234126 Primula v
22	439.6	29.9	1681	8	AY234124 Arabidops
23	433.4	29.5	1491	8	BT003379 Arabidops
24	433.4	29.5	1652	8	AY087345 Arabidops
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33	401.2	27.3	1633	6	AF001394 Arabidops
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35	359.6	24.4	96312	2	AP005554 Oryza sat
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37	139.2	9.5	535	6	AX050883 Sequence
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39	132.6	9.0	1572	8	AF296076 Mucor rou
40	131	8.9	1572	8	AB090360 Mucor cit
41	122.6	8.3	291	6	AR246607 Sequence
42	103.4	7.0	1467	6	AX058832 Sequence
43	103.4	7.0	2040	6	AX058830 Sequence
44	103.4	7.0	2040	8	CPU250734 Ceratodon
45	93.4	6.3	266	6	AR247897 Sequence

ALIGNMENTS

RESULT 1
AF005096
LOCUS
DEFINITION Ricinus communis desaturase/cytochrome b5 protein mRNA, complete
ACCESSION AF005096
VERSION AF005096.1 GI:4101625
KEYWORDS
SOURCE
ORGANISM Ricinus communis (castor bean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiales; Ricinus.
REFERENCE
1 (bases 1 to 1856)
Sayanova,O., Smith,M.A., Lapinskae,P., Stobart,A.K., Dobson,G.,

TITLE
Sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition
JOURNAL
Patent: US 5959175-A 1 28-SEP-1999;
FEATURES
source
1.1684
Location/Qualifiers
BASE COUNT 430 a 277 c 358 g 619 t
ORIGIN

Query Match 38.0%; Score 559.4; DB 6; Length 1684;
Best Local Similarity 62.8%; Pred. No. 4.7e-148;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
60 AAGAGCATTTCGCAAGCAGACCTTGCAGACATTAACCAACAGAGATTATGATC 119
58 AAGAAATACATTAACCTCAGATGATCAAGAACAGATTAACCCGAGATCTATGATC 117
120 TCTATCAAGGAAAGATTAGATATCTCAGATGATCAAGAGCATCCGATGATGAG 179
118 TCGATTCAAGGAAAGCTATGATGTTGAGATTGGGTGAAGAACATCCATCCAGTGGCAGC 177
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RESULT 3
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LOCUS
DEFINITION
Sequence 1 from patent US 5977436.
ACCESSION
AR084177
VERSION
AR084177.1 GI:10010948
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 1684)
AUTHORS
Thomas, T.L. and Li, Z.
TITLE
Oleolin 5' regulatory region for the modification of plant seed
lipid composition
JOURNAL
Patent: US 5977436-A 1 02-NOV-1999;
FEATURES
source
1.1684
Location/Qualifiers
BASE COUNT 430 a 277 c 358 g 619 t
ORIGIN
Query Match 38.0%; Score 559.4; DB 6; Length 1684;
Best Local Similarity 62.8%; Pred. No. 4.7e-148;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
60 AAGAGCATTTCGCAAGCAGACCTTGCAGACATTAACCAACAGAGATTATGATC 119
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 LOCUS
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 A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition.
 ACCESSION
 BD062571
 VERSION
 BD062571.1 GI:22608174
 KEYWORDS
 JP 2001518795-A/1
 SOURCE
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 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Thomas, T.L., Beremand, P.D. and Nunberg, A.N.
 1 (bases 1 to 1684)
 A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition
 Patent: JP 2001518795-A 1 16-OCT-2001;
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 PN JP 2001518795-A/1
 PD 16-OCT-2001
 PR 09-APR-1998 JP 1998543140
 PR 09-APR-1997 US 08/831570
 PI TERRY L THOMAS, PHILLIP D BEREMAND, ANDREW N NUNBERG PC
 C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC
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 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
 QY 60 AAGAACACATTTGCGACAGACCTTGCMAAGCATTAAGCAACAGAGATTTATGATC 119
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DB 1435 TGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1464
 RESULT 5
 BD070919
 LOCUS
 DEFINITION An oleosin 5' regulatory region for the modification of plant seed
 accession
 BD070919
 VERSION BD070919.1 GI:22616522
 KEYWORDS JP 2001519668-A/1.
 SOURCE unclassified
 ORGANISM unclassified
 REFERENCE
 1 (bases 1 to 1684)
 AUTHORS Thomas, T.L. and Li, Z.
 TITLE An oleosin 5' regulatory region for the modification of plant seed
 lipid composition
 JOURNAL Patent: JP 2001519668-A 1 23-OCT-2001;
 RHOE POULENC AGRO
 COMMENT
 OS Unidentified
 PN JP 2001519668-A/1
 PD 23-OCT-2001
 PF 09-APR-1998 JP 1998543141
 PR 09-APR-1997 US 08/831575
 PI TERRY L. THOMAS, ZHONGSEN LI
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 ORIGIN
 Query Match 38.0%; Score 559.4; DB 6; Length 1684;
 Best Local Similarity 62.8%; Pred. No. 4.7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
 QY 60 AAGAGCATTTCGACAGACCTTGCAGATTAAGCAACGAGAGATTATGATC 119
 DB 58 AAGAAATACATTAATCTCGATGATGATCAAGAACACGATTAACCGGAGATATGATC 117
 QY 120 TCTATCAAGGAAAGTTTACGATATCTCAAGTGAATTAAGACATCCCGGTGTGAG 179
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 DB 298 GTTCTGAGTTTCTTAAGATTAATGAGAGCTGTTGTTGATTTCTTAAGATGGGTTG 357
 QY 360 TTCAAGACACAGGCAAGGGGTCTACTGCTCAATCTTTTGTGCTGTGCTGCTGCT 419
 DB 358 TATGACAAAAAGGATATATATGTTTGCACATTTGTGCTTATGCAATGCTGTTTCT 417
 QY 420 CTGAGTGTTCGGGTCTCTACTGCAAGAGCACTGGGCTCATCTTGTGCTGCTGCTG 479

Db	418	ATGATGTTTAAAGGGCTTTTGTGTTTGTGAGGGTGTTTGTGATCAATTGTTTCTG86GCT	477
Qy	480	CTAATGGGTAAGCTATGGCTCCAGAGTGTTGGGTGGGCGATGATCTTGTCACTAACCA	539
Db	478	TTGATGGGGTTCCTTTGGATTCAGAGTGTTGGATTTGGAACATGAGATCGGGCATTAATG	537
Qy	540	GTTATGCGCTAACCGTAAGCTTAATGCTCTTTTCAATTCATTTGACGGAAATGTAATGCT	599
Db	538	GTAAGTCTGATTCAGAGCTTATATAGTTTATGGGATTTTTCCTGCAATTTGCTTTCA	597
Qy	600	GGTGTAGTGTGCATGCTGGAAGTTGGAACCTAAACCCATCACTTGGCTGTAAATGC	659
Db	598	GGAATTAAGTATGTTGGTGGGAAATGGAACCAATATGACATCATTCGCTGTAAATGC	657
Qy	660	GCCAAATCGAATCCGATATTCAGAGCCTTCCATATATGGCATATGCCCAATATTTTTC	719
Db	658	CTTGAAATATGACCCGATTTTACAAATATATATACCATTCCTTGTGTCTTCCAAAGTTT	717
Qy	720	AACTCCCTTACATCATATCATACAACTGCAAAATGACCTATGATCGGCTCCAGT	779
Db	718	GGTTCACCTCACTCTCATTTCTATATGAAAAAGTTGACCTTTTGACTTTTATCAAGATTC	777
Qy	780	TTTGTAGCTTTCAAGACTGACATTTTATCCTGCATTTGTAAGCGTTAGGCTCTATCTT	839
Db	778	TTTGTAAATATCAACATTTGACATTTTAACTTATATGTGTGCTGATAGGCTCAATATG	837
Qy	840	TTTATTCGTCTTTTAAAGTGGTGTTTCCAAACAAAGGGTATPACAAGAAAGTACG	899
Db	838	TATGTACATCTCTCATATATGTTGTGACCAAGAGAAAT--GTGTCTATGAGCTGAG	894
Qy	900	GAAATTTTAAAGCTATGACGCTTCTTGACTTGTATTTCTCATCTCTTCTGCGCTAAC	959
Db	895	GAACTCTGGATGCGCTAGTGCTGATTCGATTTGTGATCCGTTGCTTGTCTTGTGCTC	954
Qy	960	AATTGGCCTGAAAGGTCATGATTTTCAAGCTCTTTAGCATGTGCGCGGTTTCCAACT	1013
Db	955	AATTGGGGTGAAGAAATTAATGTTGTATGTGCAATTTTATCATGTAAGCTGAATGTACA	1014
Qy	1020	TGGCAGTTCACCTTGAAATCATCTTGTCTTAAATGTTTACATCGTGTGGCTGACGCTAAT	1072
Db	1015	GTTCAAGTCTCTTGAACCACTTCTCTTCAAGTGTATATGTTGAAAGCTTAAGGAAT	1074
Qy	1080	GATTGCTTACCAAGCAGACAAAGGGCAGCTCAACATPAACAGCTTGTGTTGTGGAT	1133
Db	1075	AATTGGTTTGAAGAAACAAACGGAATGGGACACTTGACATTTCTGTCTCTTGAATGAT	1134
Qy	1140	TGGTTTCAATGATGCGCTGACCTTTCAGATTTAGACATCATCTGTTTCCAAAGATGCTTAAG	1199
Db	1135	TGGTTTCAATGATGATTTCAATTTCCAAATGTGACATATGTTTCCAAAGATGCTTGA	1194
Qy	1200	TGCCATTTACAGAAATATCTCAACCACTTGTGAAACAATCTTGGCAGAGACATATTTGCTC	1253
Db	1195	TGCAACCTTAAGAAATATCTCGCCCTACAGTATCGAGTTATGCAAGAAACATATTTGCTC	1251
Qy	1260	TATGAAATCTGCTACATGTGGAGGGCCAAATAAATGATATACTCCACCCTGCTGCTGTG	1315
Db	1255	TACAAATTAATGATCTTCTCCAAAGGCCAATGAATGAACATTCAGAACTTGTGGAACA	1314
Qy	1320	GCTATGGAAGCTAAGATGTTTACCAAGCAGTTCCTCAAGAAACATGCTCGGGAGACATG	1372
Db	1315	GCATTTGACGGCTAAGGATATATACCAAGCCGCTCCGAAAGAAATTTGTATGGAAAGCTCTT	1374
Qy	1380	AACACTTTGGGGTGAACCTTATTTAAATCAAGATGCTGTCTTTCCCGTAAAGCTTCAG	1438
Db	1375	CACACTCATGTTAAATTAACCTTATGTCATGATATATTAATTTGAGATTAATGATCTCCGA	1433
Qy	1440	TCCCAATGTTCTTTTTTTTTTTTTTTTTT 1469	
Db	1435	TGTTGTGTCTGTCTTGTTCTACTCTGTT 1464	

RESULT 6
AR020904

LOCUS	AR020904	1685 bp	DNA	linear	PAT 05-DEC-1998
DEFINITION	Sequence 4	from patent US 5789220.			
ACCESSION	AR020904				
VERSION	AR020904.1	GI:3975519			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1685)				
AUTHORS	Thomas,T. L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freysinet,G.L.				
TITLE	Production of gamma-linolenic acid by a DELTA-6-desaturase				
JOURNAL	Patent: US 5789320-A 4 04-AUG-1998;				
FEATURES	location/Qualifiers				
source	1..1685				
	/organism="unknown"				
BASE COUNT	431 a	277 c	357 g	620 t	
ORIGIN					

Query Match	Similarity	38.0%	Score 559.4	DB 6	Length 1665			
Best Local	Similarity	62.8%	Pred. No. 4.7e-148					
Matches	885	Conservative	0	Mismatches	522			
				Indels	3			
				Gaps	1			
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Qy	120	TCATCA	AGGAAAGTTT	ACGATAT	CTCCAA	GTGACT	TAAGACATCCCGGTGTAG	179
Db	119	TCGATT	CAAGGAAAGCCT	TATGATG	TTTGGATT	GGGAAAG	CCATCCAGGTGGCAGC	178
Qy	180	CTCCAT	TGTTAAATTTT	CCGGCC	CAAGATG	CTCATATG	GGCTCATTCACATCT	239
Db	179	TTCCCT	TGAAGAGCTTG	CTGGTCA	AGGTAATG	ATGATTTG	ATTCATCT	238
Qy	240	GGCAG	CTGTTGGC	ATATAC	CTTGACAG	GTTCCTTA	CTGCGTCAAGATTA	299
Db	239	GCCTC	TAATGGAAGAA	CTTGATTA	AGTTTTC	ACTGGTAT	TATCTTAAGATTA	298
Qy	300	GTCCT	AGATGTC	CAAGAC	TACAGA	AGCTGCT	CTGAGTTTCTAAGATGG	359
Db	299	GTTCT	GAGGTTTCT	AAAGATT	TAGGAAG	CTTGTTG	ATTTCTAAATGGGTTG	358
Qy	360	TTCAAG	CACAGG	CAAGGG	GCTACT	GCCTCA	CTTTTTCGTGTGTGTTG	419
Db	359	TATGAC	AAAAAG	GTCAAT	TATATGT	TTGCA	CTTTGCTTAATAGCATCTGTTG	418
Qy	420	CTGAG	TGTTAC	GGGTTCT	CTAC	GCAGAC	AGCCTGGGCTCATCTTGTGCTGGTTG	479
Db	419	ATGAG	TGTTAT	GGGGTTT	TTTTTG	AGGGGT	TTTTTGATCAATTTGTTTCTGGGCT	478
Qy	480	CTAA	TGGTAT	GTATG	CTCCAG	ATGTTGG	GTGGGCATGATCTTGTCACTACCA	539
Db	479	TTGAT	GGGGTTTCT	TGGAT	TCAGAG	GTGTTG	ATGATGCAATGATGCGGCATTAATG	538
Qy	540	GTTAT	TGCC	CTAAG	CTTAAT	CTGCTTTT	CAATCATTGCAGCAAAATGTATGCT	599
Db	539	GTATG	TCGTAT	CAAGCT	TAAATG	ATTATG	GGTATTTTGTGTCAAATGTCTTCA	598
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Db	599	GGAA	TAAATG	ATGTTGGT	GTGAAAT	TGGAAC	ATATATGCAATCACTTGCCGTAAATAGC	658
Qy	660	GCCAT	CTGAT	CTGAT	TATTCAG	ACCTTCT	CTTAATTTGCCATATCCCAAAATTTTTC	719
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Qy	720	AATC	CCCTTA	CAATAT	CTATCA	CACTG	CAAAATGACATATGATGCGCGTCCAGTTT	779
Db	719	GGTT	CAC	CTC	CTCATTT	CTATG	AGAAAGTTGACTTTTGACTTTTCAAGATTC	778
Qy	780	TTGT	TAGCTT	CA	GTGAC	ATTTTAT	CTCTGATGTTAAAGCTTAAGCTCTATCTT	839

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 Db 1016 GTTCACTTCTCTGTAACCACTTCTCTCAAGGTTTAAAGTTAGGAAAGCTTAAAGGGAAT 1075
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 Db 1076 AATTGGTTTGAAGAAACAAACGATGGGACACTTGACATTTCTGTCTCTTGATGAT 1135
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 QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1469
 Db 1436 TGGTTGTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1465

RESULT 7
 AR200408
 LOCUS AR200408 1685 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 4 from patent US 6355861.
 ACCESSION AR200408
 VERSION AR200408.1 GI:20250482
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1685)
 AUTHORS Thomas, T.L.
 TITLE Production of gamma linolenic acid by a DELTA-6-desaturase
 JOURNAL Patent: US 6355861-A 4 12-MAR-2002;
 FEATURES
 source Location/Qualifiers
 1..1685
 /organism="unknown"
 BASE COUNT 431 a 277 c 357 g 620 t

Query Match 38.0%; Score 559.4; DB 6; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 4,7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
 QY 60 AAGAACACATTTGCAAGAGAGCTTGCACAAAGCATTAAGCAACGAGAGATTATGATC 119
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Db 59 AAGAAATACATTACCTCAGATGAATCAAGAAACCAAGATTAACCCGAGATCTATGATC 118
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 Db 599 GGAATTAAGTATGTTGTTGGTGAAGATGGAACCAATTAAGCATCAATGCTGCTTAAATG 658
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LOCUS AF007561 1685 bp mRNA linear PLN 05-JAN-1999
 DEFINITION Borago officinalis delta 6-desaturase mRNA, complete cds.
 ACCESSION AF007561
 VERSION AF007561.1 GI:4102020
 KEYWORDS
 SOURCE Borago officinalis
 ORGANISM Borago officinalis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Lamiales; Boraginaceae; Borago.
 REFERENCE 1 (bases 1 to 1685)
 AUTHORS Numberg,A.N., Beremand,P.D. and Thomas,T.L.
 TITLE Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid (GLA)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1685)
 AUTHORS Numberg,A.N., Beremand,P.D. and Thomas,T.L.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-1997) Biology, Texas A&M University, College Station, TX 77843, USA
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CDS

BASE COUNT 431 a 277 c 357 g 620 t
 ORIGIN

Query Match 38.0%; Score 559.4; DB 8; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 4.7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

60 AAGAAGACATTTGCGACAGACCTTGAAAGCATATACCAACCCAGAGATTATGATC 119
 59 AGGAATATATTAATCTCAAGTGAATCAAGAACCAAGATTAACCCGGAATCTATGATC 118
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 180 CTCCCATTTGTAAGTTTGGCCGCAAGATGTCATGATGCGTCACTTGTCTTACCTCT 239
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360 TTCAAGACACAGCAAGAGGCTACTGCTCAATCTTTTCTGCTGCTGTTGCTGCT 419
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Db 1436 TGTGTGCTGCTGTTGTTTACTTGT 1465

RESULT 10
BOU79010 1687 bp mRNA linear PLN 02-MAY-1997
DEFINITION Borage officinalis delta 6 desaturase mRNA, complete cds.
ACCESSION U79010.1 GI:2062402
VERSION U79010.1 GI:2062402
KEYWORDS Borage officinalis
SOURCE Borage officinalis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiales; Boraginaceae; Borage.
1 (bases 1 to 1687)
Sayanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G., Christie, M.W., Shewry, P.R. and Napier, J.A.
Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco
Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
97268723
MEDLINE 9108131
PUBMED 2 (bases 1 to 1687)
REFERENCE Sayanova, O., Smith, M.A., Shewry, P.R. and Napier, J.A.
AUTHORS Direct Submission
TITLE Submitted (20-NOV-1996) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK
JOURNAL Location/Qualifiers
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BASE COUNT 441 a 276 c 356 g 614 t

ORIGIN

Query Match 37.8%; Score 556.2; DB 8; Length 1687;
Best Local Similarity 62.6%; Pred. No. 3.8e-147;
Matches 883; Conservative 0; Mismatches 524; Indels 3; Gaps 1;

QY 60 AAGAACCAATTTCGACAGCAGACTTCGAAGCATATAGCAACAGAGATTATGATC 119
DB 57 AAGAATACATTACCTCAAGTGAATCAAGACCAAGATTAACCGAGATCTATGATC 116
QY 120 TCTATCAAGGAAAGTTATGATATCTCAAGTGAATCAAGAGCATCCGGTGTGAG 179
DB 117 TCGATTCAAGGAAAGCTATGATGTTTCGATTGGGTGAAGACCATCCAGGTGGAGC 176
QY 180 CTCCATTGTATAGTTTGGCGGCAAGATGTCATGATGCGTTCATGTTACATCTT 239
DB 177 TTTCCCTTAAGAGCTCTGCTGCTCAAGAGTAACATGATGCTTGTGATTCATCTT 236
QY 240 GGCATGCTTGGCAATACCTGACAGGTTCTTACTGACTACGTTACGTTCAAGATTACTT 239
DB 237 GCCTCTACATGAGAAATCTTGAATGTTTTCACCTGGGATTAATCTTAAAGATTAATCTT 236
QY 300 GTCTCTGAGATGTCAGAGCATACAGAGGCTGCTCTGAGTTTCTTAAGATGGGTTTG 359

Db 297 GTTCTGAGGTTTCTAAAGATTATAGAACCTGTGTGATGTTTCTAAAGTGGGTTTG 356
QY 360 TTCAGACACAGGCAAGAGGGGTCTACTGCTCAATCTTTTGGTGTGTTGGCT 419
DB 357 TATGACAAAAGAGTCAATATATGTTTGGCACTTTTGTCTTATAGCAATGCTGTTGCT 416
QY 420 CTGAGTGTACGGTGTCTCTACTGCAAGAGCACTGGGCTCATCTTGTCTGTGTTTG 479
DB 417 ATGAGTGTATGAGGGTTTGTGTTGAGAGGTTTGTGTATCATTTGTTTCTGGGTGT 476
QY 480 CTATGGGTATGCTATGCTCCAGAGTGTGTGGGTGGGATGATTTTGTCTACTACCA 539
DB 477 TTATGAGGGTTTCTTTGATTCAGAGTGTGATGGACATATGCTGGGCAATTATATG 536
QY 540 GTTATGCGTACCGTATAGCTTATTCGCTTTTCAATCATATGAGAAATGATGATGCT 599
DB 537 GTAGTGTCTATTCAGGCTTAATTAAGTTATGAGGTTTGTGCAAAATGCTTTTCA 596
QY 600 GGTGTAGTGTTCATGTGGAAGTTGACCATATACACCATCATCTTGTGCTATATAGC 659
DB 597 GGAATAGATATGTTGTGTGGAATGGAACCATATATGACATCATCATGCTGTAATAGC 656
QY 660 GCCAATCTGGATCTGATATTCAGACCTTCTATATGTCATATCCCAATTTTTC 719
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QY 720 AACTCCCTTACATCATATATATCAACATGCAAAATGACATATGCGGCTGACAGTTT 779
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QY 780 TTTGTAGCTTTGACAGCTGACATTTTATCTGATGTTTAAAGCTTATGCTTATCTT 839
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QY 900 GAATTTTAAAGGCTATGACAGCTTCTTGAATGTTTCTTACTCTCTTGTGCTTACCC 959
DB 894 GAACCTCTGGAGTCTGTAAGTCTGATGTTTGTGATCCCTGTTTGTCTTGTGCTT 953
QY 960 AATTGACCTGAAGAGGTATGTAATTTACAGTCTGTTTACAGTCCGCGGTTTCAACAT 1019
DB 954 AATTGGGGGAAGAAATATATGTTTATGCAAGTTTGTCACTGATCGGAATGCAACAA 1013
QY 1020 TGGCAGTTACGTTGATATCACTTGTCTTATATGTTTACAGTGTGTTGCTTACCGTAA 1079
DB 1014 GTTCAGTCTCTCTTGAACCACTTCTCAAGGTTTATGTTGAAAGGCTTAAAGGGAAT 1073
QY 1080 GATTGTTTACAGAGAGCAAAAGGAGCGCTCAACATTAACAGCTTCTGTTGTGGGAT 1139
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QY 1320 GCTATGAGAGCTAAGAGTATTAACAGAGTTCCCAAGAAACATGCTGAGAGCAATG 1379
DB 1314 GCATTGAGGCTAAGAGTATTAACAGAGCGCTCCGAAGAAATTTGATGAGAGCTT 1373
QY 1380 AACACTTGGGTTGAACCTTATTAACATCAAGTGTGTTTCCGCTAAGAGCTTCCAG 1439

QY 1260 TATGAACTGCTACCATGTCGAGGCGCAATAAATGTATATCTCCACCTCGCTGTGTG 1319
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 DEFINITION Echium gentianoidee delta-6-desaturase (D6DES) gene, complete cds.
 ACCESSION AY055117 GI:17223794
 VERSION AY055117.1
 KEYWORDS Echium gentianoidee
 SOURCE Echium gentianoidee
 ORGANISM Echium gentianoidee
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Lamiales; Boraginaceae; Echium.
 1 (bases 1 to 1478)
 Ruiz,J.R., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Marco,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Marco,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Ruiz,J.R.
 Direct Submission
 Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria,
 Campus Universitario, La Canada s.n., Almeria 04120, Spain
 LOCATION/Qualifiers
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 Bull. Herb. Boiss., ser. 2, 4: 498 (1903)"
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 BASE COUNT 364 a 258 c 365 g 491 t
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 Query Match 37.5%; Score 551.4; DB 8; Length 1478;
 Best Local Similarity 63.8%; Pident 0.8; e-16;
 Matches 853; Conservative 0; Mismatches 481; Indels 3; Gaps 1;
 QY 60 AAGAAGCATTTTCGACAGACCTTTCGAAGCATTAAGCAACGAGAGATTATGATC 119

Db 52 AAGAAGCATTTTCGACAGACCTTTCGAAGCATTAAGCAACGAGAGATTATGATC 111
 QY 120 TCTATCAAGGAAAAGTTTACGATATCTCAAGTGAATTAAGAGATCCGGTGGAG 179
 Db 112 TCAATCAAGGCAAGGCTATGATGTTTACGATGTTTGAAGCAATCCAGGAGAG 171
 QY 180 CTCACATTTGTAATTTTCCGCGCAAGATGTCATGATGCGTTCAATGCTTCAATCT 239
 Db 172 TTCCTTGTGTGACCTTGTGTGAGCAAGGTAAGATGATGATTTGTGATTTCT 231
 QY 240 GGCATGCTTGGCAATACCTTGACAGGTTCTTACTGGGTAAGCTTCAAGTTACTCT 239
 Db 232 GATTCAACTGGAAAGTTCTTGATGATTTCTTCACTGGCTATTATCTTAAGATTACTCT 291
 QY 300 GTCTGAGATGTCAGAGACTACAGAGGCTCGTCAAGTTTCTAAGATGGGTTTG 359
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 QY 360 TTCAGACACACAGGCAAGGCTCTACTGCTCAATCTTTTCGTCGTGTTGCT 419
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 Db 652 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
 QY 720 AACTGCTTACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 779
 Db 712 AGCTGCTACCTCTCATTTCTATGAAGAAGAACTGATGATGATGATGATGATGATGAT 771
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 Db 772 TTGTTAGCTTTCAGACTGACATTTTATCTGATGATGATGATGATGATGATGATGAT 831
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 Db 949 AATTGCTGAAAGGCTATGATTTTACGCTCTGTTAGACAGTCCGGGTTCCAAAT 1008
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 QY 1320 GCTATGGAAGCTAAGATGTTACCAAGCCAGTTCCCAAGAACATGCTTGGAGCAATG 1379
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 QY 1380 AACACTTGGGGTGAGC 1396
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RESULT 13
 AY131238 1347 bp mRNA linear PLN 17-AUG-2002
 DEFINITION Argania spinosa delta-6-desaturase mRNA, complete cds.
 VERSION AY131238
 ACCESSION AY131238.1 GI:22296825
 KEYWORDS Argania spinosa
 SOURCE Argania spinosa
 ORGANISM Argania spinosa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Asteridae; Ericales; Sapotaceae; Argania.
 1 (bases 1 to 1347)
 El Filali, A., Anderson, M. and Abbas, K.
 Characterization and cloning of delta-6-desaturase in Argania
 spinosa fruit
 Unpublished
 2 (bases 1 to 1347)
 El Filali, A., Anderson, M. and Abbas, K.
 Direct Submission
 Submitted (12-JUL-2002) Biologie Moleculaire, Faculte des Sciences,
 Ibn Batouta, Rabat, Rabat 1014, Morocco
 Location/Qualifiers
 1. 1347
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BASE COUNT 346 a 239 c 298 g 464 t

Query Match 36.6%; Score 538.2; DB 8; Length 1347;
 Best Local Similarity 63.2%; Pred. No. 5.1e-142;
 Matches 844; Conservative 0; Mismatches 488; Indels 3; Gaps 1;

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Qy 1380 AACACTTTCGGTGA 1394
Db 1333 CACACTCATGTGTTAA 1347

RESULT 14
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LOCUS Aquilegia vulgaris sphingolipid long chain base delta 8 desaturase
DEFINITION mRNA, complete cds.
ACCESSION AF406816
VERSION AF406816.1 GI:22652110
KEYWORDS
SOURCE Aquilegia vulgaris
ORGANISM Aquilegia vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaceae; Aquilegia.
1 (bases 1 to 1341)
Longman, A.J., Michaelson, L.V. and Napier, J.A.
Isolation and characterization of a cDNA encoding a delta 8
sphingolipid desaturase from Aquilegia vulgaris
Unpublished
2 (bases 1 to 1341)
Longman, A.J., Michaelson, L.V. and Napier, J.A.
Direct Submission
Submitted (07-AUG-2001) Cell Biology, IACR-Long Ashton Research
Station, Long Ashton, Bristol BS41 9AF, UK
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BASE COUNT 346 a 226 c 293 g 476 t
ORIGIN

Query Match 36.0%; Score 529.4; DB 8; Length 1341;
Best Local Similarity 63.1%; Pred. No. 1.6e-119;
Matches 850; Conservative 0; Mismatches 491; Indels 6; Gaps 2;

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Qy 288 CAAATTAATCTCTCTCTGATGATGTCAGAGACTACAGAAAGCTCTCTGAGTTTCT 347
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Qy 348 AAGATGAGTTTGTCAAGACACAGCAAGGGGTCTACGTCATCTTTTCTGTCCT 407
Db 298 AAAGCAGGTTTATGATGATTAAGGATCAATCACTTTTCTCTACTTTTGTCACT 357
Qy 408 GTGTGTCGCTCTGAGTGTTTTACGGTGTCTCTACCTGCAAGACACCTGGGCTACTT 467
Db 358 ATTTTAATGAGCTATTAATGATGATGAGGTTTGTGTCTGATAGACTTGGGCTACTT 417
Qy 468 TGCTGTGTTTGTCAATGGGTATGCTATGAGCTCAGAGTGTGGGGCATGATCT 527
Db 418 GCTTGTGCTGCTGTTTGGGGCTTCTTGGATGCAAAATGGGTTGTGGGCATGATTC 477
Qy 528 TGTCACTACCAATTAATGCTTAACCGTAAGCTTAATGCTTTTTCAAATCATTTGACGA 587
Db 478 GACATTAACAATTAATCAATGCTTACTCTTAATTAATGATTAATGACATTTTACCGGA 537
Qy 588 AATGTGATTCCTGATGTTAGTGTGATGAGTGGAGAGTGGACCATTAACCCATCACTT 647
Db 538 AATGTATTAACAGAAATCAATGATGAGTGTGAGAGAGGAAACCAATGGGCATCACTT 597
Qy 648 GCTGTAAATAGCCCAATCTGATCTGATTAATGACACCTTCTTAATTTGCCATATCC 707
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Qy 828 AGGCTATCTTCTTATTTCTGCTTTTAAAGTGTGTTTCCAAACAAAGGATATAC 887
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Qy 888 AAGAGATCAGAAATTTTAAAGCTATGACGTTTCTGACTTGTATTTCTACTCTT 947
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Qy 948 TCTGCTACCAATTTGAGCTGAAAGGATCATATTTTACGCTGTTTAAAGATCGCC 1007
Db 895 GCTTGTGCTGCAATTTGGGGGAGAGACGATATATGTTCCATGATGATTTGGGTTCT 954
Qy 1008 GGGTTCCAATTTGGAGTTCACTTGAATCACTTGTCTTAATGTTTAACTGTGTTG 1067
Db 955 GGGTATCAGATTAATCAATTTCTGCTTGAACATTTTTCAGCTCACTTAATGTTGGCCT 1014
Qy 1068 CTTAGCGTAAATATGTTGTTTACACAGACAGACAAAGGACAGCTCAACATACGTTCT 1127
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Db 1075 ACTTGATGATTTGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1134
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Db 1135 CAAATGCTGCGGATTTGAAGAAATTTGCTTTTGTGAAGAACTCTGACAGGAAA 1194
Qy 1248 CATTAATTTGCTATGAAGTCTACATGTTGGAGGCCAATTAATGATATCTCAACC 1307
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QY 1308 CTGCGTCTGTGGCTATGGAAGCTAATGTTACCAAGCAGCTTCCCAAGACATGTC 1367
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RESULT 15
 HACTYB5N 1591 bp mRNA linear PLN 03-FEB-2001
 LOCUS Helianthus annuus mRNA for stereo-unselective delta 8-sphingolipid
 DEFINITION desaturase (sld1 gene).
 ACCESSION X87143
 VERSION X87143.1 GI:1040728
 KEYWORDS cytochrome b5 domain; delta-8 sphingolipid desaturase, sld1 gene.
 SOURCE Helianthus annuus (common sunflower)
 ORGANISM Helianthus annuus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.

REFERENCE
 1 Sperling, P., Schmid, H. and Heinz, E.
 A cytochrome-b5-containing fusion protein similar to plant acyl
 lipid desaturases
 Eur. J. Biochem. 232 (3), 798-805 (1995)
 MEDLINE 56028121
 PUBMED 7588718

REFERENCE
 2 Sperling, P., Blume, A., Zahrlinger, U. and Heinz, E.
 Further characterization of Delta(8)-sphingolipid desaturases from
 higher plants
 Biochem. Soc. Trans. 28 (6), 638-641 (2000)
 MEDLINE 11171153
 PUBMED 11171153

REFERENCE
 3 (bases 1 to 1591)
 Sperling, P.
 Direct Submission
 Submitted (10-MAY-1995) P. Sperling, Univ Hamburg, Inst. fuer
 Allgemeine Botanik, Ohnhorststr. 18, 22609 Hamburg, FRG
 Related sequences: AJ224160, AJ224161, AF133728.

COMMENT
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 WMQIAYIGDAGHYQMAATGMNKFPAGIFPGNCITGISIAMWKTNHHIICNSIDY
 DPLQHLPMIAVSSKLFNSITSVYRGQLTDPDLAPFVSYOHLYLYPIMCVAVNLY
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polysite 1577
 /gene="sld1"
 BASE COUNT 412 a 338 c 355 g 486 t
 ORIGIN

Query Match 31.3%; Score 460.8; DB 8; Length 1591;
 Best Local Similarity 59.2%; Pred. No. 6, 2e-120;
 Matches 805; Conservative 0; Mismatches 552; Indels 3; Gaps 1;

QY 42 ACTTCGAATGGAAGACCAAGAAGACATTTGGCAAGCAGCTTGCAGATTAAGCAA 101
 Db 100 AATTCATTTGCTGATGGAAGAAAATACATACATCAAAAGATTAAAGAGATTAAC 159
 QY 102 CCAGAGATTATGATCTATCAAGGAAAAGTTAGATATCTCCAGTGGACTAA 161
 Db 160 CCTAATGACCTTTGGATCTCAATTTGGGCAAGTTTACAGTTACAGAAATGGGCTAA 219
 QY 162 GAGCATCCCGGTGGAGTCCCATTTGATTTTCCGGGCAGATCTGATGGG 221
 Db 220 GAGCATCCCGGTGGAGTCCCATTTGATTTTCCGGGCAGATCTGATGGG 279
 QY 222 TTCATTGCTTACCATCTGCGACCTGCTGGCAATACCTTGACAGGTTCTTACTGGGTAC 281
 Db 280 TTTATGCAATTTCAATCCGGATCTGCGTGAAGCATCTAGACAACTACCGGAT 339
 QY 282 TAGCTTCAAGATTACTCTGCTCTGAGATGTCAGAGATCAAGAGAGCTGCTTGA 341
 Db 340 CACTTAAAGATTACACAGTTTCTGACATTTCTAGAGACTACCGAACTCGCTTCA 399
 QY 342 TTTTCTAAGATGGTTTGTTCAGACACAGCAAGAGGCTTACTGCTCATCTTTTC 401
 Db 400 TTTGCAAAAGCCGGATATGTTGAGAAAGATCAAGGATTAATTAATCACTTTGTTT 459
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 QY 462 CATCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 521
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 QY 522 GATCTTGTCTACTACCAATTAATGCTTAACCTGATACCTTAATGCTTATGCTTCAATCAT 581
 Db 580 GACGGGGCATTTACCAATGATGCGACCCCGGGGTGAAACAGTTTGGCGGAATATT 639
 QY 582 GCAGGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
 Db 640 ATCGGAATTTGATTAACCGGAATTAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
 QY 642 CACTTGTCTGATTAAGCGCAATCTGATCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 701
 Db 700 CACATGCTTGAACAGTCTTAT 759
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 QY 942 CTCCTTTTCGGCTACCAATTTGGCCTGAAGGCTCATGATATTTCACGCTCTGTTAGCA 1001

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:38:37 ; Search time 279.13 Seconds
(without alignments)
14225.873 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1470	99.9	1471	21	ABD01349	florida bitebush
2	559.4	38.0	1684	19	AAV34398	boraginella-6-des
3	559.4	38.0	1684	20	AAV24417	boraginella-6-des
4	559.4	38.0	1685	17	AAV30395	boraginella-6-des
5	559.4	38.0	1685	25	ABK49502	DNA encoding Boraginella
6	559.4	38.0	1685	25	ABK15366	boraginella-6-des
7	526.4	35.8	1934	21	AAAD01552	Soybean sphingolipid
8	460.8	31.3	1606	21	AAW44851	Soybean sphingolipid desat

9	459.4	31.2	1594	21	AAZ24832
10	458.6	30.5	1465	21	AAC24832
11	433.4	29.5	1650	21	AAC33846
12	433.4	29.5	1650	21	AAC31462
13	423.4	29.5	1678	21	AAZ44833
14	429.4	29.2	1350	24	ABZ12753
15	399.4	27.2	1972	21	ABD12753
16	377.8	25.7	1702	24	ABK495003
17	377.8	25.7	1702	25	ABK41536
18	352	23.9	1764	21	AAAD1356
19	197.4	13.0	880	21	AAAD1351
20	176.4	12.0	657	24	ABQ65917
21	139.2	9.5	535	22	AAPE5733
22	133.2	9.1	476	24	ABE3274
23	122.6	8.3	291	25	ABK35008
24	117	8.0	287	25	ABK11201
25	106.2	7.2	480	25	ABK1024
26	103.4	7.0	1467	22	AAPE5739
27	103.4	7.0	2040	22	AAPE5739
28	93.4	6.3	266	25	ABK47468
29	84	5.7	1578	24	ABQ76782
30	84	5.7	1578	24	ABV74266
31	84	5.7	2012	22	AAPE6040
32	84	5.7	2012	25	ABK13450
33	84	5.7	15430	24	ABO76796
34	84	5.7	15430	24	ABV74274
35	84	5.7	17752	24	ABO76797
36	84	5.7	17752	24	ABV74275
37	81.8	5.6	2160	22	AAPE5733
38	81.4	5.5	1463	25	ABK73166
39	76.8	5.2	1404	25	ABV76916
40	63.8	4.3	823	21	AAAD1354
41	60.8	4.1	405	24	ABK21395
42	58.8	4.0	554	25	ABK7142
43	58.6	4.0	1374	21	AAPE5739
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ALIGNMENTS

	RESULT	1
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ID	AAD01349	standard; cDNA; 1471 BP.
AC	AAD01349;	
DT	12-OCT-2000	(first entry)
DE	Florida bitterbrush delta-6 fatty acid desaturase cDNA.	
KM	Florida bitterbrush; delta-6 fatty acid desaturase; tartaric acid	
KW	transgenic plant; fatty acid; membrane-bound desaturase; ss.	
XX	Picroamia pentandra.	
OS		
XX		
FH	Key	Location/Qualifiers
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FT		/*tag= a
FT	/product= "Delta-6 fatty acid desaturase"	
XX		
PN	WO200032790-A2.	
XX		
PD	08-JUN-2000.	
XX		
PF	02-DEC-1999;	99WO-US28589.
XX		
PR	03-DEC-1998;	98US-0110784.
XX		
PA	(DUPO) DU PONT DE NEMOURS & CO E I.	
XI	Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;	

B. napus sld1 DNA.
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
A. thaliana sld1 D
Arabidopsis thaliana
Mest sphingolipidid
DNA encoding Evenin
Evening primrose c
Corn sphingolipid
Soybean sphingolipid
Arabidopsis thaliana
C. purpureus deltec
Arabidopsis thaliana
Corn ear-derived f
Human GDP-mannose
Arabidopsis thaliana
C. purpureus deltec
C. purpureus deltec
Corn ear-derived f
P. patens D6 desat
Physcomitrella pat
P. patens delta-6-e
P. patens delta-6-e
PB-DHGA encoding
Plant specific exp
PBAR1 encoding de
Plant specific delte
C. purpureus deltec
Human GDP-mannose
Nucleotide sequenc
Wheat sphingolipid
Arabidopsis thaliana
Arabidopsis thaliana
Fungal delta-6-desat
Nucleotide sequenc
cDNA encoding a de

XX MPI: 2000-412336/35.
 DR P-PSDB; AAY71551.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 39; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding delta-6 fatty acid desaturase
 CC from clone pps-pk0011.ds; this isolated from Florida bluebush developing
 CC seed cDNA library, pps. The delta-6 desaturase enzyme catalyzes the
 CC formation of trienic acid, a fatty acid that has a triple bond at the
 CC delta-6 carbon. The present sequence is useful for producing
 CC transgenic plants having altered levels of delta-6 desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 CC
 XX Sequence 1471 BP; 353 A; 330 C; 313 G; 474 T; 1 other;
 SO
 Query Match 99.9%; Score 1470; DB 21; Length 1471;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 841 TTATTTCTGCTTTTAAAGTGTGTTTCCAAACAACAAAGGATATCAAGAAAGTACAG 900
 DB 841 TTATTTCTGCTTTTAAAGTGTGTTTCCAAACAACAAAGGATATCAAGAAAGTACAG 900
 QY 901 AAATTTAGGCTATGAGCTTTCTTGAATTTGATTTCTGACTCTTTCTGCTGCTACCA 960
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 QY 1081 ATTGGTTTACGAGCAACAAAGGCAAGCTCAACATTAAGCTTTCTGTTGGGATTT 1140
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 DB 1141 GGTTCATGCTGCTGCACTTTCAGATTTGAGCATCTGTTTCCAAAGATGCTTAAGT 1200
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 QY 1321 CTATGAGCTAAGATTTTACCAACAGCTTCCAAAGACATGCTTGGGAAGCATGA 1380
 DB 1321 CTATGAGCTAAGATTTTACCAACAGCTTCCAAAGACATGCTTGGGAAGCATGA 1380
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 DB 1381 ACACTTTCGGGTGAACCTTATTAACATCAAGTCTGCTTTCCGTAAGCTTCAAGT 1440
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 DB 1441 CCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1471

RESULT 2
 AAV34398
 ID AAV34398 standard; DNA; 1684 BP.
 XX
 AC AAV34398;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Borage delta-6 desaturase gene.
 XX
 KM Upstream region; regulatory region; sunflower; albumin; seed; expression;
 XX lipid metabolism; delta-6 desaturase; transgenic plant; ds.
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..1389
 FT /*tag= a

FT	primer_bind	/product= "delta-6 desaturase"
FT	primer_bind	/complement (616..632)
FT	primer_bind	/tag= b
FT	primer_bind	/tag= c
FT	primer_bind	/tag= c
XX	MO9845460-A1.	
XX	15-OCT-1998.	
XX	09-APR-1998;	98WO-US07178.
XX	09-APR-1997;	97US-0831570.
XX	(RHON) RHONE-POULENC AGROCHIMIE.	
XX	Beremand PD, Nunberg AN, Thomas TL;	
XX	WPI; 1998-583201/49.	
XX	P-PSDB; AAM67471.	
XX	New sunflower albumin 5' regulatory region - useful for directing	
XX	altered lipid metabolism in plant seeds	
XX	Example 2; Fig 1; 38bp; English.	
XX	This sequence is the gene encoding the borage (Borago officinalis)	
XX	delta-6 desaturase enzyme. The lipid metabolism gene is an example	
XX	of a heterologous gene which can be expressed at high levels in a	
XX	seed-specific manner in transgenic plants, when placed under control	
XX	of the sunflower albumin gene 5' regulatory region (AAV34397).	
XX	Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;	
XX	Query Match	38.0%; Score 559.4; DB 19; Length 1684;
XX	Best Local Similarity	62.8%; Pred. No. 3.2e-158;
XX	Matches	885; Conservative 0; Mismatches 522; Indels 3; Gaps 1
OY	60 AAGAGACATTTGCGAAGCAGACCTTGCAAGCATTAAGCAACGAGATTATGATC	119
DB	58 AAGAAATACATTACTCGATGAACTCAAGAACACAGATTAACCGGAGATCTATGATC	117
OY	120 TCTATCAGGGAAGATTACGATATCTCCAGTGGACTTAAGAGATTCGGGTGTAG	179
DB	118 TCGATTCAAGGGAAGCCTATGATGTTTCGATTTGGTGAAGAACATCCAGGTGCAGC	177
OY	180 CTCCATTGTTAAGTTTGGCCGCAAGATGACATGATGGTTCATTGCTTACCATCCT	239
DB	178 TTTCCCTTGAAGAGCTTGGCTGTGTAGAGGTAACATGATGATTTGTTGCACTCT	237
OY	240 GGCACTGCTGGCAATACCTTGACAGGTTCTTTACTGGGTACTACGTTCAAGATTACT	299
DB	238 GCGCTTACATGGAAGAAATCTTGATAGTTTTCACCTGGTATTACTTAAGATTACTCT	297
OY	300 GTCTCTGATGATGCCAAGACTACGAAGGCTGCTCTGATTTTCTAAGATGGGTTG	359
DB	298 GTTCTGAGGTTTCTAAGATTAATGGAAGCTTGTTGATTTGATTAATGAGGTTTG	357
OY	360 TTCAAGACACAGGGAAGGGGTCACTGCTCAATCTTTTCGTGTGTGTGTTGCT	419
DB	358 TATGCAAAAAAGGTCATATTAATGTTTGCACACTTGTGCTTAATGCAATGCTGTTGCT	417
OY	420 CTGAGTGTTAACGAGTCTCTACTGCAAGACACCTGGGCTCACTTGTGCTGGTTTG	479
DB	418 ATGATGTTTAAGGGGTTTGTGTTGTAGGGGTGTTTGTATCATTTGTTTCTGGGTGT	477
OY	480 CTAATGGGATGCTATGGCTCCAGAGTGGTGGGTGGGCGATGATTTCTTGCTACCA	539
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OY	540 GTTATGCTTAACCGTAAGCTTAATGCTTTTTCAAATATGACGAGAAATGATATGT	599
DB	538 GTAGTGTCTGATTCAGGCTTAATTAAGTTATGGGTATTTTGTGCAATATGCTCTTCA	597

QY	600	GGGTGATGCTGTCATGCTGGAAGTTGGACATTAACCCATCACTTGGCTGTAAAGC	659
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Db	658 <td>CTTGAAATATGACCCCTGATTTACAAATATATACATCTCTGTGTGTGCTTCCAAAGTTTTC</td> <td>717</td>	CTTGAAATATGACCCCTGATTTACAAATATATACATCTCTGTGTGTGCTTCCAAAGTTTTC	717
QY	720 <td>AAGTCCTCTTACATCATCTATCACACTGCAAAATGACCTATGATGGCGCTGCAGGTT</td> <td>779</td>	AAGTCCTCTTACATCATCTATCACACTGCAAAATGACCTATGATGGCGCTGCAGGTT	779
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QY	780 <td>TTTGTGTAGCTTTAGACACTGGAACATTTTATCTGTCATGTGTTAGCGTTAGGCTCTATCTT</td> <td>839</td>	TTTGTGTAGCTTTAGACACTGGAACATTTTATCTGTCATGTGTTAGCGTTAGGCTCTATCTT	839
Db	778 <td>TTTGTATAGTTATCAACATTTGAGACATTTTACCCTTATATGTGTGTGCTGTAGGCTCAATATG</td> <td>837</td>	TTTGTATAGTTATCAACATTTGAGACATTTTACCCTTATATGTGTGTGCTGTAGGCTCAATATG	837
QY	840 <td>TTTATTTCTGTCCTTTAAGTGGTGTGTTTCCAAACAAAGGATATCAAGAGAATGAC</td> <td>899</td>	TTTATTTCTGTCCTTTAAGTGGTGTGTTTCCAAACAAAGGATATCAAGAGAATGAC	899
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QY	900 <td>GAAATTTTAGGCTATGACGCTTTCTTGACTTGGATTTCTACTCTCTTTCTCGGCTACCC</td> <td>959</td>	GAAATTTTAGGCTATGACGCTTTCTTGACTTGGATTTCTACTCTCTTTCTCGGCTACCC	959
Db	895 <td>GAACTCTTGGAGATGCCCTAGAGTTCTCATATTTGGTACCCGTGCTGTGTTCTGTGTTCCCT</td> <td>954</td>	GAACTCTTGGAGATGCCCTAGAGTTCTCATATTTGGTACCCGTGCTGTGTTCTGTGTTCCCT	954
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Db	955 <td>AATTGGGGGTAAAGAAATTAATGTTGTTATTTGCAAGTTTATCAAGACTGGAATCCAAACAA</td> <td>1014</td>	AATTGGGGGTAAAGAAATTAATGTTGTTATTTGCAAGTTTATCAAGACTGGAATCCAAACAA	1014
QY	1020 <td>TGGCAGTTGACGCTTGAATCACTTGTCTCTAATGTTTACACTGCTTTGCTTACGGGTAAAT</td> <td>1079</td>	TGGCAGTTGACGCTTGAATCACTTGTCTCTAATGTTTACACTGCTTTGCTTACGGGTAAAT	1079
Db	1015 <td>GTTCAGTTCTCTTGAACCACTTCTCTTCAAGTGTATGTTGGAAAGCCTTAAGGGAAAT</td> <td>1074</td>	GTTCAGTTCTCTTGAACCACTTCTCTTCAAGTGTATGTTGGAAAGCCTTAAGGGAAAT	1074
QY	1080 <td>GATTGCTTTTACACAGCAGCAAAAGGGACCCCTCAACATAACAGCTTCTGTTGGTGAT</td> <td>1139</td>	GATTGCTTTTACACAGCAGCAAAAGGGACCCCTCAACATAACAGCTTCTGTTGGTGAT	1139
Db	1075 <td>AATTGGTTTGAAGAAACAAACGAAAGGACACTTGACATTTCTGTCTCTCTGGATGAT</td> <td>1134</td>	AATTGGTTTGAAGAAACAAACGAAAGGACACTTGACATTTCTGTCTCTCTGGATGAT	1134
QY	1140 <td>TGTTTTATGATGGCGCCGCACTTTCAGATTTGAGCATCATCTGTTCCAAAGATGCTTAAG</td> <td>1199</td>	TGTTTTATGATGGCGCCGCACTTTCAGATTTGAGCATCATCTGTTCCAAAGATGCTTAAG	1199
Db	1135 <td>TGGTTTCATGCTGATTTGCAATTTCCAAATTTGAGCATCATTTGTTTCCCAAGATGCTCAGA</td> <td>1194</td>	TGGTTTCATGCTGATTTGCAATTTCCAAATTTGAGCATCATTTGTTTCCCAAGATGCTCAGA	1194
QY	1200 <td>TGCACTTTCAAGAAATCTCACCCATTTGTAACAACATTTGCGCAAGACATTAATTTGCTC</td> <td>1259</td>	TGCACTTTCAAGAAATCTCACCCATTTGTAACAACATTTGCGCAAGACATTAATTTGCTC	1259
Db	1195 <td>TGCAACCTTGAAGAAATCTCGCCCTACGTGATGAGATTGCAAGAAACATTAATTTGCTC</td> <td>1254</td>	TGCAACCTTGAAGAAATCTCGCCCTACGTGATGAGATTGCAAGAAACATTAATTTGCTC	1254
QY	1260 <td>TATGAAACTCTTACATGTGGAGGCCCAATTAATATGTAATATCCACCCTGCGTGTG</td> <td>1319</td>	TATGAAACTCTTACATGTGGAGGCCCAATTAATATGTAATATCCACCCTGCGTGTG	1319
Db	1255 <td>TACAAATATTCATCTTTCTCCAAAGGCCCAATGAATATGACCTCGAACAATTTGAGAACACA</td> <td>1314</td>	TACAAATATTCATCTTTCTCCAAAGGCCCAATGAATATGACCTCGAACAATTTGAGAACACA	1314
QY	1320 <td>GCTATGGAACCTAAGATGTTTACCAAGCCAGTTCCCAAGAAACATGCTCGGGAAGCATG</td> <td>1379</td>	GCTATGGAACCTAAGATGTTTACCAAGCCAGTTCCCAAGAAACATGCTCGGGAAGCATG	1379
Db	1315 <td>GCATTTGAGGCTAGAGGATATTAACCAAGCCGCTCCCGAAGAAATTTGATATGGGAAGCTTT</td> <td>1374</td>	GCATTTGAGGCTAGAGGATATTAACCAAGCCGCTCCCGAAGAAATTTGATATGGGAAGCTTT	1374
QY	1380 <td>AACACTTTGGGGTGAAACCTTATTAACAAACATCAAGTGTGCTCTTTCCGTAAAGCTTCCAG</td> <td>1439</td>	AACACTTTGGGGTGAAACCTTATTAACAAACATCAAGTGTGCTCTTTCCGTAAAGCTTCCAG	1439
Db	1375 <td>CACACTCATGTTAAATTAACCCCTTAGTTCATGTAAATTAATTTGAGATTATGATATCTCTTA</td> <td>1434</td>	CACACTCATGTTAAATTAACCCCTTAGTTCATGTAAATTAATTTGAGATTATGATATCTCTTA	1434
QY	1440 <td>TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT</td> <td>1469</td>	TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	1469
Db	1435 <td>TGTTTGTGCTGTCTTGTTCTTACTTGTGT</td> <td>1464</td>	TGTTTGTGCTGTCTTGTTCTTACTTGTGT	1464
RESULT 3			
AAAX24917			
ID	AAAX24917	standard; cDNA; 1684 BP.	
XX	AAAX24917;		
XX	AAAX24917;		
XX	21-JUN-1999	(first entry)	
XX	Borage delta-6 desaturase cDNA.		
DE	Borage delta-6 desaturase cDNA.		
XX	Delta-6 desaturase; borage; oleosin; Afs21; promoter;		

KW	transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
XV	gamma-linolenic acid; octadecatetraenoic acid; ds.
XX	
OS	Borage officialis.
XX	
FH	Key Location/Qualifiers
FT	CDS 43..1389
FT	/tag= a
XX	
PN	MO9845461-A1.
PD	15-OCT-1998.
XX	
PF	09-APR-1998; 98WO-US071179.
XX	
PR	09-APR-1997; 97US-0831575.
XX	
PA	(RHON) RHONE-POULENC AGROCHIMIE.
XX	
PI	Li Z, Thomas TL;
DR	WPI; 1999-180333/15.
XX	
P	P-PSDB; AAW98130.
PT	Nucleic acid containing oleosin 5'-regulatory region - useful for
PT	modulating fatty acid synthesis and lipid metabolism in plants,
XX	particularly to increase content of gamma-linolenic acid
PS	
XX	Example 2; Page 59-61; 101pp; English.
CC	The present sequence encodes borage delta-6 desaturase (see
CC	AAM98130) an enzyme that catalyzes the conversion of linoleic acid
CC	to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was
CC	isolated from a borage membrane-bound polyosomal cDNA library
CC	using a partial clone, obtained from an EST database search, as
CC	a probe. The borage delta-6 desaturase nucleic acid can be
CC	operably linked to the seed-specific 5' regulatory region (see
CC	AAM24916) of the Arabidopsis thaliana oleosin ACS21 gene in claimed
CC	expression cassettes of the invention. Transgenic plants, e.g.
CC	sunflower, soybean, maize, tobacco, cotton, peanut, oilseed
CC	rape or Arabidopsis are obtained that show increased levels of
CC	GLA or octadecatetraenoic acid. The levels of desirable fatty
CC	acids in oilseed crops can be manipulated to provide seed
CC	oils of use in human health and industrial applications.
XX	
SQ	Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;
Query Match	38.0%; Score 559.4; DB 20; Length 1684;
Best Local Similarity	62.8%; Pred. No. 3.2e-158;
Matches 885; Conservative	0; Mismatches 522; Indels 3; Gaps 1
OY	60 AAGAAACCATTTCCCAAGCAGACCCTTGCAAGCATTAAGCAACGAGATTATGATC 119
DB	
58 AAGAATATCATTCCTCGATGAATCAAGAACGACGATAAACCCGGAGATCTATGATC 117	
OY	120 TCTATCAAGGAAAAGTTTACGATATCTCCAAGTGACTTAAGAGCATCCGGTGTGAG 179
DB	
118 TCGATTCAAGGGAAGGCCTATGATGTTTCGATTTGGGTGAAGAACCATCCAGTGGCAGC 177	
OY	180 CTCGCATGTTAAGTTTTGCCGCAAGATGTCATGATCGCTTCAATGCTTACCATCCT 239
DB	
178 TTTCCTTGAAAGATCTTGCTGCTCAAGAGTAACTGAAGCATTTGTTGATTTCCATCCT 237	
OY	240 GGCACTGCTGGCAATACCTTGACAGGTTCTTACTGGGTACTACGTTCAAGATTACTT 299
DB	
238 GCCTTACATGGAAGAATCTTGATATAGTTTTCACATGGGATATTACTTAAAGATTACTT 297	
OY	300 GTCTCTGAGATGTCCAAGACTACGAAGGCTGCTCTGAGATTCTTAAGATGGGTTTG 359
DB	
298 GTTCTGAGGTTTCTTAAGATATTATGGAAGCTTGATGTTTGAATTTCTTAATATGGGTTTG 357	
OY	360 TTCAGAACAACCGCAAGGGGCTACTACTGCTCAATCTTTTGTGCTGTGTTGCTT 419
DB	

Db	358	TATGACAAAAAAGGTCATATTATGTTGGCAACTTGGCTTTATAGCAATGCTGTTGCT	417
Oy	420	CTAGATGTTTACGGTGTCTCTACTGCAGAGCACTGGGCTCATCTTGTCTGGT	479
Db	418	ATGATGTTTATGGGGTGTGTTTTGTCAGGGGTGTGTTGGTACATTTGTTTCTGGGGTGT	477
Oy	480	CTATAGGTAATGCATGGCTCCAGAGTGGTTGGGGGGGAGTGAATCTTGTCATCAACCA	539
Db	478	TTGATGGGGGTTTTCTTTGGATTCAAGATGGTGTGGANTGGACATGATGCTGGGCAATTATG	537
Oy	540	GTTATGCTTAACCGTAAGCTTAATCGTCTTTTCAAAATCATTTGACGAGAAATGTGATTC	599
Db	538	GTAATGTCGTATTAAGAGCTTAATAAGTTATGGGATTTTTGTGCGAAATGTGCTTCA	597
Oy	600	GGTGTAGTGTTCATGGTGGAGGTTGGACCATTAACACCATCACTTGTCTGTATATGC	659
Db	598	GGAAATTAAGTATGGTTGGTGAAATGGAACCATATGACATCATCATTCCTGTATATAGC	657
Oy	660	GCCAAATCGAATCCTGAATATTCACACCTTCTATTAATGCGAATATCCCAAAATTTTC	719
Db	658	CTTGAAATATGACCCGTGATTTACAAATATATACATCTCTGTGTGCTTCCAAAGTTTTT	717
Oy	720	AACTCCCTTACATCATCTATCATCAACATGCAAAATGACCTATGATCGGCTCCAGGTTT	779
Db	718	GGTTCACCTCACCTCTCATTTCTATGAGAAAAAGTTGACTTTGACTCTTATCAAGATTC	777
Oy	780	TTGTGTAGCTTTCAGCACTGGACATTTTATCTGCATATGTTAAGCGTTAGGCTCTATCTT	839
Db	778	TTTGTATGATTTCAAACTATGGACATTTTACCCTTATATGTGCTGCTAGGCTCAATATG	837
Oy	840	TTTATCTGTCCTTTTAAGTGGTGTTTTCCAAACAAGGAGTATCAAGAGAAGTACG	899
Db	838	TATGTACATCTCTCATATATGTATGTATGACCAAGGAAT--GTTGCTTATCGAGCTACG	894
Oy	900	GAAATTTTAGGCTATGACGCTTTCGTGACTGTATCTCTACTCTTTCGCGCTACCC	959
Db	895	GAACTCTTGGGATGCCATAGTGTCTCATTTTGGTATCCCGTGTCTTGTGTTTGCT	954
Oy	960	AATTGGCCCTGAAGGGTCAATGATTTTCACTGCTGTTTGAAGCATGCCGGTTCACAT	1019
Db	955	AATTGGGGTGAAAGAAATATGTTTGTATATGCAAGTTTATCAGTAGACGTGAATCAACAA	1014
Oy	1020	TGGGAGTTTCACTGGAATCACTTTGCTTCTATATGTTTACACTGGTTGCCTAGGGTAT	1079
Db	1015	GTTTCAAGTCTCTTGAACCACTTCTCTTCAAGTGTATATGTGTGAAGGCCTTAAGGGAT	1074
Oy	1080	GATTGGTTTCCAGCAGACAAAGAGGCGCTCAACATTAACAGCTTTCGCTTGGGGAT	1139
Db	1075	AATTGGTTTGAAGAACAAACGAGTGGGACACTTGACATTTTGTGCTCTCTTGAGTATGAT	1133
Oy	1140	TGATTTCATGGTGGCTGCACTTTCAGATTTGAGCATCATCTGTTTCCAAAGATGCTAAG	1199
Db	1135	TGATTTCATGGTGGATTTGCAATTCGAATTTGAGCATCATTTGTTTCCAAATGCTGAGA	1194
Oy	1200	TGCCATTTCAAGAAAATCTCACCAATTTGTAAACAACTTTGCCAGAGCATTAATTTGCTC	1255
Db	1195	TGCAACCTTGAAGAAAATCTCGCCCTAGCTGATGCAATTAATGCAAGAAACATTAATTTGCT	1254
Oy	1260	TATGAAATCGCTACATGTGGGAGGCGCAATTAATGATATCTCAACCTGCTGCTGTG	1319
Db	1255	TACAAATTAATGATCTTTCTCCAGGGCCAAATBAATGACATCAAGAACTTATGAGAACCA	1314
Oy	1320	GCTATGGAAGCTAAGATGTTACCAAGCGCACTTCCCAAGACATGCTGTGGGAACAATG	1379
Db	1315	GCATTTGACGGCTAAGGATATTAACCAAGCGCTCCGAAAGAAATTTGATTTGGGAAGCTTT	1374
Oy	1380	AACACTTTGGGGTAAACCTTATTAACAATCAAGTGTCTCTTTCCCGTAAAGCTTCCAG	1438
Db	1375	CACACTCATGGTTAAATTAACCTTAGTTCATGTAATTAATTTGAGATTATGATCTCTTA	1434
Oy	1440	TCCCAATGTTCTTTTTTTTTTTTTTTTTTTT 1469	
Db	1435	TGTTTGTGTCTGTCTGTGTTCTTACTGT 1464	

Db	1316	GCATTGACGGCTAGAGGATATACCAAGCCGCTCCCGAAGATTGGTATGGGAAGCTCTT	1375
Qy	1380	AACACTTTGGGGTGAACCTTATMAACATCAAGTGTCTTTTCCCGTAAAGCTTCGAG	1439
Dy	1376	CACACTATAGGTAAATTAATACCTTAGTTCATGTAATTAATTGAGATTGTATCTCCTA	1435
Oy	1440	TCCGATGTTCTTT	1469
Db	1436	TGTTGTGCTTGTGTTGTTGTTCTACTGTT	1465
RESULT 5			
ID	ABK49502	standard; DNA; 1685 BP.	
XX	ABK49502;		
AC			
XX			
DT	15-JUL-2002	(first entry)	
XX			
DE	DNA encoding Borago officinalis delta6-desaturase.		
XX			
KW	delta6-desaturase; sunflower; soybean; maize; tobacco;		
KM	peanut; carrot; oil seed rape; gamma linolenic acid; GLA;		
KM	chilling tolerance; gene; ds; borago.		
XX			
OS	Borago officinalis.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	44..1390	
FT		/*tag= a	
FT		/product= "delta6-desaturase"	
FT		/trans_except= (pos:1151..1153, aa:Ser)	
XX			
PN	US6355861-B1.		
PD	12-MAR-2002.		
XX			
PF	19-SEP-1997;	97US-0934254.	
XX			
PR	13-OCT-1992;	92US-0959952.	
PR	10-OCT-1991;	91US-0774475.	
PR	08-JAN-1992;	92US-0817919.	
PR	14-SEP-1994;	94US-0307382.	
PR	28-JAN-1997;	97US-0789936.	
XX			
PA	(RHON) RHONE-POULENC AGROCHIMIE.		
XX			
PI	Thomas TL;		
DR	WPI; 2002-380944/41.		
DR	P-PSDB; AAU79830.		
XX			
PT	Novel nucleic acid encoding evening primrose delta6-desaturase which		
PT	converts linoleic acid to gamma linolenic acid useful for producing		
PT	gamma linolenic acid in transgenic plant or bacteria		
XX			
PS	Example 9; Column 29-32; 53pp; English.		
XX			
CC	The invention describes an isolated nucleic acid encoding an evening		
CC	primrose Delta6-desaturase. The nucleic acid and a vector expressing the		
CC	nucleic acid are useful for producing a plant such as sunflower, soybean,		
CC	maize, tobacco, peanut, carrot or oil seed rape plant, with increased		
CC	gamma linolenic acid (GLA) content, and also for inducing or increasing		
CC	production of GLA in a bacteria or plant deficient, lacking in or		
CC	producing low levels of GLA. The nucleic acid is also useful for inducing		
CC	chilling tolerance in plants. This sequence encodes the borago delta6		
CC	desaturase involved in the production of gamma linoleic acid.		
XX			
SO	Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;		
Query Match	38.0%; Score 559.4; DB 24; Length 1685;		
Best Local Similarity	62.8%; Pred. No. 3.2e-158;		

	Matches	885;	Conservative	0;	Mismatches	522;	Indels	3;	Gaps	1				
QY	60	AAGAAGCA	CA	TTTGGC	AGACGAC	CTTGCC	AAAGCA	TA	TAAGCA	ACCA	GGAGATTATGATC	119		
Db	59	AAGAAATAT	CA	TTTACCT	CGATGA	AACTCA	AGAACCA	CGATTA	AACCCGGAGATCTATGATC			118		
QY	120	TCATCAAGG	AAAGTTTAC	ATATCTCC	AAAGGGA	CTAA	AGACAT	CCGGG	GGGTAG			179		
Db	119	TCGATCAAGG	AAAGCC	TATGATGTTTCG	ATGGGTG	GAAGAAC	CAATCC	AGTGGCAGC				178		
QY	180	CTCCCAT	TGTTAA	GTGTTTGG	CCGGCC	AGAGTGC	TA	CTAGTGG	TCATGCTTAC	CAATCCT		239		
Db	179	TTTCCCTTGA	AGATCTTTG	CGTGGTCA	AGAGTA	CTATGAT	TA	TGTTGCA	TTCCATC	CT		238		
QY	240	GGCAGCT	GTGGCA	TAATAC	TTTGACAG	GTCTTTTA	CTGGGTA	CTA	CGTTCA	AGATTACTCT		299		
Db	239	GCCCTCA	ATCGAAGAA	ATCTTGTA	TAAGTTTTC	ACTGGGTAT	ATCTTAA	AGATTACTCT				298		
QY	300	GTCCTGA	AGATGCC	AGAC	TA	AGAAAGGTG	CGTCTG	AGTGTTC	TA	ATAATGGTTTG		359		
Db	299	GTTTCTGA	GGTTCTTAA	AGATTAA	AGAAAGCTTG	TGTTGATGTTTCTTAA	AAATGGGTTTG					358		
QY	360	TTCAAGAC	CACGAGGCA	AAAGGGGTCT	ATGCTCA	ATCTTTTCG	GTGCTGTG	TCGCT				419		
Db	359	TATACAAAA	AGGTCA	TATATG	TTTGCA	ACTTTGCTTTA	TAGCAATG	CTGTTGCT				418		
QY	420	CTGAGGT	TTTACGG	TGTTCTCT	TA	CTGACAG	ACCTGGG	CTCATCTT	TGCTGTG	TTTG		479		
Db	419	ATGAGT	TTTATAG	GGGTTTTGTTT	TGAGGGGT	TTTGGTAC	ATTTGTTTCTGGGGTGT					478		
QY	480	CTATGGG	TAATGCA	TAGGCTCA	AGAGTGGGTGGG	GCATGAT	TTCTGTCA	TACCA				539		
Db	479	TTGATGG	GGTTTCTTTG	GAATTC	CAGAGTGGTGA	ATGACATGATG	CTGGGCATTA	TATG				538		
QY	540	GTTATG	CCCTAAC	CGTAA	CTTAATCGTCTTTTCA	ATATG	AGAGAAATG	TATGCT				599		
Db	539	GTA	GTCTGA	TATTAAG	CTTAATAG	TTTATG	GGTATTTTGTG	CCAAATG	TCCTTCA			598		
QY	600	GGTGTAG	TGTCAGTGG	TGAGAG	TTGGA	CCATTA	CCCATCA	CTTGTG	CTGATATAGC			659		
Db	599	GGATTA	GTATG	TGGTGGTGA	AAATGGA	CCATTA	GCATCA	ATTCCTG	TATATAGC			658		
QY	660	GCCAT	CTGAT	CCTGATAT	TCAG	ACCTTC	CTATAT	TGCCAT	TATCCCAA	ATTTTC		719		
Db	659	CTTGAA	TATAG	ACCCTGATTTA	CA	TATATAC	ATTCCTGTGTG	CTCCAA	ATTTTTT			718		
QY	720	AAC	CCCTTAC	ATCATCTAT	CA	CAAC	CTGCAAA	TGACTATG	ATCCGCTG	CCAGGTTT		779		
Db	719	GGT	CACTCA	CTCTCATTTCT	AT	AGAAAA	AGTTGACTTT	TGACTTT	TATCA	GAATTC		778		
QY	780	TTTGTAG	CTTTCAG	CACTGGA	CA	TTTTAT	CTGCA	TGTTAA	CGTTAA	CGGCTTATCTT		839		
Db	779	TTTGTAG	TTATCA	CAATGGA	CA	TTTTTACC	CTATAT	TGTTG	CTGATAGG	CTCAATATG		838		
QY	840	TTTAT	TTCTGCTTTAA	GGTGGT	TTTTCC	AA	CAAAA	GGGTAT	AC	AGAGATGAG		899		
Db	839	TAT	GTACA	AACTCTCAT	TAA	TGTTGT	TACCA	AGAGAA	AT--GTGTCTTAT	CGAGCTAG		895		
QY	900	GAA	ATTTTAA	GCATGAG	CTTTCTTGA	CTTGGAT	TTCTG	ATCTTTC	CGCTG	CTACCC		959		
Db	896	GAA	CTCTTGGA	ATGCTTAG	TGTTCTG	CAATTTGG	ATACCCG	TGCTGTTTCTT	TGTTGCT			955		
QY	960	AAT	TG	CCCTAAA	AGGTCA	TGATATTT	CA	CGTCCG	TTTAA	CGAGTCCGCGGGTTCC	AT	1019		
Db	956	AAT	TG	GGGTTAA	GAATAT	TGTTTGT	AT	TGCA	AGTTTAT	CA	GTGATGCA	ATCA	1015	
QY	1020	TGG	CAGTTCA	GCTTGA	ATCACTT	TGCTTAT	TGTTTAC	ATG	GTGTTG	CTTACG	GTAT	1079		
Db	1016	GTT	CA	AGTTTCTCTTTGA	ACCACTTCTCTTCA	AGTGTAT	TGTTGGA	AGGCTTAA	GGGAAT			1075		
QY	1080	GAT	TG	TTGTTTCA	CA	CGACGA	CAAAAGG	GCCTCA	CA	ATTA	CA	AGCTTCTG	CTGGTGGAT	1139
Db	1076	AAT	TG	TTGTTTGA	AAACAA	CGAATGG	GA	CACTTG	CA	ATTTCTGTCTCT	CTGATG	AT	1135	

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OY 1140 TGGTTTCAGTGGCCCTGCACCTTTCAGATTGAGCATCTGTTCACAGATGCGCTAG 1199
DB 1136 TGGTTTCAGTGGCCCTGCACCTTTCAGATTGAGCATCTGTTCACAGATGCGCTAG 1195
OY 1200 TGGCAATTCAGGAAATCTCACCCTATGTAACAACTTGCAGAGCATATTTGTC 1259
DB 1196 TGCACCTTACGAAATCTCGCCCTACGATGATGATGACAAAGAAATATTTGCT 1255
OY 1260 TATGAATCTGCTACCTATGAGGAGGCAATTAATGATCTCCACCTGCTGCTG 1319
DB 1236 TACCAATTCAGATCTTTCACAGGCAATGAAATACACTAGAACATTTGAGAAC 1315
OY 1320 GGTATGAGAGTATAGATGTTACCAAGCAGATGCCAAGAACATGCTGGAGCAATG 1379
DB 1316 GCAATTCAGGCTAGGATATTAACCAAGCCGCTCCGAAAGAAATTTGATGGAAGCTCTT 1375
OY 1380 AACACTTTCGGGTGACCTTATTAACATCAAGTGTCTTCCGTAAGACCTTCAG 1439
DB 1376 CACACTCAGTGTAAATTAACCTTACGATGATATTAATGAGATTAATGATCTCCA 1435
OY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1469
DB 1436 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1465

RESULT 6
ABX15366
ID ABX15366 standard; cDNA; 1685 BP.
AC ABX15366;
XX
XX 17-APR-2003 (first entry)
DE Borage delta-6-desaturase #1 cDNA.
XX
XX Delta-6-desaturase; gene; ss: delta-12-desaturase; sunflower; soybean;
XX maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
XX octadecatretenoic acid; alpha-linolenic acid; delta-15-desaturase;
XX borage.
XX
XX Borage officinale.
XX
XX
XX Key Location/Qualifiers
XX CDS 44..1390
XX FT /tag= a
XX FT /product= "Borage delta-6-desaturase #1"
XX FT /transl_except= (pos:1151..1153, aa:Ser)
XX
XX US2002108147-A1.
XX
XX 08-AUG-2002.
XX
XX 21-DEC-2001; 2001US-0029756.
XX
XX 13-OCT-1992; 92US-0959952.
XX 19-SEP-1997; 97US-0934254.
XX 10-OCT-1991; 91US-0774475.
XX 08-JAN-1992; 92US-0817919.
XX 14-SEP-1994; 94US-0307382.
XX 28-JAN-1997; 97US-0789936.
XX
XX (THOM/) THOMAS T L.
XX
XX Thomas TL;
XX
XX P-PSDB; ABG73095.
XX
XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
XX for producing plant with increased gamma linolenic acid content, and
XX for inducing octadecatretenoic acid production in plant
XX

```

PS Example 9; Fig 5A; 55pp; English.

XX The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatretenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatretenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding a borage delta-6-desaturase polypeptide.

XX Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

Query Match 38.0%; Score 559.4; DB 25; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 3.2e-158;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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OY 60 AAGAAGCAGATTCGACAGACCTTCGAAAGCATTAAGCAACAGAGATTATGATC 119
DB 59 AAGAATATCTTACCTCAGATGATGATCAAGAACAGATTAACCGAGATCTATGATC 118
OY 120 TCTATCAAGGAAAGTTTACGATATCTCCAGATGAGACTAAAGACATCCCGTGTAG 179
DB 119 TCGATTCAGGAAAGCCATGATGATGTTGCGATGGGTGAAAGACCATCAGGTGAC 178
OY 180 CTCCCATTTTAACTTTTCCCGGCAAGATGCTAGATGCTGATGCTTACATGCTTAC 239
DB 179 TTTCCCTGAAAGCTTCTGCTGCTCAAGAGTACGATGATGATGATGATGATGATGAT 238
OY 240 GGCATGCTTGGCAATACCTTGACAGAGTTCTTACTGCGTATACGTTCAAGATTACT 299
DB 239 GCTCTACATGGAAGAACTTGTATGATGATGATGATGATGATGATGATGATGATGAT 298
OY 300 GTCTGTAGATGCTCAAGACTACGAAGGCTGCTCTGATGATTTCTTAAGTGGTTTG 359
DB 299 GTTCTGAGGTTCTTAAGATTAAGAAAGCTTGTGATGATTTCTTAAGTGGTTTG 358
OY 360 TTCAAGACACAGGAAAGGCTCTACGCTCAATCTTTTGTGTGTGTGTGTGTGTGT 419
DB 359 TATGACAAAAGGCTCATATTAATGTTGCAATTTGCTTATGCAATGCTGTGTGT 418
OY 420 CTGAGTGTTCAGGTTCTCTACTGCAAGACCTGCGCTCATCTTGTCTGTGTGTG 479
DB 419 ATGAGTGTTCAGGTTCTCTACTGCAAGACCTGCGCTCATCTTGTCTGTGTGTG 478
OY 480 CTAATGGGTATGCTATGCTCCAGAGTGGTGGTGGGAGATGATTTCTGATCAACAA 539
DB 479 TTGATGGGTTCTTTGATTCAGAGTGGTGGTGGTGGGAGATGATTTCTGATCAACAA 538
OY 540 GTTATGCTTACCGTAAGCTTATGCTTTTCAATTCATGCAAGAAATGATGTGT 599
DB 539 GTTATGCTTACCGTAAGCTTATGCTTTTCAATTCATGCAAGAAATGATGTGT 598
OY 600 GGTGTTAGTGTGCAAGGTTGAGGTTGACCAATACCATCATCTTGTCTGTAATAGC 659
DB 599 GGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
OY 660 GCCAATCTGATCTGATATTCAGACCTTCTTATATTTGCAATATCCCAAAATTTTC 719
DB 659 CTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
OY 720 AACTCCCTTACATCTATCATACAACTGCAAAATGACTATGATGATGATGATGATGAT 779
DB 719 GGTGATCTCACTCTCATTTCTATGAAAGGTTGACTTTGATCTTTTATCAAGATTC 778
OY 780 TTTGTTAGCTTACAGACTGACATTTTATCTGATGATTTTAAAGGTTAGGCTTATCTT 839

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Db 779 TTTGTAATATCAACATTGACATTTTACCCTATATATGTCGCTAGGCTCAATATG 838
 Qy 840 TTTATCTGCTTTTAAAGTGTGTTTCCACAAACAAAGGGATATCAAGAGTCA 899
 Db 839 TATGTAATCTCTCAATATGTTTGAACCAAGAAAT---GCTCTTATCAAGCTCA 895
 Qy 900 GAAATTTAGGCTATGACGCTTCTTGTATGTTATCTACTCTCTTCTGCTTACC 959
 Db 896 GAATCTTGGAGTCCAGTGTCTCATTTGGTACCCGTTGCTGTTCTGTTGCTTCC 955
 Qy 960 AATTGGCTGAAAGGCTATGTTTACGCTCTGTTTACAGTCCGCGGCTTCAACAT 1019
 Db 956 AATTGGGCTAAGAAATATGTTTATGTAAGCAATTATCAGATGCAATGCAACAA 1015
 Qy 1020 TGGCAGTTCACTTGAATCACTTGTCTTAAATGTTTACATGGTGTCTTACGCTTAA 1079
 Db 1016 GTTCAGTCTCTTGAACCACTTCTTCAAGTCTTATGTTGAAGCTTAAAGGAAAT 1075
 Qy 1080 GATTGTTTACACAGACAGACAAAGGAGCCTCAACATTAACGCTTGTGCTGGAT 1139
 Db 1076 AATTGGTTTGAAGAAACAAACGATGGGACATTTCTGCTCTCTGCTGGATGAT 1135
 Qy 1140 TGGTTTCATGTCGCTGACCTTTCATGATGAGATGATCTGTTTCCAAAGATGCTTAA 1199
 Db 1136 TGGTTTCATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1195
 Qy 1200 TGGCATTTCAGAAATCTCAACCATTTGTGAACAACTTGGCCAGAGATTAATTTGCC 1259
 Db 1196 TGCACTTTCAGAAATCTGCTCTTCAAGTCTTATGTTGAAGCTTAAAGGAAAT 1255
 Qy 1260 TATGAACTGCTTACATGTCGAGGAGGCAATTAATGTTATCTTCACTGCTGCTG 1319
 Db 1256 TACAATATCATCTTCTTCTCAAGGCAATGAATGACACTGACAACTTGAAGAAC 1315
 Qy 1320 GCATGGAACCTAAGATGTTTACCAAGCCAGTTCCTCCAGAAACATGCTGAGAGCAT 1379
 Db 1316 GCATGGAAGCTAAGATGTTTACCAAGCCAGTTCCTCCAGAAATGTTGATGAGAGCT 1375
 Qy 1380 AACATTTTGGGATGAACTTATTAACATCAAGTGTCTTCTCCCTTAAAGCTTCCAG 1439
 Db 1376 CACATCTATGTTAAATTAATCCCTTATGTTATGTTAATTTGAGATTAATGATCTCT 1435
 Qy 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1469
 Db 1436 TGTGTGTCCTGCTGTTCTTACTTGT 1465
 RESULT 7
 AAD01352 standard; cDNA; 1934 BP.
 ID AAD01352;
 AC AAD01352;
 XX 12-OCT-2000 (first entry)
 DT 12-OCT-2000 (first entry)
 DE Soybean sphingolipid desaturase cDNA #2.
 XX Soybean sphingolipid desaturase; membrane-bound desaturase;
 KM transgenic plant; fatty acid; ss.
 XX Glycine max.
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 305..1657
 FT /tag= a
 FT /product= "Sphingolipid desaturase"
 XX
 XX MO200032790-A2.
 XX PN 08-JUN-2000.
 XX PD 02-DEC-1999; 99MO-US28589.
 XX

PR 03-DEC-1998; 98US-0110784.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 XX WPI; 2000-41236/35.
 DR P-PSDB; AAY71554.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 XX transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 46; 57bp; English.
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone sbl.pk0017.b4.f15 isolated from soybean seedling cDNA
 CC library, sbl. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;
 XX
 Query Match 35.8%; Score 526.4; DB 21; Length 1934;
 Best Local Similarity 61.3%; Pred. No. 3.3e-148;
 Matches 864; Conservative 0; Mismatches 542; Indels 3; Gaps 1;
 Qy 49 TGGAGAGCCAAAGAACCAATTTGCAAGACAGACCTTGCAAGCATTAAGCAACAGAG 108
 Db 315 TTGAGAGAGGAAGAAAGTACATTAACCTCAAGAGAGCTGAAGGGTCAACAAAGAGGAG 374
 Qy 109 ATTATGATCTCTATCAAGAGGAAAGTTTACATATCTTCCAGTGAATTAAGACATC 168
 Db 375 ATTATGATCTCTATCAAGAGGAAAGTTTACATATCTTCCAGTGAATTAAGACATC 434
 Qy 169 CCGGTGAGTCCCATGTTTAAAGTTTGGCCGCAAGATGTCATGATGCTTATG 228
 Db 435 CTGATGATGTTTCAATCTCAACCTTCTGTCGAGATGTCATGATGATGATGATGAT 494
 Qy 229 CTTACCATCTGACAGTCTGTCGCAATTAACCTTGAAGTCTTCTTCTGATCTTAC 288
 Db 495 CATACCATCTGACAGTCTGTCGCAATTAACCTTGAAGTCTTCTTCTGATCTTAC 554
 Qy 289 AGATTAATCTCTCTGATGATGTCGCAATTAACCTTGAAGTCTTCTTCTGATCTTAC 348
 Db 555 GTGACTTCAAGTCTCTGATGATGTCGCAATTAACCTTGAAGTCTTCTTCTGATCTTAC 614
 Qy 349 AGATGAGTTTGTCAAGACACCGCAAGAGGGGTCTACTGCTCAATCTTTTCTGCTG 408
 Db 615 AATTGAGTCTTTTGTCAAGACACCGCAAGAGGGGTCTACTGCTCAATCTTTTCTGCTG 674
 Qy 409 TGTGTTGCTCTGATGATGTTTACGATGTTCTTCTTCTTCTTCTTCTTCTTCTTCT 468
 Db 675 TTAATGTTCCATGATGATGATGTTTCTGATGATGATGATGATGATGATGATGAT 724
 Qy 469 GCTCTGTTTCTTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
 Db 735 GTTCAGCATGCTCTTAAAGGATGATGATGATGATGATGATGATGATGATGATGAT 794
 Qy 529 GTCACTCAAGATTAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 588
 Db 795 GCCACTATGTTGTTAAGCAACCAATGTTTCAACAGGTTGACAGATCTCTTGGGA 854
 Qy 589 ATGTGATGCTGTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 648
 Db 855 ACTGCTTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 914
 Qy 649 CCGTATATGCGCAATCTGATCTGATATTAAGCACTTCTTCTTAAATGATGATGAT 708
 Db 915 CGTCAACAGCTTGAACATGACCTGATCTGACAGACATGCGGCTTGTGAGTTTGGT 974

QY 709 CAAATTTTCAATCCCTTACATCATATCAACAAGTCAAAATGACCTATGATCGG 768
 DB 975 CGCGGTTTCAATTCATTAACCTCTCATTTCTATGAGGAGAGATTGATTTCA 1034
 QY 769 CTGCGAGTTTGTGTTAGCTTTGACACTGACATTTTATCTGATGTTAAGCTTA 828
 DB 1035 TTGCTAGTTCTTGATCTGTACACGACTTTACTTTTACCGGTAATGTGTGCA 1094
 QY 829 GGCTCATCTTTTATTTCTTTTAAAGTGTGTTTCCAAACAAAGGATTAACA 888
 DB 1095 GGGTCACTTGTATCTGACAGACAATCTGTATGTTTTCAGCGCAAAA--GTGCAAG 1151
 QY 889 AGAGAGTCAAGAAATTTTAGGCTATGACCTTTCTGATGTTATCTGATCTCTT 948
 DB 1152 ATGAGCTTGAACATTAATGAGGATCTGTGTTTGGACTTGTCTCTTTTATGT 1211
 QY 949 CTGCGCTACCAATTTGGCTGAAAGGATCATATTTTCAAGTCTGTTAGAGTGG 1008
 DB 1212 CTGCTGCAATTTGGCTGAGAGGATTAATGTTGCTGTGCTGCTGCTGTTGTT 1271
 QY 1009 GGTTCACATTTGGCTGAGTCTGATTAATCTTTGCTTATGTTTACATGTTG 1068
 DB 1272 CCATTCAGACATTTCAATCTGTTTGAATCACTTTGCTGCAAAATGATATGTCGGCC 1331
 QY 1069 CTAGCGTATGATTTGTTTCAACGAGACAAAGGCAAGCTCAATTAACAGTTCTG 1128
 DB 1332 CGAGTGGAAATGCTGTTTGAAGAGACAAAGTGTATGATGATCTCTGTTGCT 1391
 QY 1129 CTGCTGAGTGTGTTTCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1188
 DB 1392 CTTCGATGATTTGTTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1451
 QY 1189 GGAATGCTTAAATGCTTCAATGAGAAATCTCACCAATGTTGAACAACTTTGCGCAAG 1248
 DB 1452 GGTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1511
 QY 1249 ATAAATTTGCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1308
 DB 1512 ATAAATTTGCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1571
 QY 1309 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1368
 DB 1572 TCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1631
 QY 1369 GGAAGCAATGAACACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
 DB 1632 GGAAGCTGTTATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1691
 QY 1429 AAGCTTCCAGTCCCATGTTCTTTT 1457
 DB 1692 AAGCTTCTTTTCTTTTCTTTTCTTT 1720

RESULT 8
 ID AA244851 standard; DNA; 1606 BP.
 AC AA244851;
 XX
 XX 27-APR-2000 (first entry)
 DE Sphingolipid desaturase DNA.
 XX
 XX Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material; ds.
 XX unidentified.
 OS
 XX
 FH Key Location/Qualifiers

FT CDS 88..1464
 FT /tag= a
 FT /product= "sphingolipid desaturase"
 XX
 XX DE19828850-A1.
 XX
 XX 30-DEC-1999.
 XX
 XX 27-JUN-1998; 98DE-1028850.
 XX
 XX 27-JUN-1998; 98DE-1028850.
 XX
 XX (GVSE-) GVS ERWERB & VERW LANDWIRTSCHAFTLICH.
 PA Heinz E. Zaehneringer U. Schmidt H. Sperling P;
 PI
 XX WPI; 2000-127549/12.
 DR P-PSDB; AAV51348.
 XX
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 PS Disclosure; Fig 15; 62pp; German.
 XX
 XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence encodes a sphingolipid desaturase protein
 CC described in the method of the invention.
 CC
 XX Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 other;
 SQ

Query Match 31.3%; Score 460.8; DB 21; Length 1606;
 Best Local Similarity 59.2%; Pred. No. 26-128;
 Matches 805; Conservative 0; Mismatches 552; Indels 3; Gaps 1;

QY 42 ACTCAATGGAAGGCAAGGCAATTTGCAAGGACCTTGCATAGCA 101
 DB 115 AATTCATTTGCTGATGGAAGAAATATCATTAACAAAGATTAAAGACATTAACA 174
 QY 102 CCAGAGATTATGATCTCTATCAAGGAAAGTTTACATATCTCAAGTGAATAA 161
 DB 175 CCTAATGACCTTTGATCTCATATTTGGCAAGTTTAAAGATTACAAAGTGGCTTAA 234
 QY 162 GAGCATCCGGTGTGAGCTCCCATTTTAAAGTTTTCGCGCAAGATCTACTGATGG 221
 DB 235 GAGCATCCGGTGTGAGCTCCCATTTTAAAGTTTTCGCGCAAGATCTACTGATGG 294
 QY 222 TTCAATGCTTACATCTGCGGCTGCTGCAATCTTGAAGATCTTCTTCTGCTGAT 281
 DB 295 TTATGCAATTTCAATCTGCGGCTGCTGCAATCTTGAAGATCTTCTTCTGCTGAT 354
 QY 282 TAGCTCAAGATTACTCTGCTGATGATGCAAGGATCAAGAGGCTGCTCTGAG 341
 DB 355 CACTTAAAGATTATCAAGATTCTGCAATTTTGAAGATCAAGAGGCTGCTCTGAG 414
 QY 342 TTTTCTAAGATGGTGTGTTCAAGACCAAGCAAGGCTCTACTGCTCAATCTTTTC 401
 DB 415 TTTGCAAAAGCGGATATGTTTGAAGAAAGGCTCAAGGATTAATTAATCACTTTGTT 474
 QY 402 GTGTCTGTGTTGCTGCTGATGTTTAAAGGTTCTTACTGCAAGGACCTGGGCT 461

Db	475	GTGTGCTACTGCTTTCCGCTTGTGTGTATGTGGCGTTATATTCGGGAAGCTTTCAGAT	534
Qy	462	CATCTTTGCTCTGTTTGTCTAATGGGTAATGCTATGGCTCCAGAGTGTGGGTGGCGAT	521
Db	535	CATATGCTTTGGGGGCGATATTTGGGAATTAGCATGGAATGCATAATGCCATATTTGGGTCAT	594
Qy	522	GATCTTTGCTACTACCAAGTATATGGCTTAACCGGTAAAGCTTAATCGCTTTTTCAAATCAAT	581
Db	595	GACCGGGGTCAATTACCAATATATGGCGACCCCGGGGTGGMAACAAGTTTCCGGAAATATT	654
Qy	582	GCAGGAATGTGATTTGCTGTGTATGTGTGATAGTGTGAAAGTTGGAACCAATTAACCAT	641
Db	655	ATCGGGAATTTGTATAACCGGAATAAGCATTCGGTGTGGAAATGAGCAGCATTAACCCAGAT	714
Qy	642	CACTTTGCCTGTAAATAGCGCAATGTGATTCCTGATTTACGACCTTCTTAATATATGCC	701
Db	715	CACATCGCTTTGTAACAGTCTTGATTTATATCTGTATCTTCAGCATTTAACCGATTTGTAGCC	774
Qy	702	ATATTCGCCAAATTTTTCACCTCCCTTAATCATATATATCAACATGCAAAATAGCTAT	761
Db	775	GTTCCTTCCAGCTTTTAACTCAATACTTCTGTTTTCATAGGAGACAGTGTACCTTT	834
Qy	762	GATGCGCTGCCAGGTTTTTTGTATAGCTTTCAAGCACTGGACATTTTATCTGCATTTGTA	821
Db	835	GACCCGTTAGCCCGGTTCTGTGTGATCAACAGCAATTCATTAATATACCCGATCATGTGT	894
Qy	822	AGCGTTAGGCTCTATCTTTTATTTATTTGCTTTTAAGTGTGTGTTTCCAAACAACAAAG	881
Db	895	GTGGCCGGGTCAACCTCTATTTACAAACATCTGTGTGTGATTTCAAAACAGAAAG--	952
Qy	882	GTATTAACAAGAAAGTCAGAAAATTTTAGGCTATGCAAGCTTTCTTGACTTGTATTTCTTA	941
Db	953	-TTCCGACACAGGTTTAAACATATCTCGGAACCCCTAATCTCTGACGCTGTTCCTGTTA	1011
Qy	942	CTCCCTTTGCGCTAACCCAAATTTGGCGTAAAGGGCTAGTATTTCAACGCGCTTTAGCA	1004
Db	1012	CTTGTCTTCGCTTACCGAATCTGGCCCAACGCGTGGCTTTGTGTGTATGCTTCTGT	1077
Qy	1002	GTGCGCGGGTTCCAACATTTGGCAGTTTCAGCTTGAATCACTTGTCTTAATGTTTAACT	1063
Db	1072	GTAAACGGGTATACAACATATTCAGTTTACACTGAACCAATTTTCTGGGAATGTTTACGNG	1133
Qy	1062	GCTTTCCTACCGTAATGATTTGCTTTTCAACAGACGAACAAAGGCAACGCTCAACATTAAC	1122
Db	1132	GGCCCGCCAAAGAGACAAATTTGTTCAGAAACAAACGCGTGGAGCAATGATATCCGG	1197
Qy	1122	GCTTTCGCTTGGTGAGATTGTTTCATGAGTGCCCTGCACCTTTCAAATTTAGCATCATCTG	1181
Db	1192	TGTTCTTCTTGGATGGAATTGGTTTTTGGGAAGTTTACAGTTTCAACTTGAAGCACATTTG	1255
Qy	1182	TTTCCAGAGATGCTTAAGTGCATTTCAAGAAATCTCAACCATTTGTGAACAACATTTGC	1244
Db	1252	TTTCTTAGGTTTGCACCGGTGTCACTGTAGTGCAATTTCTCCATATGTAGAAACCTCTCG	1311
Qy	1242	CAGAAGCAATATTTGCTCTATGAACCTGTAACATGTGGAGAGCCAAATPAATGCTATAC	1303
Db	1312	AAGAAATATTAACCTTAATGTAGTGTGTGCTTTATGATGCAATGTAAACACCTTG	1377
Qy	1302	TCCAACCTGCGTGTGTGCTATGGAAGCTAAGATGTTTACCAAGCCAGTTTCCAAAGAC	1367
Db	1372	AAGACGCTTAAAGACAGCGGCTCTACAGGCAAGTACCTTAAGAACCCGCGCCACAGAAAT	1433
Qy	1362	ATGCTGTGGGAAGCAATGACACTTTCCGGTGAACCTTAT	1401
Db	1432	TTAGCTTGGGAAGCTTTCAACCCCATGATGTGAACCTTCT	1471

RESULT 9	
AAZ44832	
ID	AAZ44832 standard; DNA; 1594 BP
XX	
AC	AAZ44832;

DT	27-APR-2000	(first entry)	
XX			
XX			
DE	B. napus sld1 DNA.		
XX			
XX			
KW	Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;		
KW	transgenic plant; crop plant; delta-8-unsaturated long-chain base;		
KW	tolerance; resistance; soil salinity; ion stress; toxicity; drought;		
KW	cold; frost; phytophogenic microorganism; flowering time; cosmetic;		
KW	pharmaceutical; food; chemical raw material; ds.		
XX			
OS	Brassica napus.		
XX			
FX			
FT	Key	location/Qualifiers	
FT	CDS	51..1400	
FT		/*tag=	
FT		a	
FT		/product= "sld1"	
XX			
PN	DEL9828850-AL.		
XX			
PD	30-DEC-1999.		
XX			
XX			
PF	27-JUN-1998;	98DE-1028850.	
XX			
PR	27-JUN-1998;	98DE-1028850.	
XX			
PA	(GVSE-) GVS GBS ERWERB & VERW LANDWIRTSCHAFTLICH.		
PI	Heinz B, Zaehring U, Schmidt H, Sperling P,		
PI	WPI, 2000-127549/12.		
DR	P-PSDB; AAY51333.		
XX			
PT	New sphingolipid desaturase that selectively introduces double bond		
XX	into sphingolipids and capnoids -		
PS	Claim 11, Fig 1; 62pp; German.		
XX			
CC	This invention describes a novel sphingolipid desaturase that selectively		
CC	introduces a double bond into the sphingobase of the ceramide residue of		
CC	sphingolipids and capnoids. A DNA sequence encoding the sphingolipid		
CC	desaturase, or a vector containing the DNA sequence, can be used to		
CC	produce transgenic plants, especially crop plants, with an increased or		
CC	decreased delta-8-unsaturated long-chain base content or an altered		
CC	delta-8-unsaturated long-chain base cis/trans ratio, especially to		
CC	compensate for a delta-8-unsaturated long-chain base deficiency, to		
CC	exclude production of delta-8-unsaturated bases, to increase tolerance		
CC	or resistance to soil salinity, ion stress or toxicity, drought, wet		
CC	conditions, cold or frost and/or phytophogenic microorganisms, or to		
CC	alter size growth and flowering time. Cells, transgenic organisms or		
CC	plants containing the DNA sequence can be used to produce sphingolipids		
CC	and capnoids with unsaturated sphingobases. The sphingolipids or capnoids		
CC	can be used in cosmetics, pharmaceuticals and foods and as chemical raw		
CC	materials. This sequence encodes the Brassica napus sphingolipid		
CC	desaturase sld1 protein described in the method of the invention.		
XX			
SO	Sequence 1594 BP; 382 A; 369 C; 375 G; 468 T; 0 other;		
XX			
Query Match	31.2%;	Score 459.4;	DB 21; Length 1594;
Best Local Similarity	59.6%;	Pred. 0.54e-128;	
Matches 794;	Conservative 0;	Mismatches 536;	Indels 3; Gaps
XX			
QY	60 AAGAGCACATTTGGCAGACGACCTTGCAAGCATTAAGCAACGAGAGATTATGATC	119	
DB	69 AAGAGATTCAATTACAGGAGATGATCTGAAAAAACCAACCAACCGGAGATTATGATC	128	
QY	120 TCTATCAAGGAAAGTTTACGATATCTTCAAGTGGACTAAAGAGCATCCGGGTGTAG	179	
DB	129 TCAATCCAGGCAAGTCTACGAGCTCCACATGGGTGCAATCCATCCCGAGGCGAA	188	
QY	180 CTCACATGTTAAGTTTGGCGGCGCAAGATGTCATGATGGTTCATGTTACCATGCT	239	
DB	189 GCAGGATCTTAAACCTCGCCGGTCAAGACGTCAACGAGCGGTTCATGCTTACCATCC	248	

QY 240 GGCACTGCTGGCAATACCTTGACAGGTTCTTACTGGGACTAGCTGCAAGATTACTCT 299
DB 249 GGAACCGCATGSGCCCACTCGAAGACCTTCCACAAGGCTACCACTGGAAGACCCAC 308
QY 300 GTCTCTGAGATGTCAGAGCTACAGAGGCTGCTGTGAGTTTCTTGAAGTGGGTTTG 359
DB 309 GTGTCCGAGGTGTGGGTGACTACCGTGTGTTAGCCGGGAGTTTCCAAAGCGGACTC 368
QY 360 TTCAAGACACAGGCAAGGGGCTCTACTGCTCATCTTTTGGTGTCTGTGTTGGCT 419
DB 369 TTTCGATMAAAGGTACGCTCTTTTACCGCTCAACGCTCCCTGCTGCAATGCTGCG 428
QY 420 CTGAGTGTATAGGTTTCTCTACTGCAAGAGACCGGGCTGATCTTTGCTGTGTTG 479
DB 429 GCGGTGTATACGGTGTGTTGCTGATGACAGCATATGGCCCACTTAATATCCGCGTC 488
QY 480 CTAAATGGATATGCTATGCTCCAGAGTGTGGTGGGCGGAGTATCTTGTCACTACCA 539
DB 489 TTGCTGGGCTTCTCTGATACAGAGCGCTTACGTGGACATAGACTGTGCTATTACAC 548
QY 540 GTTATGCTTACCGTAACTTAATCGTCTTTTCAATCATTCAGAGAAATGATGCT 599
DB 549 GTGACGCTCAACGAGCGGTGTATTAATCTGCTGCTGTCTGTGTAATGCTATCACC 608
QY 600 GGTGTAGTGTGCTAGTGGAGTGGAGTGGACATTAACCCATCTTGTGCTGTAATAGC 659
DB 609 GGGATATCCAGTCCGTGGTGGAAATGAGCGCATTAAGCATTAATCTTGTATTAAGT 668
QY 660 GCCAATCTGGATCTGATATATTCAGCACTTCTATTAATGSCATATCCCAAAATTTTC 719
DB 669 CTGACCAAGATCTCTGATCTCCAGCAATCCCTGTGTAGCGGTCTTCCAAAGTTCTTT 728
QY 720 AACTCCCTTACATCACTAATCACTCAACTGCAAAATGACTATGATGCGCTGCCAGTT 779
DB 729 AAGTCATGACGCTCAGCTTCTATGGAGGAAAGTTGACGTTCCATCAGTACATTC 788
QY 780 TTGTGTAGCTTGAAGCTGAGATTTTATCCGCAATGTTAGCGTTAGGCTCTATCTT 839
DB 789 TTGATAGCTTACCAACACTGTGTGTTTATCCATCATGTTGTGGGAATCAATCTC 848
QY 840 TTATATCTGCTTTTAAAGTGTGTGTTTCCAAACAAAGGTTATCAAGAGAAATCAG 899
DB 849 TTTATCCAAAGCTTACTTTTGTCTATCTCGAAGCTTAC---GTCTGATGAGCTTG 905
QY 900 GAAATTTAGGCTATGCACTTTCTTGAATCTGCTTACTCTCTTCTGCTTACC 959
DB 906 AATATAGCTGGGATCTTGTGTTTCTGGAAGTGTCTCTTGTATGATCTTCTTACCA 965
QY 960 AATTTGCTGAAAGGCTATGATATTCAGCTCTGTTTACAGTCCGCGGTTCCAACT 1019
DB 966 AATGCGCAAGAGGATCATCTTGTCTTTTAAAGCATGGCCGCTCACGGGATTCAGCAC 1025
QY 1020 TGCACTTGAAGTGTGATCACTTGTCTTAAATGTTTAACTGCTTACGCGGTAAAT 1079
DB 1026 GTTCAAGTCTGTTTAAACATTTTGGCGGAGATGTTTACCGGTCCGCTTAATGGAAC 1085
QY 1080 GATTTGCTTACAGAGACAGAAAGGCGAGCTCAACATTAACAGCTTCTGCTGTGGAT 1139
DB 1086 GATTTGCTTGAAGAGCAACAGCGGTGAGCTTGAATATCGTGTAGTGTATGAT 1145
QY 1140 TGGTTTCAATGTGCTGCTGCTGCTTCAATGATGATCTGTTTCCAGAGATGCTTAA 1199
DB 1146 TGGTTTCTTGGCGGTGCTGCTGCTTCAAGATCATCTGTTCCCTAGGCTACCGCT 1205
QY 1200 TGCACTTGAAGAAATCTACCATTTGTGAACAACTTTGCGCAAGAGATTAATTTGTC 1259
DB 1206 TGCACTTGAAGGAGATTTGCTGTGTGCTTCAAGAGCTTTGTAAGAGCATTAATCTAC 1265
QY 1260 TATGAAATGCTCAATGTTGGAAGGCAATAAATGATATCTCAACCTGCTGCTGTG 1319
DB 1266 TATAGAGTCTTCTGTGTGGGAGGCTAATGTGTGAGCGCTCAGAGACTTGAAGAAAGCG 1325

QY 1320 GCTATGAGCTAAGATGTTTACCAAGCCGTTCCCAAGACATGCTTGGAGCAATG 1379
DB 1326 GCGGTTCAGAGCTAGAGATGTGACTATCTGTGTTGAGAAATTTGCTATGGAGCTTG 1385
QY 1380 AACCTTTGCGGT 1392
DB 1386 AATACTCATGCT 1398
RESULT 10
AAC42244
ID AAC42244 standard; DNA; 1465 BP.
XX
AC AAC42244;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
XX
XX Hybridization assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; 88.
XX Arabidopsis thaliana.
XX
PN BP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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Query Match

30.5%; Score 448.6; DB 21; Length 1465;

Best Local Similarity 59.0%; Pred. No. 9,5e-125; Matches 768; Conservative 0; Mismatches 544; Indels 3; Gaps 1;

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QY 120 TCTATCAAGGGAAGATTACGATATCTCCAAAGTGAAGATCCCGGTGTAG 179
 DB 194 TCGATTCAAGGTAAGTTACGACGTTCCGATTGGGTTAAATCTATCCCGAAGCGAA 253
 QY 180 CTCCCATTTGTAAGTTTGGCGGCAAGATGTCATGATGCGTTCACTTGCTTACATCC 239
 DB 254 GCAGCATTTCTCAATCTCCGCGGCAAGATGTCACGACGCGTTCACTTCCATCC 313
 QY 240 GGCACGTTGGCAATACCTGACAGTCTTACTGGGACTACGTTCAAGTTACTCT 299
 DB 314 GGAACCGCATGGACCACTTGAAGGCTTACAAATGGCTATCAGTAGAGACCAAC 373
 QY 300 GTCTCTGAGATGTCAGAGACTACAGAAAGCTGCTCTGAGTTTCTAAGATGAGTTG 359
 DB 374 GTGTGACAGTCTCAGGTACTACCGTCTTGACCGCGAGTTCTCCAAAGCGGCTTC 433
 QY 360 TTCAAGACACCAAGCAAGGAGTCTACTGCTCAATCTTTTCTGTCGTGTTGCT 419
 DB 434 TTGCACAAAAAGGTACGTCGCTTTACACTACGTCGCGTCCGCGTCACTGCGG 493
 QY 420 CTGAGTGTACGCTGTTCTCTACTGCAAGAGACTGGGCTCATCTTGTGTTG 479
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 QY 480 CTAAATGGATATGCTATGCTCCAGAGTGGTGGGAGATTTCTTGCTACTACCA 539
 DB 554 TTAATCGGCTCTCTCTGATCCAAAGCGCTTACGTCGCGCAAGTTCCGCTCACTACG 613
 QY 540 GTTATGCTTAACCGTAAGCTTAACTGCTTTTCAATCAATGTCAGAGAAATGATGCT 599
 DB 614 GTGACGCTCAACCAACCGGTGTAACAACTAATCACTTCTCCGCTAAGTGTCTCAC 673
 QY 600 GGTGTTAGTGTGATGCTGAGAGTGGAGTGAACATCAACCATCTTGTGCTGTAATAG 659
 DB 674 GGCATCTCAATCGCGGTGGAGAAATGAGCAACAGCTCAACCATCTGTTGTAACAG 733
 QY 660 GCCAATCTGGATCTGATATTCAGACCTTCTATATGCGCATCCCAAAATTTTTC 719
 DB 734 CTGACACAGATCCGATCTACAAACATCCGATCTTGCCGCTCTCTCAAAATTTCTTC 793
 QY 720 AACTCCCTTAACATCACTATCAACATGCAAAATGACCTATGATGCGCTGACAGTT 779
 DB 794 AATTCGATGACGTCAGTTTCTATGACAGAAATTAACATGATGATCTCTAGTGCATTC 853
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Query Match 29.5%; Score 433.4; DB 21; Length 1650;
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QY 120 TCTATCAAGGAAATTTAAGATATCTCTCAAGTGAATTAAGATATCCGGTGTAG 179
DB 283 GCGATTCAAGGAGGCTTACAAAGCTCTCGATTGATTAATACTATCCCGAGCGAGC 342
QY 180 CTCCCATTTGATTTGCGGCGCAAGATGCTAGTATGCTTCAATGCTTACATCTCT 239
DB 343 ACGGTATCTCATCTCTGTTGCTCAAGATCAAGATCTTCAATGCTTCAATCTCT 402
QY 240 GGCATGCTTGGCAATACCTTGAAGGCTTCTTACTGAGTCTTCAAGATGCTTCT 299
DB 403 GGAACCGCTTGGACATCTCGACATCTTCAACCGGTTACCAATCAAGATTTCCAA 462
QY 300 GTCTCTGAATGTCAGAGATCTCAAGAGCTGCTCTGAGTCTTCAAGATGCTTCT 359
DB 463 GTCTCGAAGTCTCAAGCATTAACGCTGATGCTGCGAGTTTGTAAATCTCGCTCT 522
QY 360 TTCAAGACACAGGCAAGGGGCTCTAGTCTCAATCTTTTGTGCTGCTGCTGCT 419
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DB 763 GGAATCTCAATGCGGTGAGAAATGAGATCAACATGCTCATATGCTGCTGCTGCT 822
QY 660 GCCAATCTGATCTGATATTCAGACCTTCTTATATGCTATGCTATGCTATGCT 719
DB 823 CTGATTAAGATCAAGATCTACAAACATCTGCTGCTGCTGCTGCTGCTGCTGCT 882
QY 720 AACTCCCTTAACATCACTATCAACATCAACATCAACATCAACATCAACATCAACAT 779
DB 883 TCTCTATTAACCTGATCTTACGATCGAAATCAACATGCTGCTGCTGCTGCTGCT 942
QY 780 TTTGTTAGCTTCAAGATGATTTTATCTGATGCTTGAAGCTTGAAGCTTGAAGCT 839
DB 943 TTAGTAGATCAACATTTACTTATTAACATGCTTGAAGATCAATCTCTC 1002
QY 840 TTTATTTCTGCTTTTAAGGCTGCTTCAACAAAGGCTATTAAGAGAGATCAG 899
DB 1003 TTCAATCAACAGTTTCTTGTGCTTCTCAACAGTGA---GTACCAATGCTGCTT 1059
QY 900 GAAATTTTGGGATGCTGCTTCTGATGCTGCTTCTCTACTCTTCTGCTGCTGCT 959
DB 1060 AACTTTCGCGGAATCTTATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
QY 960 AATTGCTGTAAGGCTCATGATTTTCAAGTCTGCTTGAAGCTGCTGCTGCTGCT 1019
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QY 1140 TGGTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199
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QY 1380 AACCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1407
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RESULT 12
AAC51462
ID AAC51462 standard; DNA; 1650 BP.
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XX AAC51462;
AC
XX
XX 18-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 68612.
DE
XX
XX Hybridization assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 29.5%; Score 433.4; DB 21; Length 1650;
 Best Local Similarity 58.1%; Pred. No. 4e-120;
 Matches 783; Conservative 0; Mismatches 562; Indels 3; Gaps 1;

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 DB 225 AAAAGATACATTCGAACAGAGATCTTAAAAACAAACAAATCTGAGATCTATGATC 284
 QY 120 TCTATCAGGAAAGATTACGATATCTCCAGTGTGACTAAAGAGATCCCGTGTGAG 179
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 DB 285 GCGATTCAAGGAGGCTACAAAGCTCGATTTGATTAACATCATCCCGAGGCGAG 344
 QY 180 CTCCATTTGTAAGTTTGGCCGCAAGATGTCACTGATGCGTTCAATTGCTTACCTCT 239
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 DB 345 ACGGTATCTCAATCTGTTGCTCAAGAGCTCAGCAGATGCTTTCATTCGATTTCAATCCC 404
 QY 240 GGCATCTTTGGCAATACCTTGAAGGCTTCTTACTGGGGTACTAGCTTGAAGTTACTCT 299
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 DB 405 GGAACCGCTTTGGACCAATCTCGACATCTCTTACCGGTTACCAACAGAGATTTCCAA 464
 QY 300 GTCTCTGAGATGTCAAGAGACTACAGAGGCTGCTCTGAGTTTCTAAGATGGGTTTG 359
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 DB 465 GTCTCGAAGTCTCAGCGGATTTACGATGCGTATGGCGGAGTTTGTAAATCGGCTTC 524
 QY 360 TTCAAGACACAGGCAAGGGGCTTACTGCTCAATCTTTTGGTGTGTGTTGCT 419
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 DB 525 TTGCAAAACAAAGGTACGTTACTCTCTACATCTTACCTTCCTCCCGCAATGTTCTTC 584
 QY 420 CTGAGTGTTAGGGTCTCTCTACTGCAAGAGACCTGGGCTATCTTGGTGTGTTG 479
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 DB 585 GGAATCTCTACGGTGTGTGGCTTGTACTCCGTCTGCTCAAAATGCGCGCGG 644
 QY 480 CTAAATGGTATGCTATGCTCCAGAGTGTGGTGGGAGGATTTCTGTCACTACCA 539
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 DB 645 CTCTCGGTCTCTCTCGAATCCAGAGGCTTACATAGTCAAGATCTGTCTATTACGTT 704
 QY 540 GTTATGCTTACCGTATGCTTAAATGCTTTTCAATATGTCAGAGAAATGATGTGCT 599
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 DB 705 ATCATGTCAACAAATCTTATTAACAGATTCGCTCAGCTTCTCCGGTAACTGTCTACC 764
 QY 600 GGTTGATGTTGATGCTGATGAGAGTGTGAGCAATACCAACCATTAATGCTGTATAGC 659
 |||||
 DB 765 GGAATCTCAATCGCGTGGTGAATGAGCTCAAAATGCTCATATCTAGTGTGTAAACAG 824
 QY 660 GCCAATCTGATCTGATATTTAGCACTTCTATATATGCAATCCCAAAATTTTTC 719
 |||||
 DB 825 CTGATTTAGATCAATCTTACAAACATCTCTGTCTTGGCGCTCTCCACCAATTTCTTC 884
 QY 720 AACTCCCTTACATCACTATACAACTGCAAAATGACCTATGATCGCGTCCAGGTTT 779
 |||||
 DB 885 TCCTCATTTGACCTCGAGATCTTACGATCGGAAATCACTCAGTTTATCCAGTCGAGATTC 944
 QY 780 TTGTGATGCTTTAGACCTGAGATTTTATCTGCAATGTTAAGCGTTAGGCTTATCTT 839
 |||||
 DB 945 TTAGTAGCTATCAACATTTACTTATATCCAGTTATGCTTGTGAAGAAATCAATCTTC 1004
 QY 840 TTATATCTGCTTTTAAAGTGTGTTTCCAAACAAGAGGATATACAGAGATGAG 899
 |||||
 DB 1005 TTATATCAACGTTTCTCTGCTCTTCTTCCAAACGTGA---GTACCAAGATCGTCTTAA 1061
 QY 900 GAAATTTAGGCTATGAGCTTTCTTGAATGTTGATTTCTTACTCTTTCTGCGCTACCC 959
 |||||
 DB 1062 AACTGCGCGGATCTTAGTCTTCTGGAATGTTGCCCACTTTAGTCTTATGATCTTACCA 1121

QY 960 AATTGGCTTGAAGGGTCAATGATTTTCAAGCTCTGTTTGAAGATGCGCGGTTCCAAAT 1019
 |||||
 DB 1122 AACTGGCTTGAAGGGTCAATGATTTTCAAGCTCTGTTTGAAGATGCGCGGTTCCAAAT 1181
 QY 1020 TGGCAGTTGAGTTGATTTTCAAGCTCTGTTTGAAGATGCGCGGTTCCAAAT 1079
 |||||
 DB 1182 ATTCAATTCACCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1241
 QY 1080 GATTGGTTTCAAGGGTCAATGATTTTCAAGCTCTGTTTGAAGATGCGCGGTTCCAAAT 1139
 |||||
 DB 1242 GATTGGTTTCAAGGGTCAATGATTTTCAAGCTCTGTTTGAAGATGCGCGGTTCCAAAT 1301
 QY 1140 TGGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
 |||||
 DB 1302 TGGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1361
 QY 1200 TGGCAGTTGAGTTGATTTTCAAGCTCTGTTTGAAGATGCGCGGTTCCAAAT 1259
 |||||
 DB 1362 TGGCAGTTGAGTTGATTTTCAAGCTCTGTTTGAAGATGCGCGGTTCCAAAT 1421
 QY 1260 TATGAAATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1319
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 DB 1422 TATGAAATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1481
 QY 1320 GCTATGAAATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1379
 |||||
 DB 1482 GCTATGAAATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1541
 QY 1380 AACACTTTGCGGTGAACCTTAATMAACA 1407
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 DB 1542 AATACTCATGCTTAATGATTTTAAATCA 1569

RESULT 13
 AA244833
 ID AA244833 standard; DNA; 1678 BP.
 XX
 AC AA244833;
 DT 27-APR-2000 (first entry)
 XX
 DE A. thaliana sld1 DNA.
 XX
 KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 172..1521
 FT /tag= a
 FT /product= "sphingolipid desaturase"
 PN DE19628850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GBS ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E, Zaehneringer U, Schmidt H, Sperling P;
 XX WPI; 2000-127549/12.
 DR P-PSDB; AAY51334.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 into sphingolipids and capnoids -

XX	.
PS	Claim 11; Fig 3; 62pp; German
VV	

This invention describes a novel sphingolipid deaturase that selectively introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid deaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence encodes the Arabidopsis thaliana sphingolipid deaturase sld1 protein described in the method of the invention.

SQ Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 other;

Query Match	29.5%	Score	433.4	DB	21	Length	1678
Best Local Similarity	58.1%	Pred	No. 4e-120				
Matches	783	Conservative	0	Mismatches	562	Indels	3
						Gaps	1

QY	60	AAGAAGCAATTTCCCAAGCAGCAACCTTGGAAAAGCAATAAACAACCAAGAGATTATGATC	119
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QY	120	TCATCAAGGAAAAGTTTACGATATCTCCAAATGGACTAAAGAGATCCCGGTGGTAC	179
Db	250	GCGATTCAAGGCAAGGTCATCAACGTCCTCCGATTGGATTAAAACTCATCCGGAGCGAC	309
QY	180	CTCCATTTGTAAGTTTGGCCGCAAGATGTACATGAATGCCGTATTTGTTACATCTT	239
Db	310	ACGGTATTTCTCAATCTCGTTGGTCAAGACGTCAACGAATGCTTTCATGCGATTTCATCCC	369
QY	240	GGCATCGCTTGGCAATTAACCTTTGACAGAGTCTTTTACTGGGTACTACGTTCAAGATTACTCT	299
Db	370	GGAAACGGTTTGGCAACATCTGCAACATCTCTTCAACCGGTTACCAKATCAGAGATTTCCAA	429
QY	300	GTCCTCGAGATGTCCAGAGACTACAGAAAGCTGTCCTGAGTTTTCATAAGATGGGTTTG	359
Db	430	GTCTCCGAAGTCTCAGCGGATTACCGTCTGATGGCTCCGAGTTTGTATACTCCGATCTC	489
QY	360	TTCAAGAACAAGGCAAGGGGCTACTGCTCATTTTTCGTGTCTGTGTTTGCT	419
Db	490	TTCGAAAACAAGGTCACGTTACTCTTACACTTACGCTTACGCTTGGTCGCCGCAAGTTCTTC	549
QY	420	CTGAGTGTTAACGAGTTCCTACTGCAAGACACCTTGGGCTCATTTTGGCTGTGGTTTG	479
Db	550	GGAGTTCCTACGAGTGTTTTGGCTGTACTCCGTCCTTGGCTACCAAAATGCCGCCGG	609
QY	480	CTAAATGGGTAATGCTATGGCTCCAGAGTGTGGGTGGGAGCATGATTTCTTGTCACTAACAA	539
Db	610	CTTCTCGGTCCTCTGTGATCCAGAGCGGTTACATAGTCAAGATCTGTGCTATTAAGTT	669
QY	540	GTTATGGCTAACCGTAACCTTATATGTCCTTTTCAAAATCATGTACAGAAATGTGATTTGCT	599
Db	670	ATCATGTGAAACAATCTTATTAACAGATTCGCTCAGCTTCTCTCCGTAACGTGTACACC	729
QY	600	GGTGTAGTATGTGCATGTGTGAAAGTTGACACATAACCCCATCATTTTCCCTGTATAGC	659
Db	730	GGAAATCTCAATCGCGTGTGGAAATGAGACTCAACATGCTCATATCTTACTGTTTAAACG	789
QY	660	GCCAAATCTGAATCTGTATATTACAGACCTTCTTATTAATTTGCCATATCCCAAAATTTTTC	719
Db	790	CTCATATTACGATCCGATCTACACACATCCCTGTCTTGGCGGTCTCCACAAATTTCTTC	849
QY	720	AATCCCTTAATCATATCTATTCACAACATGCAAAATGACCTATAGTGGCGCTGCAGGTTT	779

Db	850	TCCGATCATTGACCTCGAGATGTTACGATCCGAAATCAACGTTTGATTCGACGTCGGCAGATTC	909
Qy	780	TTTGTAGACTTTTCAGCACTGACATGTTTATCTCGATGTTTAAAGCTTAGGCTATCTT	839
Db	910	TTAGTCAGCTATGCAACCTTTACTTATATATCCAGTATGTGCTTTGGAAAGATCAATCTC	969
Qy	840	TTTATTCGTCGTTTAAAGTGTGTTTTCCAAACAACAAAGGGATATCAAGAGAAGTCAG	899
Db	970	TTCAATTCAAAAGTTTCTCTTGCTCTCTCTCCAAACGTGA--GTAACGATCGTCTTTA	1028
Qy	900	GAATATTTAGGCTATGACGCTTTCGTGACTTGTGATTTCTTACTCTCTTCTCGGCTACCC	959
Db	1027	AACTTCGGCGGAATCTTAGTCTTCTGAGACTTGTTCCACGCTTAGTCTGATCTACCA	1086
Qy	960	AATTGGCCTGAAGAGGTCATGATTTTCAAGTCCTGTTTAGAGTCGCGGGTTCACAT	1019
Db	1087	AACTGGCCTGAGAAATTTCTTCTGTCTTCAAGCTTCAACCGTCACGCGGCTTCAACAC	1146
Qy	1020	TGGAGATTGAGCTTGAATACCTTGTCTTAAAGTTTACACTGGTGTTCCTAGGGGTAA	1079
Db	1147	ATTCAATTCACGCTTAAACCATTTTCGCTGATGTCTACGTTGTCACCCACCGGTAGC	1206
Qy	1080	GATTGGTTTCCACGACAGACAAAGGACGCTCAACATTAACAGCTTCTGCTGTGGGAT	1139
Db	1207	GACTGGTTTCAAGAACGAAGGGGGGAAACAATGATATCTGTTAGATCATATCATGGAT	1266
Qy	1140	TGTTTTTCAATGCTGGCTGCACTTTCAATGAGCATCATCTGTTTCCAAGATGCTTAAG	1199
Db	1267	TGTTTTCTTTGGTGGATTACAGTTTCACTTGAGCATATTTGTTCCCTCGCTTACCTCGT	1326
Qy	1200	TGCGATTTTCAGGAAATCTCAACCATTTGTGAACAACATTTGCCAGAGCATTAATTGTCC	1259
Db	1327	TGCCATCTCCGGAAAGTTTCTCCGGTGTTCAGAGCTTTGCAAGAACATTAATCTTCG	1386
Qy	1260	TATGAAACTGCTACATGTGGGAGGCCAATAAATGATATCTCACCTGCGTGTGTG	1319
Db	1387	TATAGAGATATGTCGTGTGTTGAAGCAAAATGTGTGACATTAACATTTGGAACACAGCA	1446
Qy	1320	GCTATGGAAGCTAAGATGTTTACCAAGCCAGTTCCCAAGAACATGTCTGGAAGCAATG	1379
Db	1447	GCTTATCAAGCTAGACAGTGGCTTAATCCGGTGGTTAAGAACTTGTTGGGAAGCTTTG	1506
Qy	1380	AACACTTTGGGGTGAACCTTATTAATAA	1407
Db	1507	AATACTCATGGCTAAATGATTTTAATCA	1534
RESULT 14			
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XX	AC	AB212753;	
XX	AC		
XX	DT	21-JAN-2003 (first entry)	
XX	DB	Arabidopsis thaliana stress regulated gene SEQ ID NO 558.	
XX	KW	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	
XX	OS	Arabidopsis thaliana.	
XX	PN	WO200216655-A2.	
XX	PD	28-FEB-2002.	
XX	PF	24-AUG-2001; 2001MO-US26685.	
XX	PR	24-AUG-2000; 2000US-227866P.	
XX	PR	26-JAN-2001; 2001US-264647P.	
XX	PR	22-JUN-2001; 2001US-300111P.	
XX	PA	(SCRI) SCRIPPS RES INST.	
XX	PA	(SYGN) SYNGENTA PARTICIPATIONS AG.	

XX Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI, 2002-304127/34.
 DR Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 XX
 PS Claim 6; SEQ ID NO 558; 577bp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stresses. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 CC
 XX
 SQ Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 other;
 Query Match 29.2%; Score 429.4; DB 24; Length 1350;
 Best Local Similarity 58.1%; Pred. No. 5.8e-119;
 Matches 776; Conservative 0; Mismatches 556; Indels 3; Gaps 1;

QY 60 AAGAACATTTTCGACAGACCTTGCAGAAAGCATACAGACAGAGATTTATGATC 119
 DB 19 AAAAAATATTAAGCAAGCAAGATCTTAAACAAACAAATCTGGAAATCTATGATC 78
 QY 120 TCTATCAAGGAAAGATTACGATATCTCAAGTGAGTAAAGAGATCCGGTGTAG 179
 DB 79 GGGATTCAAGGAGGATCTACACGCTCGATGATTAATACTATCCGAGGCGAC 138
 QY 180 CTCACATTTGATTTTCCGCGCAAGATGTCATGATGCGTTACCTTACATCTC 239
 DB 139 ACGGTATTTCTCAATCTCGTTGGTCAAGCGTACCGATGCTTTATGCAATTTATCC 198
 QY 240 GGCATGCTTTGGCAATACCTTGACAGGTTCTTTACTGCGTACTACCTTAAGTTACT 299
 DB 199 GGAACCGCTTTGGCACCATCTCGACCATCTCTTCAACCGGTACCAATCAGAGTTTCCA 258
 QY 300 GTCTCGAGATGTCAGAGACTACAGAGGCTGCTGAGGTTTCTTAAGATGGGTTG 359
 DB 259 GTCTCGAGATCTACAGCGATTTACGCTGATGCTGCGAGTTTGTAACTCGGCTTC 318
 QY 360 TTCAAGACACAGGCAAGGAGGCTACTGCTCAATCTTTTGTGTTGCTGTTGCT 419
 DB 319 TTGCAAAACAAAGGTACGTTACTCTTACATCTTACGCTTGTGCTGCGCAATGTTCTTC 378
 QY 420 CTGAGTGTTTAGGTTTCTTACTGCAAGAGCACTGCGCTCATCTTTGCTGTGTTG 479
 DB 379 GGAATCTCTACGAGTGTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438
 QY 480 CTAAATGGATGATGATGCTGCGAGAGTGTGGGTGGGCAATGATCTTGTACTACCA 539
 DB 439 CTTCTCGGTTCTCTTGAATCAGAGCGCTTACATAGTCAATCTGCTACATTAAGTT 498
 QY 540 GTTATGCTTAACGTAAGCTTAATCGTCTTTTCAATCATTTGACAGAAATGATGCT 599
 DB 499 ATCATGTCGAACAATCTTATAACAGATTGCGTCACTTCTCTCGGTAACTGCTCAC 558
 QY 600 GGTGTGATGTTGATGATGTTGAAGTGAACATTAACCATCACTTGTGCTGTAATAC 659
 DB 559 GGAATTCATCGCGTGTGGAATGAGTCAACATGCTCATCATCTGTTGTAACAG 618
 QY 660 GCAATCTGATCTGATATTAAGCACTTCTTAAATTTGCAATCCCAAAATTTTTC 719

DB 619 CTCGATTACGATCCAGATCTAACACATCCCTGCTTCCGCGTCCACCAATTTCTTC 678
 QY 720 AACTCCCTTACATCATATATACACAACTGCAAAATGACTATGATCGGCTGCCAGTTT 779
 DB 679 TCCCTATTGACCTCCAGATTTACGATCGGAACCTCAAGTTTGAATCCAGTCCGAGATT 738
 QY 780 TTGTGATCTTACGACCTGACATTTATTCCTGATGATTAAGGTTAGGCTTATCTT 839
 DB 739 TTATGACATATCAACATCTTATTTATTTATTCAGTTATGCTTTGGAAGATCAATCTC 798
 QY 840 TTTATTTCTGCTTTTAAAGTGTGTTTTCACAAACAAAGGATTAACAGAAATGATCAG 899
 DB 799 TTCAATCAAGATTTCTGCTGCTTCCCAAGCTGAA---GTACAGATGCTGTTA 855
 QY 900 GAAATTTAGGCTATGACGCTTTCTTGAAGTTGATTTCTTACCTTTCTGCTTACC 959
 DB 856 AACTTCCGCGGATCTTGTGCTTGTGACCTTGTCCACTCTTGTCTCATGCTTACCA 915
 QY 960 AATTGCGCTGAAGGCTGATGATTTTCAAGTCTGTTAGAGAGTCCGCGGTTCAACAT 1019
 DB 916 AACTGCGCTGAAGATTTCTTCTGCTTTCACAACTTCAACGCTGACGCGCTTCAAC 975
 QY 1020 TGGCAGTTCAAGCTTGAATCACTTGTCTTATGTTTACACTGTTTCCAGCGTAAAT 1079
 DB 976 ATTCAATTCAGCTTAAACATTTGCTGCTGATATGCTAGTTCACACCGGATGAC 1035
 QY 1080 GATTGCTTCAACGACGACAAAGGCAAGCTCAACATTAACAGCTTGTGCTTGGAGAT 1139
 DB 1036 GACTGCTTGAAGAGCAAGCGCGGGAACATGATATCTCTTGTAGATCATACATGAT 1095
 QY 1140 TGGTTTCAAGTGGGCTGCTGCTTCAAGTATGATGATGATGATGATGATGATGATG 1199
 DB 1096 TGGTTTCTTGGGATTAACGATTTGCTGATGATGATGATGATGATGATGATGATG 1155
 QY 1200 TGGCATTTCAGGAAATCTCAACCTTGTGAACAACTTTCAGAGACATTAATTTGCTC 1259
 DB 1156 TGCCATCTCCGGAAGTTTCTCCGCTGTTCAAGGCTTTGCAAGATATATCTTCCG 1215
 QY 1260 TATGAACCTGCTACATGATGAGGCAATTAATGATATCAACCTGCTGCTG 1319
 DB 1216 TATAGAGATGATGCTGCTTGAAGCAATGATGATTAACATTTGAAGACAGA 1275
 QY 1320 GGTATGAGATTAAGATGTTACCAAGCACTTCCCAAGAAATGCTGGAACATG 1379
 DB 1276 GGTATCAAGCTAAGAGCTGCTAATCCGCTGTTAAGAACTTGTGGAACTTTG 1335
 QY 1380 AACACTTCCGGTGA 1394
 DB 1336 AATACCTATGGCTAA 1350

RESULT 15
 AAD01353
 ID AAD01353 standard; cDNA; 1972 BP.
 XX
 AC AAD01353;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Wheat sphingolipid desaturase cDNA #1.
 XX
 KW Wheat; sphingolipid desaturase; membrane-bound desaturase;
 KW transgenic plant; fatty acid; ss.
 XX
 OS Triticum aestivum.
 XX
 PH Key Location/Qualifiers
 FT CDS 124..153
 FT /*tag= a
 FT /product= "sphingolipid desaturase"
 XX
 PN MO20032790-A2.

XX		08-JUN-2000.	
PD			
XX	PF	99WO-US28589.	
XX	02-DEC-1999;		
XX	03-DEC-1998;	98US-0110784.	
PR			
XX	(DUFO) DU PONT DE NEMOURS & CO E I.		
XX			
PI	Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;		
XX	WPI; 2000-412336/35.		
DR	P-PSDB; AAY71555.		
PT	Polynucleotide encoding delta-6 desaturase enzyme useful for producing		
PT	transgenic plants and for producing antibodies specific to which is		
PT	useful for screening cDNA expression libraries -		
XX			
PS	Disclosure; Page 48-49; 57pp; English.		
XX			
CC	The present sequence is a cDNA encoding sphingolipid desaturase		
CC	from clone wrel .pk0004.c7.fis isolated from wheat etiolated		
CC	seedling root cDNA library, wrel.		
CC	The present sequence is useful for producing		
CC	transgenic plants having altered levels of sphingolipid desaturase which		
CC	in turn would alter the fatty acid composition. The enzyme is useful		
CC	for producing polyclonal or monoclonal antibodies. The polynucleotide		
CC	is also useful as primer or probe for screening cDNA libraries to		
CC	isolate desired full-length cDNA clones.		
SQ	Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 other:		
	Query Match	27.2%; Score 399.4; DB 21; Length 1972;	
	Best Local Similarity	58.1%; Pred. No. 8.4e-110;	
	Matches 763; Conservative	0; Mismatches 542; Indels 9; Gaps 3	
OY	103	CAGGAGATTATMGATCTCTATCAAGGGAAGAAGTTTACGATATTCGAAGTGACTAAAG	162
Db	245	CGGACGACCTTGATCTTCATCTCCGGAGAGCTTACGACCTCACGCCGTGCGCC	304
OY	163	AGCATCCCGGTGTGAGCTCCCATTTTAAGTTTTGCCGCAGATGTCACTGATGCGT	222
Db	305	ACCACCCGGGGCGAGGTCGGCTCATCACCCTGCCGGCCAGAGCCGACCGACGCT	364
OY	223	TGATTGCTTACCATCTGGGACCTGTTGGCAATFACCTTGACAGGTTCTTTACTGGGACT	282
Db	365	TCATGGCTTACCAACCGCCCTCCGCGCCGCTCTCCGCGCTTTCGTCGCG---CC	421
OY	283	ACGTTCAAGATTACTCTGCTCTGAGATGTCCAGAGACTACGAGAGCGCTGCTGAGT	342
Db	422	GCTTCTCCGACTACCGTCCCCCGGCTCCGCGACTTCCGCGCTCTCGGCGAGC	481
OY	343	TTTCTAAGATGGGTTTGTTCAGAACACAGGCAAGAGGGGTACTGCTCAATCTTTTCG	402
Db	482	TCTCTCGCGGGGCTCTTTCAGAGCGCGTGGGACACACCCCAAGTTCCTGCTCTCGCAA	541
OY	403	TGTCGTGTGTTGCTGCTCTGAGTGTTAACGATGTTTCTTACTGCAAGACACTGGGCTC	462
Db	542	TGTGCGTCTCTTTCGCAATCGCCCTCTACTGGCTCTCGCTTCACGACCGGGGCC	601
OY	463	ATCTTTTGCTGTGCTTTCGTAATGGGTATGCTATGGCTCCAGAGTGGTGGTGGGCAATG	522
Db	602	ACATGTTGCGCGGCGGCTCATTTGCTTCATCTGGAATCCAGTCGGGCTGGATTGGCCATG	661
OY	523	ATTCTGTTCACATAACAAGTTATGCTAACCCGTAATGCTCTTTTCAATCAATG	582
Db	662	ACTCGGCGCACCAACCAATCACAGGACCCCGGCTCAACCGCTCTCGCAGGTGCT	721
OY	583	CAGGAATGTGATTGCTGGTGTAGTGTTCATGTGCAATGGTAGAAGTTGACCAATACACCATC	642
Db	722	CCGGGAATGCTGCTCAACGGGCTTCGGCATGCTGGGTGAAGTTCAACCAACACACACACC	781
OY	643	ACTTTGCTGTATATGCGCCAATCTGGATCTCGATATTCAGACACTTCTCTAATATTCGA	702

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Db      782  ACATCTCTCGCAACAGCCTGGACCATGACCAGGACCTCCAGCACTGGCCGCTCTTCGGCG  841
Oy      703  TATCCCAAAATTTTTCATCTCCTTACATCATATCTATCACACTGCAAAATGACCTATG  762
Db      842  TTTCCACCAACAGCTTTTCAACAACTTTTGTCGTCTGCTAGAACGCACTTGGCGTTTG  901
Oy      763  ATCGGCGTCGACAGGTTTTTTTGTGTAGCTTTGACACTGGACATTTTATCTCATGTGTA  822
Db      902  ATGCCAATATCCAAAGTTCTTGCTGACCTACCAAGCACTGGACATTTTACCCGGTATGGAT  961
Oy      823  GCGTTAGGCTCTATCTTTTATTTCTGTCTTTTAAAGTGTGTTTTCCAAACAAAGAGG  882
Db      962  TTGCAAGGATTAATCTTCTGTGTGAGTCAATCCGTCTTCTGATCAGCAAAAGAA---GG  1018
Oy      883  TATACAAAGAGAATCAGAGAAATTTTAAAGCTATGACAGCTTCTTGACTTGTGATTTCTTAC  942
Db      1019  TCGCGAGACGTTGGCTGGAGATCCCGAGATGTGACAGCGTTCTGGGTTTGTAAACCCCTTGC  1078
Oy      943  TCCTTTCTCGCTTACCCAAATGGCGCTGAAGAGGTCATGTATTTACGCTCTGTTTAGCAG  1002
Db      1079  TGGTCTCTTGCTCTCCGAATTTGGAGAGAGGATGTGCTTTGTGCTTGCACAGCTTTGGA  1138
Oy      1003  TCGCGCGGTTCCAACTTGGCAGTTTCAGCTGAATTCACCTTGTCTTATGTTTTACACTG  1062
Db      1139  TCACGGGATTCACAGATGTTCAAGTTCTGCTGAAACCACTTCTCATCCGCTGTGTATGTTG  1198
Oy      1063  GTTTCCTTAAGCGGTATGATGATGTTTTCACCAAGCAACAAAGGAGCGCTCAACTAACG  1122
Db      1199  GGCACCAAAAGGGAAACGACTGTTTGAAGAGGCAAAACGGCGGACACTTGATATCAAGT  1258
Oy      1123  CTTTCCTGTTGGGGAATTTGTTTATGTGTGCGCTGCACTTCAAGTTGAGCATCATCTGT  1182
Db      1259  GCTCCCGGTGATGATTTGTTTCATGATGTTGCTGCAAGTTTCAGATGTGAACACATTTGT  1318
Oy      1183  TTCCAAAGGATCCCTAAGGCCATTTTCAGAAAAATCTCAACCATTTGTGAACAAACTTGGC  1242
Db      1319  TTCTTCGCTGCTCGCTGCTCCACTATAGAGATGGTGGCGCGCATTTGTGCTGACCTTTGCA  1378
Oy      1243  AGAAGCATTAATTTTGTCTTATGAAACCTGTACATGTGGGAGGCCAATAAATGTGTATACT  1302
Db      1379  AGAAGCATGGGCTGTCTTATATGTATCCGCACTTCTGGGAGGCAAAATGTATATGACATGGA  1438
Oy      1303  CCACCTCGCTGCTGTGGCTATGSAAGCTAAGATG--TTACCAAGCCAGTTTCCCAAGA  1358
Db      1439  AGAGCGCTAAGGCGCTGCAGCACTTGCAGCGCCAGGGGAAGCCACTACCTGAGACTCTCCAAAGA  1498
Oy      1360  ACATGTCTTGGGAAGCAATGAACCTTTGGGTGAACCTTATATTAACATCAAGT  1413
Db      1499  ATCTGTCTTGGGAAGCTTTGAACACTATGATATCTGGGATCAGACGCTGGAGT  1552

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Search completed: December 31, 2003, 16:16:32
Job time : 284.13 secs

maize cDNA sequences is either Virginia Malbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZMBB: www.zmbl.iasatate.edu.

FEATURES

Source

Location/Qualifiers

1. 1764
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:634923"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/Dubont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 310 a 602 c 456 g 396 t

ORIGIN

Query Match 23.9%; Score 352; DB 11; Length 1764;

Best Local Similarity 55.9%; Pred. NO. 6.8e-52; Matches 730; Conservative 0; Mismatches 566; Indels 9; Gaps 3;

103 CAGAGATTATGATCTCTATCAAGGAAAGTTTACGATATCTCCAGTGAATAAG 162
189 CCGACGACCTCTGGATTCATCTCCGGCAGCGTGAAGTACGACCTGGCTCCCC 248
163 AGCATCCGGTGTAGCTCCCATTTTAAAGTTTCCGGCCAAAGATGCTAGTCCGT 222
249 ACCACCCGGGGGCGACCTCCGCTTCTACCCCTGGGGGAGAGCCACGACCCCT 308
223 TCATGCTTACATCCGCGACCTTGGCAATACCTGAAGTCTTACTGGGACT 282
309 TCGCCGCTACACCGCCCTCGCGCGCCGCTCTCCGCGCTTGTGGTGG---CC 365
283 ACCTTCAGATTAATCTGTCTGAGATGTCAGAGATCAAGAGGCTGTCTAGT 342
366 GCCTCTGTGACTACCGCTCTCCCGCGCTCCGCGCATACCGCGCTCTCGCGAGC 425
343 TTTTAAAGATGGTTTGTCAAGACACAGGCAAAAGGGTCTACTGCTCAATCTTTTCG 402
426 TATCTCCGCGGCGCTCTCGAAGCGCTCGGCCCAACCCCAAGATCACTGCTCTGA 485
403 TGTCTGTGTGTCTGCTCTGAGTGTAAAGTGTCTCTCACTGCAAGACACCTGGCTC 462
486 TGGCCGCTCTTCTTACGCGCGCTGATCTGCTCTGAGTGGCCAGCGCTCGCGCGC 545
463 ATCTTGTCTGTGTTGCTATAGGATAGCTATAGGCTCCAGAGTGTGGTGGCGATG 522
546 ACCTCCCTCGGGGGGCTCTATGGCTTGTGATCCAGTCCGAGTGGATGGCCACG 605
523 ATTCTGTCTACCAAGATTAAGCTTAACCGTAACTTAATGCTTTTCAATCATTTG 582
606 ACTCGGGCCACCAACCGCATACCGGCTCGCTCGACCGGCTGTGAGTGTCTCT 665
583 CAGGAATGATGTTGCTGTGTTAGTGTGATGCTGGAAGTTGAGCAATTAACCATC 642
666 CCGGAACTGCTCAACCGGCTCAAGATGCTGTGGTGAAGTGAACCAACACGACCC 725
643 ACTTGTCTGTTATAGCGCAATCTGATCTGATATTTACGACCTTCTATATTTGCA 702
726 ACATCGCTTCAACAGCTGGAACATACCCGACCTCCAGACATGCCCTCTTGGCG 785
703 TATCCCAAAATTTTCACTCCCTTACATCATATATCAAACTGCAAAATGACTTANG 762
786 TCTCCCAAGCTGTGGCAACATATGCTTACTTCAACACGACCTGGCGTTG 845
763 ATGCGGTGCAAGTTTGTGTTAGCTTTAGACACTGGAATTTTATCTGCAATTTAA 822
846 ATCCCGCTGAAATTTCTTATCATGCTACGACCTGAGACCTTCTACCCGATATGCA 905
823 GCGTTAGGCTCTATCTTTATCTGTCTTTAAAGTGTGTTTCAACAAACAAAGGG 882

106 TCGCCAGATTAATCTTCTCGCCAGCTCGCCCTGTTCCTT---CAGGAGAAAGGG 962
883 TATCAAGAAATCTCAGAAATTTTAGGCTATGACCTTTCTGATCTGATTTCTTAC 942
963 TCGCGAGCGGTGTGATGATGCGGGGTCCCAATTTCTGGGCTGTGATCCCTTGC 1022
943 TCTTCTCGCCCTTACCAATTTGAGCTGAAAGGCTCATATTTACGCTCTGTTAGCAG 1002
1023 TGTGCTTCTTCCCTGCGCAATTTGTGGAGAGGCTCCGCTTGTGCTTTTACGTTACCA 1082
1003 TCGCCGGTTCACCAATTTGACCTTGAATCACTTTGCTTATATGTTTACATG 1062
1083 TCGCGGATATGACAGCTCAATTTGCTGTAACCACTTCTGCTGACGATGATGTCG 1142
1063 GTTGTCTTACCGTATGATGTTGTTTACACGAGACAAAGGACGCTCAATTAACAG 1122
1143 GGCACCCAAAGGCAATGACTGTTTGAAGAGAGCGGACAGGCTGACATCTCTGT 1202
1123 CTCTGCTGTGATGATGATGTTTATGATGAGCTGCTGACCTTTGATTTGACATCTGT 1182
1203 GCTCTCTTGTGATGATGTTGTTTCAAGGTGCTGACATTTCCAGATTTGACACATCTGT 1262
1183 TTCAAGATGCTTAAAGTGCATTTGAGAAATCTCACCCATTTGAACTTTGCC 1242
1263 TTTCCGCTTACTCTGCTGCTGACCTTGCACAGGTTGACACGCGCTCCGACCTTTGCA 1322
1243 AGAAGATATTTGTCTTATGAAATGCTACCAATGTTGAGAGCCATTAATGATTAAT 1302
1323 AGAAGATAGGCTCACTTATTTCTGACGACCAATTTCTGGGATGCAAAATGCTTACATGGA 1382
1303 CCACCTGCGGTGCTGCTGATGAGCTAAGATTTTACCA---AGCCAGTTCCCAAGA 1359
1383 AGACACTCAGGGCTGCTGATTTGACAGCCAGACCGCTTCAAGTGGTGTCTCCAGAA 1442
1360 ACATGCTTGGGAGCAATGAACATTTGCGGTGAACCTTATTA 1404
1443 ATTGGTATGGAGGCTGTGAACACCATGATTAATGAGATGA 1487

RESULT 2

CB972537

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
Unpublished
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGTACCGACATATGCC.
Location/Qualifiers

FEATURES

Source

1. 721
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultiivar="Cabernet Sauvignon"
/db_xref="taxon:29760"

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/clone="CAB30001_11a_Fa_D04"
/sex="Hermaphrodite"
/lab_host="DH5alpha"
/clone_lib="Cabanet Sauvignon Berry Stage I - CAB3"
/notes="Organ: Berry; Vector: pDNA; Site_1: Sfil; Site_2:
Sfil; CAB3 is a cDNA library of Vitis vinifera 'Cabanet
Sauvignon' Clone 8 berries. Samples were collected after
berry set from field-grown vines during stage I of berry
growth, 17 days after full bloom. The average berry size
was 6 millimeters. Sampled vines were located at the
University of California, Davis, Experimental Vineyard.
cDNAs were made by oligo-dt priming and directionally
cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGGATCAAGCAGAGGCGCATTCAGCGCGG-3' and
5'-ATTCTAGAGGCCGAGCGCGCGCATTC-3'. Library was
constructed using the Clontech Creator SMART Kit and
size-selected to contain the 0.5-3 kb size fraction."

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BASE COUNT 171 a 131 c 168 g 251 t

Query Match 22.2%; Score 326.4; DB 14; Length 721;
 Best Local Similarity 65.8%; Pred. No. 2.8e-47;
 Matches 474; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

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91 AGCATAGCAACAGGAGATTATGATCTCTATCAAGGAAAGTTACATATCTCCA 150
2 AGCATACAGCAAGCGAGGATCTGTGATCTCTATACAGGTAAGTTACATATCTCCA 61
151 AGTGAATAAGAGATCCCGGTGTGAGCTCCCATTTTAACTTTTGCAGGCAAGATG 210
62 ATTGGCTTAAGTTATCCGGGTGGGAGATCCCTCTCCGAATTTGGCGGCAAGATG 121
211 TCACTAGTGGTTCATTTGCTTACCATCTGCTGGCAATCTTGAAGTTCT 270
122 TTACAGACGCTTCATTCATTCATTCAGATCTGCTGGCAATCTTGAAGTTCT 181
271 TTATCGGGTCTACGTTCAAGATTACTCTGCTGTGATGATCCAGAGATACAGAGG 330
182 TTATCGGGTCTACGTTCAAGATTACTCTGCTGTGATGATCCAGAGATACAGAGG 241
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242 TCGCTATGATTTTCAAACTTGGGTTTGTGAAGAAAGGCAATCTGATCTACTACA 301
391 CAATCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
302 CCGTTCATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 361
451 GCACCTGGGCTCATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 510
362 GTTTCGCGGTTCATCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
511 GGGTGGGCGGATCTTGTCTACCAAGTTATGCTTAACCTTAAGCTTAATCTGCTTT 570
422 ATCTGGGATATGTTCTGGGCTTATTCAGATATGCTCACTCTGGGTTTAACTCTTG 481
571 TTCAATCATTCAGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 630
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631 ATTAACCATCATCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
542 ATATATCCCATCATATAGCTTGTATATGCTTGTATATGCTTGTATATGCTTGTAT 601
691 CTATTAATGCTCATATCCCAAAATTTTCACTCCCTTACATCATATCAATCTGCA 750
602 CAGTGTGAGTTCCTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
751 AAATGACCTATGATCGGCTGCAAGTTTGTGTTAGCTTGAAGCACTGAGCAATTTAT 810
662 TATTGAATTTGATTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721

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RESULT 3
LOCUS BQ409001
DEFINITION BQ409001. 651 bp mRNA linear EST 22-MAY-2002
ACCESSION GA_Ed0014D02r Gossypium arboreum 7-10 dpa fiber library Gossypium
VERSION BQ409001
KEYWORDS arboreum cDNA clone GA_Ed0014D02r, mRNA sequence.
SOURCE BQ409001.1 GI:21096688
ORGANISM EST.
Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 651)
Wing,R.A., Friesch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
'D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 563
Seq primer: TAATAGCTCACTATAGG
High quality sequence stop: 628.
Location/Qualifiers
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/mol_type="mRNA"
/strain="AXA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ed0014D02r"
/risue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XhoI"

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BASE COUNT 170 a 138 c 152 g 191 t

Query Match 20.4%; Score 299.8; DB 13; Length 651;
 Best Local Similarity 68.4%; Pred. No. 1.3e-42;
 Matches 415; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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105 CAGGAGATTATGATCTCTATCAAGGAAAGTTAGATATCTCAAGTACTAAG 164
163 AGCATCCCGGTGAGTCCCATTTGTAAGTTTGGCCGCAAGATGTCATGATGCT 222
165 AACACCTTGAAGAGACTTCCTTGTGCTGATATCTGCTGCAAGATGCAAGAGCT 224
223 TCATTGCTTACATCTCTGCACTGCTTGGCAATACCTTGAAGTTCTTTACTGGTACT 282
225 TTGTAGCTTATATCTCTGCTTGAAGTCTGCAATATCTTGAAGATCTTTTACCGGCTATT 284
283 AGTTCAAGATTAATCTCTGCTGATGATGTCAGAGATCAAGAGGCTGCTGATGCT 342
285 ATCTCAAGATTAATCTCTGCTGATGATGTCAGAGATCAAGAGGCTGCTGATGCT 344
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345 TTTCATGATGAGTTTGTTCAGAGACACGAGAAAGGCTTACTGCTCAATCTTTTTCG 404

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QY 403 TGTCTGTGTTGCTGCTGAGTGTACGGTGTCTCTACTGCAGACGACCTGGGCTC 462
 DB 405 TAGCATTCGCTGTTTCTCATAGTGTTCAGGCTTTTATGCTCTAACAGCGCTTGGTGC 464
 QY 463 ATCTTTCCTGTGTTTCTTAATGGGTAATGCTAGGCTCAAGTGTGTGGGGGCGATG 522
 DB 465 ATCTTCCTTGGGGGCTTTACTGGGATTCATCATGATACAGAGTGGGTGATGACATG 524
 QY 523 ATTTCTTCTACTACCAAGTTATGCTTAACCGTAAGCTTAATGCTTTTCAATCATTTG 582
 DB 525 ATTCGGGCAATTAACAGGTAATGTCAGCAAGAAATTAACAAGGTTGCTCAGATCCCTTA 584
 QY 583 CAGGAATGATGATGCTGCTGTTAGTGTGTCATGGTGAAGTTGACCATTAACCCATC 642
 DB 585 CTGGGATTCGCTTTCAGGATCATGATGTTGTTGGTGAATGACCAATCTCTACC 644
 QY 643 ACTTTGC 649
 DB 645 ACATTGC 651
 RESULT 4
 BQ864828
 LOCUS 721 bp mRNA linear EST 14-AUG-2002
 DEFINITION OGC27M12. y9. ab1 QG ABCDI lettuce salinas Lactuca sativa cDNA clone
 ACCESSION OGC27M12. mRNA sequence.
 VERSION BQ864828
 KEYWORDS BQ864828.1 GI:22250293
 SOURCE EST.
 ORGANISM Lactuca sativa
 Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; Lactuca.
 1 (bases 1 to 721)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
 P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Church, S., Jackson, L. and Bradford, K.
 Lactuce and Sunflower ESTs from the Compositae Genome Project
 http://compgenome.ucdavis.edu/
 Unpublished
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
 belongs to contig QG_Ca_contig2376, see http://cgpdb.ucdavis.edu/
 for details.
 Plate: OGC27 row: M column: 12.
 Location/Qualifiers
 1..721
 /organism="Lactuca sativa"
 /mol_type="mRNA"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="OGC27M12"
 /lab_host="E.coli"
 /clone_lib="QG_ABCDI lettuce salinas"
 /note="Vector: pARCDSAT1AB. The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_lib=QG_ABCDI lettuce salinas

TAG TISSUE=flowers pre-fertilized
 TAG_SEQ=GGTACCGG"
 BASE COUNT 194 a 153 c 163 g 211 t
 ORIGIN
 Query Match 20.1%; Score 295.6; DB 13; Length 721;
 Best Local Similarity 65.7%; Pred. No. 6, 6e-42;
 Matches 430; Conservative 0; Mismatches 224; Indels 0; Gaps 0;
 QY 29 CTTCCTCTGTGCTCACTTCAATGGAAGCCAAAGACACATTTCCCAAGACACCTTGC 88
 DB 51 CTTTCCTTCAGGCTTTTCAATGACAGAACCCAAAGAGTATGTCATCTGAAGAGCTCAA 110
 QY 89 AAGCATTAAGCAACAGAGATTTATGATCTCTATCAAGGAAAGTTATACATATCTC 148
 DB 111 AACTCACAACAAACAGGGGATCTGAGATCTGTATACAGGAAAGTTATACATCTC 170
 QY 149 CAATGGAATTAAGACATCCCGGTGTGAGCTCCCATTTGTAAGTTTGGCCGCAAGA 208
 DB 171 AGAGTGATGAATAACCAACCTGTGTGACCTGCATTTGTAATCTTGTGTCAGA 230
 QY 209 TGTCACTGATGCTTCAATGCTTACCATCTGSCACTGCTTGGCAATCTTACAGGTT 268
 DB 231 CGTCACCGATGCTTACGCTGCTCTTCATCATCTACCTGCTTGGCAATATCTGACAGATT 290
 QY 269 CTCTACCTGAGTACATGATTAATCTCTGCTCTGAGATGTCACAGACTACAGAAAG 328
 DB 291 CTTCATGAGTATTAATCTCAAGACATACGCCGTTCCGAGATCTCCAAAGATTAACGAAA 350
 QY 329 GCTGCTCTGATGTTTCTTAAGATGGGTTTGTCAAGACACAGGCAAAAGGGCTTACTG 388
 DB 351 GCTTACTTCTGAATTCACAAAATGGGTTGTTCGAAAAGAGGCAATGAGATTGAT 410
 QY 389 CTCAATCTTTTGTGCTGTGTGTTTGGCTCTGAGATTTTACGGTGTCTCTACTGCAA 448
 DB 411 ATCATGATGCTATGACATATGATGTTCTCCGTTGTGTTTATGATTCAGCCA 470
 QY 449 GAGCACCCTGGGCTCATCTTTGCTCTGTTTGTCTAATGAGGATCTAATGCTCCAGAGTGG 508
 DB 471 GAGTCTTTTGTTCATTTGATTTGGGTGATTAATGAGGTTCTTTGATTAAGAGTGG 530
 QY 509 TTGGGTGGGCGATGATTTCTTGTGCTACATCAAGATTAATGCTTAATGCTCT 568
 DB 531 GTGGCTAAGCGCATGATTCGGGCAATCATGATTAATGATGATCGAAATTCATCGTTT 590
 QY 569 TTTTCAATATATGACAGAAATGATGATGCTGTGTTAGTTCATGATGATGGAATTGGA 628
 DB 591 TGTCTCAGATCTTACCGGAAATGCTCTCCCGGAAATCAGCATTTGCGTGGAAAGAAA 650
 QY 629 CCAATACACCCATCACTTGGCTGTAATAGCGGCAATCTGATCTGATATTC 682
 DB 651 CCACTGTCAGATCATATGCTGTTACAGCTTTGATATGATCTGACCTTCA 704
 RESULT 5
 CB002504/c 674 bp mRNA linear EST 10-JAN-2003
 LOCUS VVB017E10.131866 An expressed sequence tag database for abiotic
 DEFINITION VVB017E10.131866 An expressed sequence tag database for abiotic
 ACCESSION CB002504
 VERSION CB002504
 KEYWORDS CB002504.1 GI:27579809
 SOURCE EST.
 ORGANISM Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; Vitaceae; Vitis.
 1 (bases 1 to 674)
 Cramer, G.R. and Cushman, J.C.
 An expressed sequence tag database for abiotic stressed leaves of
 Vitis vinifera var. Chardonnay
 Unpublished

COMMENT

Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer

Plate: 0 row: E column: 10

Seq primer: T3 20mer

High quality sequence stop: 674.

Location/Qualifiers

FEATURES

source

1. 674
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVB017E10"
/issue_type="leaf"
/dev_stage="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

BASE COUNT

236 a 183 c 125 g 130 t

ORIGIN

Query Match 19.7%; Score 289.8; DB 14; Length 674;

Best Local Similarity 65.3%; Pred. No. 6,9e-41;

Matches 442; Conservative 0; Mismatches 232; Indels 3; Gaps 1;

497 GCTCGAGTGGTGGGCGCATGATTTCTGCACTACCAAGTTAGCCGTA 556
674 GATTGAGAGTGGGCGCATGATTTCTGCACTACCAAGTTAGCCGTA 615
557 GCTTATCGCTTTTCAATCATTTGAGGAAATGATGCTGCTGTTAGTTGCA 616
614 TTGAAACCGTTTGTGCAAGTGTGAGGAAATGCTGCTGCGGATCGATTCG 555
617 GTGGAAGTTGACCATTAACACCATCATCTTGCCTGTAATAGGCCAATCTG 676
554 GTGGAAGTTGACCATTAACACCATCATCTTGCCTGTAATAGGCCAATCTG 495
677 TATTCAGCACTTCTGTAATATGATTCATCCCAAAATTTTCACTCCCTTA 736
494 TCTTCAGCACTTCTGTAATATGATTCATCCCAAAATTTTCACTCCCTTA 435
737 CATTCAGCACTTCTGTAATATGATTCATCCCAAAATTTTCACTCCCTTA 796
434 TTTCTATGAAAGGAATGATTTTATGTTGCTAGGTTTCTAGTACAGCA 375
797 CTGCAATTTTATCTGCAATGTTTAAAGCTGATCTTATCTGCTTTAA 856
374 CTGCAATTTTATCTGCAATGTTTAAAGCTGATCTTATCTGCTTTAA 315
857 GGTGTTGTTTCCAAACAAAGGTTATCAAGAGAGTCAAGAAATTTTAAAG 916
314 TTTGTTGTTGTC---CAAGAGAGGTTGCTACAGGCGTCAAGAGATTTT 258
917 AGCTTTCTGACTGTTGTTTCTTACTCTTCTTCTGCTTACCAATTTGCT 976
257 TGTGTTTGGATTGTTGTTGTTTCTTCTTCTTCTGCTTACCAATTTGCT 198
977 CATGATTTTCAAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1036
197 GATGTTTGTGTTCTGAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 138
1037 TCACITTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1096
137 TCATTTCTGATTCAGTGTGTTATGTTGTTGTTGTTGTTGTTGTTGTTG 78

QY 1097 GACAAAGGCGACGCTCAACATACAGCTTCTGTTGGTGGATTGGTTTCATGGTGGCT 1156

DB 77 GACTCATGGGCTCTTCGATTAATTTCTGCTCTTGGATGAGCTGTTTCATGGTGGCT 18

QY 1157 GCACITTCAGATTGAGC 1173

DB 17 GCAGTTTCAGATTGAGC 1

RESULT 6

CB002410 673 bp mRNA linear EST 10-JAN-2003

LOCUS

VVB016E06.131678 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera

DEFINITION

CDNA clone VVB016E06 5, mRNA sequence.

ACCESSION

CB002410 GI:27579715

VERSION

EST.

KEYWORDS

EST.

SOURCE

Vitis vinifera

ORGANISM

Vitis vinifera

REFERENCE

1 (bases 1 to 673)

AUTHORS

Cramer, G.R. and Cushman, J.C.

TITLE

An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay

JOURNAL

Unpublished

COMMENT

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer

Plate: 0 row: E column: 06

Seq primer: T3 20mer

High quality sequence stop: 673.

Location/Qualifiers

1. 673

FEATURES

source

1. 673
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVB016E06"
/issue_type="leaf"
/dev_stage="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

BASE COUNT

236 a 182 c 125 g 130 t

ORIGIN

Query Match 19.7%; Score 289.4; DB 14; Length 673;

Best Local Similarity 65.3%; Pred. No. 8.1e-41;

Matches 441; Conservative 0; Mismatches 231; Indels 3; Gaps 1;

499 TCCAGAGTGGTGGTGGGCGATGATTTCTGCTACTACCAAGTTATGCCAATCCGTA 558
672 TTCAGAGTGGTGGTGGGCGATGATTTCTGCTACTACCAAGTTATGCCAATCCGTA 613
559 TTTATGCTTTTTCAAATCATTTGAGGAAATGATGCTGCTGTTAGTGTTCATGCT 618
612 TGAACCGCTTTTGTGAGGCTGAGTGGGAAATGCTTGGCGGATCAGTATTTGCTGT 553
619 GGAAGTTGACCATTAACACCATCATCTTGCCTGTAATGAGCGCAATCTGATCCGTA 678

Db 552 GGAAGTGAATCAACAAGCTCATCATGCTGCAACAGCCTGATTCGATCCGATC 493

Qy 679 TTGAGCAGCTTCTATATATGCGATATCCCAAAATTTTCACTCCCTTACATCATCT 728

Db 492 TTGAGCAGCTTCTATATATGCGATATCCCAAAATTTTCACTCCCTTACATCATCT 433

Qy 739 ATGACATGCAAAATGACCTATGATGCGCTGCGAGCTTTTGTATGCTTACAGACT 798

Db 432 TGTATGAAAGAAAGATGATTTTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTG 373

Qy 799 GACATTTTATCTGCACTTTGTAAGCTTATCTTTTATCTGCTTTTAAAG 858

Db 372 GACATTTTATCTGCACTTTGTAAGCTTATCTTTTATCTGCTTTTAAAG 313

Qy 859 TGGTGTTCCTCAACAAGAGGATATACAGAGATGCAAGATTTTGTAGGCTATGAC 918

Db 312 TGTGTGTGTC--CAAGAGAGGATGCTGCAAGAGGATTTTGTAGGCTATGAC 256

Qy 919 CTTTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 978

Db 255 TGTGTGTGTC--CAAGAGAGGATGCTGCAAGAGGATTTTGTAGGCTATGAC 136

Qy 979 TGTATTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038

Db 195 TGTGTGTGTC--CAAGAGAGGATGCTGCAAGAGGATTTTGTAGGCTATGAC 136

Qy 1039 ACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1098

Db 135 ATTTCTATCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 76

Qy 1099 CAAGAGGAGCTGCAACAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1158

Db 75 CTATGAGGCTGCTGCAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16

Qy 1159 ACTTTCAGATTGAGC 1173

Db 15 AGTTTCAGATTGAGC 1

RESULT 7

LOCUS B0861565

DEFINITION OGC18P18.yg.abi OQ.ABCDI lettuce salinas Lactuca sativa cDNA clone

ACCESSION B0861565

VERSION B0861565.1 GI:22247030

KEYWORDS EST.

SOURCE Lactuca sativa

ORGANISM Lactuca sativa

REFERENCE 1 (bases 1 to 696)

AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.

TITLE lettuce and Sunflower ESTs from the Compositae Genome Project

JOURNAL Unpublished

COMMENT Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Aamundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu] belongs to contig OQ_CA_contig2376, see http://cgdb.ucdavis.edu/ for details.

FEATURES

source

1. .696

BASE COUNT 187 a 148 c 153 g 208 t

ORIGIN

Query Match 19.1%; Score 280.8; DB 13; Length 696;

Best Local Similarity 64.5%; Pred. No. 2,6e-39;

Matches 435; Conservative 0; Mismatches 237; Indels 2; Gaps 1;

138 TACGATATCTCCAAAGTGAAGTAAAGAGATCCCGGTGTGAGCTCCATTGTTAAGTTT 197

Db 8 GAAGAGCTCAAAAGTCAACAAACCAAGAGATCTGTGATCTGATACAGGAAAGTT 67

Qy 138 TACGATATCTCCAAAGTGAAGTAAAGAGATCCCGGTGTGAGCTCCATTGTTAAGTTT 197

Db 68 TATGAGGTCTCAAGAGTGAAGTAAAGAGATCCCGGTGTGAGCTCCATTGTTAAGTTT 127

Qy 198 GCCGCCAAGATCTACTGATGCTTACTGTTACATCTGCGACCTGCTGGCAATAC 257

Db 128 GCTGTCAAGACGTCACCATGCTTACGCTGCTTCAATCCATCCATGCTGGCAATAT 187

Qy 258 CTGAGAGGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317

Db 188 CTGAGAGGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247

Qy 318 GACTACGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 377

Db 248 GATTACGAAGGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 307

Qy 378 GGGGTCTACTGCTCAATCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 437

Db 308 GGAGTTTGTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367

Qy 438 CTCTACTGCAAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 497

Db 368 TTATTCAGCAGAGTCTTTTGTATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 427

Qy 498 CTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 557

Db 428 ATTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 487

Qy 558 CTATATGCTTTTCAATCATGTCAGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 617

Db 488 TTCAATGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 547

Qy 618 TGAAGTTGACATTAACCCATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 677

Db 548 TGAAGAGAAACCACTGCAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 607

Qy 678 ATTCAGAGCTTCTTCAATCATGTCAGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTG 737

Db 608 CTTCAC--CACATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665

Qy 738 TATCAGACTGCA 751

Db 666 ACTACGAAAGAA 679

RESULT 8
LOCUS BG647198 783 bp mRNA linear EST 24-Apr-2001
DEFINITION EST508817 HOGA Medicago truncatula cDNA clone pHOA-15P24 5' end,
 mRNA sequence.
ACCESSION BG647198
VERSION BG647198.1 GI:13782310
KEYWORDS EST
SOURCE Medicago truncatula (barrel medic)
 Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
REFERENCE 1 (bases 1 to 783)
 Hahn,M.G., Ojane-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
 Uterback,T., Cho,J. and Fraser,C.M.
 ESTs from roots of Medicago truncatula treated with
 oligogalacturonides of DP 6-20
TITLE Unpublished
JOURNAL Contact: Michael G. Hahn
 Complex Carbohydrate Research Center
 University of Georgia
 220 Riverbend Road, Athens, GA 30602-4712, USA
 Tel: 706-542-4457
 Fax: 706-542-4412
 Email: hahn@ccrc.uga.edu
 G390804e TIGR sequence name: MTMBV96TK More information is
 available at: www.medicago.org
 Seq primer: Skmod (CTA gaa cta gtc gat cc).
FEATURES
 source
 1..783
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /cultivar="A17"
 /db_xref="taxon:3880"
 /clone="pHOA-15P24"
 /tissue_type="3 day old seedling roots"
 /dev_stage="24 hours after treatment in the dark at 26 C
 with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
 presence of 100 ug/ml Gentamicin"
 /lab_host="XLOLR"
 /clone_1lb="HOGA"
 /note="Vector: pBluescript SK-; Site 1: EcoRI, Site 2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unizap XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-aseIst
 helper phage and propagated in SOLR cells."

BASE COUNT 173 a 142 c 169 g 299 t
ORIGIN
 Query Match 19.0%; Score 279.4; DB 10; Length 783;
 Best Local Similarity 60.0%; Pred. No. 4.3e-39;
 Matches 466; Conservative 0; Mismatches 311; Indels 0; Gaps 0;
QY 430 ACGGTCTTCTACTGCAAGAGCACTGGGCTATCTTGTGTTGCTATGAGTA 489
 |||||
DB 1 ATGCGTGTGGTGTGACAAAGTGTGGGCTCATTTAGGTTCTGGAATGTTGGGTT 60
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QY 490 TGGTATGCTCCAGAGTGTGGGGGATATTTCTGTCACTACCAAGTTATGCTTA 549
 |||||
DB 61 TGGTATGAGTGAAGACTTATATTTGGTCATATCTGGTCACTATGAGGTTATGCGA 120
 |||||
QY 550 ACGGTAGCTTATCGCTTTTCAATCATTTGACAGAAATGATGCTGGGCTTATG 609
 |||||
DB 121 GTGGAAGTTATCAAAATTTGACCAAAATTTCTTGTGTAATTTATGACTGGTATAGTA 180
 |||||
QY 610 TTGCATGTTGGAAGTTGACCATTAACCATCACTTGGCTGTAATGAGCCCAATCTGG 669
 |||||

RESULT 9
LOCUS CB893839 817 bp mRNA linear EST 24-Apr-2003
DEFINITION EST646631 HOGA Medicago truncatula cDNA clone HOGA-29M7, mRNA
 sequence.
ACCESSION CB893839
VERSION CB893839.1 GI:30101008
KEYWORDS EST
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
REFERENCE 1 (bases 1 to 817)
 Hahn,M.G., Ojane-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
 Uterback,T., Cho,J. and Fraser,C.M.
 ESTs from roots of Medicago truncatula treated with
 oligogalacturonides of DP 6-20
TITLE Unpublished
JOURNAL Contact: Michael G. Hahn
 Complex Carbohydrate Research Center
 University of Georgia
 220 Riverbend Road, Athens, GA 30602-4712, USA
 Tel: 706-542-4457
 Fax: 706-542-4412
 Email: hahn@ccrc.uga.edu
 TIGR sequence name: MTMDK76TK
 More information is available at: www.medicago.org
 Seq primer: Skmod (CTA gaa cta gtc gat cc).
FEATURES
 source
 1..817
 /organism="Medicago truncatula"
 /mol_type="mRNA"


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Db      295 AGGGTTCGTACAGGGCTCAGAGATTTGGGGCTGCTGTGTTTGGATTGGTACCT 236
Qy      939 CTAATCCTTTTCGCTGCTACCAATTTGGCTGAAAGGTCATGATTTCACTGCTTTA 998
Db      235 TTACTGTTTCATGTCGTCCCAATTTGGGAAAGATGTTGTTGTTCTGATTTTC 176
Qy      999 GCAGTCGCGGGTCCCAATTTGGCAGTTCACTTAATCACTTCTTCTAATGTTTAC 1058
Db      175 TCCTTACTGGAATCAGATGTTCAATTTCTGTTTAATCATTTCTCATCCAGTTTAT 116
Qy      1059 ACTGTTTCCCTAGCGGTAATGTTGTTTCAACAGACAGAAAGGCAAGCTCAACATA 1118
Db      115 GTGGGCTCTCAAGTGGAGATGTTGTTGAGAAACAGATCAGGCTCTCATAT 56
Qy      1119 AAGCTTCTGCTTGGTGGAGTTGTTTCAATGTTGCTGCTGACCTTTAGATTGAC 1173
Db      55 TCCTGCTCTCTTGTGATGATGCTGTTTCATGTTGGGCTCAGATTCAATGAGC 1

RESULT 11
LOCUS   BF268631 957 bp mRNA linear EST 07-MAR-2001
DEFINITION GA_Eb0002G08f Gossypium arboreum 7-10 dpa fiber library Gossypium
ACCESSION BF268631
VERSION  BF268631.1 GI:11199626
KEYWORDS EST.
SOURCE  Gossypium arboreum
ORGANISM Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosid II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 957)
AUTHORS  Wing,R.A., Fritsch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE    An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL  Unpublished
COMMENT  Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 714.
FEATURES
source 1..957
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Eb0002G08f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 258 a 179 c 233 g 287 t

Query Match 18.3%; Score 268.8; DB 10; Length 957;
Best Local Similarity 61.9%; Pred. No. 2,8e-37;
Matches 426; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

Qy 37 GTTGACCTTCATGAGAGCCAAAGACACATTTGGCAGACGCTTGCAACACATA 96
Db 165 GTTGAGCTTCATGAGAGCCAAAGACACATTTGGCAGACGCTTGCAACACATA 224
Qy 97 AGCAACCAAGAGTTTATGATCTATACAGGAAAGTTTACGATATCTCCAACTGA 156

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Db      225 ACAAATCGGGAGATTGTGATCTCAATCCAGGCAAGGTTATACATGTTTCAAGATGGG 284
Qy      157 CTAAGAGATATCCGGGTGTGAGCTCCCAATGTTAAGTTTTCGGGCAAGATGTCACTG 216
Db      285 CAAAGAGATATCCGGGTGTGAGCTCCCAATGTTAAGTTTTCGGGCAAGATGTCACTG 344
Qy      217 ATGCGTTCAATGCTTACACCTCGGCACTGTTGGCAATACCTTGAACAGTTCTTACTG 276
Db      345 ATGCGTTCTGCGATACCTCGGCACTGTTGGCAATACCTTGAACAGTTCTTACTG 404
Qy      277 GGTACTAGTTTCAGATTAATCTGCTCTGAGATGTCCAGAGATCAACAGAGCTGCT 336
Db      405 GTTATCATCTCAAAAGATTTGAGGTGCGAGATATCCAAAGATTAATAGAGGCTGCT 464
Qy      337 CTGAGTTTCTTAAGATGGGTTTTCAGACACAGGCAAGAGGCTTACTGCTAATCT 396
Db      465 CGAGATTGCGCAAGCCGGTATGTTGAAAGAAAGGACATGTAGCCCTTTTTCATT 524
Qy      397 TTTTGCTGCTGTGTTTGTGCTGAGTGTTCAGGTTTCTTACTGCAAGACACT 456
Db      525 CAGCTGTACCTTATTTATCTTATGCTCTTTATGTTTATAGATGTGATAGCTGT 584
Qy      457 GGGCTCATCTTGTCTGTGTTGCTAATGGTATGCTATGCTCCAGAGTGTGGTGG 516
Db      585 GGGCAATCTTGGGTGGGCACTGTTGGGCTTGTGGATGAGAAAGGCAATCATTTG 644
Qy      517 GGCATGATCTTGTACTACCAAGTTTACCTTACCTTAACTGTTTCTTTTCAAA 576
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Qy      577 TCATGACGAAATGATGATGCTGTGTTAGTTCATGTTGAAAGTTGACCAATACA 636
Db      705 TTTTATCTGGGATGTTTAAACCGGATCAAGATTCCTGGTGAATGACTCAAAAG 764
Qy      637 CCATCATCTTGTCTGTATAGCGCAATCTGATCTGATTTAGCACTTCTCTATA 696
Db      765 CTCACCAATTTGGCTGCAAGCCGTGACACAGATACCAAGATCCAGACATATCTGTT 824
Qy      697 TTGCATATCCCAAAATTTTCAATC 724
Db      825 TTGCCGTCTTTTACCACTTTTAATTC 852

RESULT 12
LOCUS   BJ111411 772 bp mRNA linear EST 20-JUL-2001
DEFINITION EST5313161 GSD Medicago truncatula cDNA clone pGSD10F10 5' end,
RNA sequence.
ACCESSION BJ111411
VERSION  BJ111411.1 GI:14985738
KEYWORDS EST.
SOURCE  Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosid I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.
REFERENCE 1 (bases 1 to 772)
AUTHORS  Grusak,M.A., Samc,D.A., Town,C.D., Van Aken,S., Uterback,T., Cho
,J. and Fraser,C.M.
TITLE    ESTs from developing reproductive tissues of Medicago truncatula
JOURNAL  Unpublished
COMMENT  Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
B398266e
TIGR sequence name: MTPAT29TK
More information is available at: www.medicago.org

```

FEATURES
source

Seq primer: Skmod (CTA gaa cta gtc gat cc).

Location/Qualifiers

1. 772
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/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="pGSD10F10"
/issue_type="immature seeds"
/dev_stage="immature seeds, 11 to 19 days after
pollination"
/clone_id="GBSD"

/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
GigaPack III Gold packaging extracts. Plasmid containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propagated in
XL10R cells."

BASE COUNT 172 a 158 c 161 g 281 t

ORIGIN

Query Match 18.2%; Score 268; DB 12; Length 772;
Best Local Similarity 59.4%; Pred. No. 4.2e-37;
Matches 454; Conservative 0; Mismatches 310; Indels 0; Gaps 0;

637 CCCATCACTTGGCTGTATAGGCCCAATCGATCTGATATTCAGACCTTCTTAA 696
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Qy 697 TTGCAATATCCCAAAATTTTCACTCCCTATCATATATATCAACATGCAAAATGA 756
Db 67 TCGCTGCTATCGCATCTTTGGTTGATTAATCTTATTTCTATGATAGACAGTTAA 126
Qy 757 CCTATGATCGCGCTGCCAGGTTTTTTTGTAGCTTTCAGACTGACATTTTATCTGCAT 816
Db 127 AGTTTATGCTTTGTCAAGGTTTCTTATCATGATACGACATATCACTTTTACCTGCT 186
Qy 817 TGTAAAGCTTAGGCTTATCTTTTATCTGCTTTTAAAGTGCTTTTCAACAACA 876
Db 187 TGTGTTTGAAGGCTTAACTTGAATCAATTTTGTCTTGTGGCATCAC 246
Qy 877 AAAGGATATCAAGAGATCAGAAATTTTAAAGCTATGACGTTCTTGAATGATAT 936
Db 247 GAATATGTTCTGATAGGCTTTAACAATCATGATGATGATGATGATGATGATGATG 306
Qy 937 CTCTACTCTTTCTCGCTTACCAATTTGCTGAAAGGCTGATATTTCACTGCTGTT 996
Db 307 CTCTGATATGTAGCCCTCCCAAGTTGGCAGAAAGCTCATGTTGTTCTGCTGTT 366
Qy 997 TACAGAGCGCGGCTTCAACATTTGAGCTTCACTGATGATCACTTGTCTTAAATTT 1056
Db 367 TTGTTGTTTTCATCAATCAATCTTAAATTTGTTGAACATTTGCTGCAAACTGT 426
Qy 1057 ACACTGTTTCTAGAGGATATGTTTCAACGACAGACAAAGGACGCTCAACA 1116
Db 427 ATCTCGGTCAACGAGGAAATGATTTGTTTGAAGAAACAGCTGGAACATGATA 486
Qy 1117 TAAACAGTTTCTGTTGTTGATTTGTTTCAATGTTGCTGACATTTCAATGATGATC 1176
Db 487 TCATTTGTTTCAACATGATGATTTGTTTCTTGTGTTGAGTTTCACTTGAACATC 546
Qy 1177 ATCTGTTTCAAGAGGCTTAAATGATTTCAAGCAATTTCAACCATTTGTGAACAAC 1236
Db 547 ATTTGTTTCAAGGCTTCAAGGCTTAAATGAGAAAGTTTGGCCATTTGTGATGATC 606
Qy 1237 TTTCGCAAGACATATTTGTTCTATGAACCTGATCATGTTGGAGGCAATTAATG 1296

Db 607 TATGCAAGAGCATATTTGCTTACAGAGTTTGTATTTGTTGAGGCAATCTTTGA 666
Qy 1297 TATATCCACCCTGCGTGTGCTATGAGACTAGATGTTTACCAACCGAGTTCCA 1356
Db 667 CTCTCAAGACTTTTGAAGCTGCTGATTTGACCAAGGATTTTACCAACTGCTTAC 726
Qy 1357 AGAAGATGCTCTGGAAGCAATGACATTTCCGGTGAACCTTA 1400
Db 727 AGAAGCTTTGTTGGAGGCTTTTATATCTGATGCTGAGCTTGA 770

RESULT 13
A1729087 622 bp mRNA linear EST 11-JUN-1999
LOCUS BNLGH112557 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
DEFINITION to (AF005096) desaturase/cytochrome b5 protein [Ricinus communis],
mRNA sequence.

ACCESSION A1729087 GI:5047939
VERSION A1729087
KEYWORDS EST.
SOURCE Gossypium hirsutum (upland cotton)
ORGANISM Gossypium hirsutum

REFERENCE 1. (bases 1 to 622)
Blewitt, M., Matz, E.C., Davy, D.P. and Burr, B.
ESTs from developing cotton fiber
Unpublished

CONTACT: Ben Burr
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Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnl.bnl.gov
Seq primer: T3 Primer.

FEATURES
source

Location/Qualifiers

1. 622
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/issue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="X11-blue"
/clone_id="Six-day Cotton fiber"
/note="Vector: pBluescript II KS+"

BASE COUNT 160 a 116 c 137 g 209 t

ORIGIN

Query Match 17.9%; Score 263; DB 9; Length 622;
Best Local Similarity 65.0%; Pred. No. 3.4e-36;
Matches 405; Conservative 0; Mismatches 215; Indels 3; Gaps 1;

770 TGGCAGTTTTTGTAGCTTACAGACATGATTTTATCCGATTTGTAAGCTTAA 829
Db 3 TACAAGCTTTTATAGTATGATCAACATTTGACATTTTACCTGATGCTTTGCTAG 62
Qy 830 GCTCTATCTTTTATTTCTGCTTTTAAAGTGTTTCCACAAACAAAGGATATACA 889
Db 63 GATCAACCTATTTGCAACATCTATCTTGTGTTGTGTTGTTGTTGTTGTTGTTGTT 119
Qy 890 GAGAGCTAGAAATTTTAAAGCTATGACGTTTCTGACTGTTGATTTCTTACTCTTTC 949
Db 120 CAAGGCTCAAGAAATTTTGGGATTTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTT 179
Qy 950 TGGCTACCAATTTGCTGTAAGGCTGATGTTTCAAGTCTCTGTTTGAAGTCCCGG 1009
Db 180 TCTCTTACCTAATTTGTTAGCAAGATTAATGTTTGTGTTGTTGTTGTTGTTGTTGTT 239
Qy 1010 GTTCAACATTTGCAAGTTGATGATCACTTGTCTTATGTTTACACTGTTTGGC 1069

Db 240 TATCCAACTGTTCACTTCTGTTGAACCATTTCTCGTAGGTTTACGTGCGCCGCC 299
 QY 1070 TAGCGGTATGATGTTTTCACAGACAGACAAAGGCGACGCTCAATACAGCTTCTGC 1129
 Db 300 GAACGGGAATGATGTTTTCAGAAACAAACCGAGGAGCTTAAATATGTTGTTGCTC 359
 QY 1130 TTGTTGGGATGTTGTTTCATGTTGGGCTGTCACCTTCAGATTGAGCATCATCTGTTTCCAAG 1189
 Db 360 TTGGATGATGTTGTTTCTATGTTGGGTTTGCAATTCAGATTGAGCATCATCTGTTTCCAAG 419
 QY 1190 GATGCTTAAGTGCATTTGAGAAATCTCACCATTTGTAACAACTTTGCCAAGA 1249
 Db 420 GTTGCTAGGTGTCATTTAGGACAAATTCACCATTTGTTAAGAGTTGTTAAGAAACA 479
 QY 1250 TAATTGTTCTTGAAGTCTCAATGTTGGAGGCGCATTAATGTTATCTCCACCT 1309
 Db 480 CAATTGTTGTTTCAATGTTGCTTCTTTTGGAAAGCTAATGCAATGAGTGAACACT 539
 QY 1310 GCGTGTGTTGCTATGGAAGCTAAGATGTTACCAAGCCAGTTCCAGAAATGTTG 1369
 Db 540 TAAATAGCTGCTTCAAGCTTAGGTTCTTACCAATGCTGTTCCAAAAAATTTGGTGTG 599
 QY 1370 GGAAGCAATGAACACTTTCGGGT 1392
 Db 600 GGAAGCTGTCACACACATGGGT 622

RESULT 14
 A1729306 668 bp mRNA linear EST 11-JUN-1999
 LOCUS BNLG113080 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
 DEFINITION to (AF007561) delta 6-desaturase [Borago officinalis], mRNA
 sequence.

ACCESSION A1729306 GI:5048158
 VERSION A1729306
 KEYWORDS EST.
 SOURCE Gossypium hirsutum (upland cotton)
 ORGANISM Gossypium hirsutum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids
 1 (bases 1 to 668)

REFERENCE Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
 ESTs from developing cotton fiber

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished
 Contact: Ben Burr
 Biology Department
 Brookhaven National Laboratory
 Upton, NY 11973, USA
 Tel: 516-344-3396
 Fax: 516-344-3407
 Email: burr@bnl.bnl.gov

Seq primer: T3 Primer.
 Location/Qualifiers

FEATURES
 source 1..668

/organism="Gossypium hirsutum"
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 /lab_host="XLI-Blue"
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 /note="Vector: pBluescript II KS+."
 BASE COUNT 184 a 134 c 131 g 219 t
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Query Match 17.6%; Score 259.4; DB 9; Length 668;
 Best Local Similarity 65.8%; Pired. No. 1,4e-35;
 Matches 377; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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Db 89 TCATTGAGACATCAATGCGGATTCAGAAAGGGGTACATTTCCAAAACAGAGCTTGAACCC 148
 QY 94 ATTAGAACACAGAGATTTATGATCTCTATCAAGGAAAGATTATCATCTTCCAACT 153
 Db 149 AAAAAAACAATGATCTCTTGTGATCTCAATCAAGGCAAGATCTATGATGTAATCTCAAT 208
 QY 154 GGAATAAAGAGATCCCGGTGAGTGAAGCTCCATTTGTAATTTTGGCGGCAAGATGTA 213
 Db 209 GGAATGACCAACACCTGATGAGGCACTTCAATTAAGTCAACTCGCGGTCAAGAGCCCA 268
 QY 214 CTGATGCGTTATGTTCTTACATCTGAGCACTGCTTGGCAATACCTTGAACAGTTCTTA 273
 Db 269 CCGATGCTTTCATAGATTATCATCCGGCATATGCTTGGCAATATCTCGAAGTTCTTCA 328
 QY 274 CTGGGATCAAGTTCAAGATTCTCTGTTCTGAGATGTCAGAGACTACAGAGCTG 333
 Db 329 CTGGTATTAACCTTGAAGGTTACTTACTCTGATATATCCAAAGATTATAGAAAGCTAG 388
 QY 334 TCTGAGTTTCTTGAAGATGGGTTGTTCAAGACACAGGCAAGGGGCTACTGCTCAA 393
 Db 389 CTGTTGAGTTCTCAAGATGGGCTTTTGAACAGAAAGACATGGACATGATTATAC 448
 QY 394 TCTTTTCTGTTCTGTTGTTGCTGCTGAGTGTTCACGTTCTCTACTGCAAGACA 453
 Db 449 TTACATCATACATGCTGTTTCTGTTTCTGTTTCTGTTTATGTTTATGTTGACAAA 508
 QY 454 CCGGCTCATATTTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 513
 Db 509 CTGGGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 568
 QY 514 TGGGCAATGATCTTGTACCTACCAAGTATGCTTAACGCTAAGCTTATGCTTTTTC 573
 Db 569 TAGACATGATTCAGACATTAACCTGATCTCTAATAAACCCTCAACAGTTGCTC 628
 QY 574 AATCATTCAGAGAAATGATGTTGTTGTTA 606
 Db 629 AACTTCTTACAGGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 661

RESULT 15
 BQ281359 744 bp mRNA linear EST 13-MAY-2002
 LOCUS WHE3020_D06_H12ZS Wheat unexpressed seedling shoot normalized cDNA
 DEFINITION library Triticum aestivum cDNA clone WHE3020_D06_H12, mRNA
 sequence.

ACCESSION BQ281359 GI:20548798
 VERSION BQ281359
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 744)

REFERENCE Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 P.S., Hela, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
 Rauch, C.J., Seaton, C.H., Tong, J.C. and Zhang, D.

The structure and function of the expressed portion of the wheat
 genomes - Normalized shoot cDNA library

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

Email: oanderson@pw.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: SK primer.

FEATURES
 source 1..744
 Location/Qualifiers

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144 a      219 c      197 g      164 t
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/mol type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE3020 D06 H12"
/tissue type="Etiolated shoot"
/dev stage="Five day old seedling"
/lab_host="E. coli DH103"
/clone_lib="Wheat unstressed seedling shoot normalized
cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
phluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
"UJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give phluescript cDNA clones before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares'. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
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Query Match	17.5%	Score 257.4;	DB 13;	Length 744;
Best Local Similarity	60.2%;	Pred. No. 3e-35;		
Matches 445;	Conservative 0;	Mismatches 291;	Indels 3;	Gaps 1;

QY	512	GGTGGGGCATATCTTGTCTACACACGAAGTATAGCTCAACGGTAAGCTTAATCGCTTT	571
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QY	572	TCAATCATTTGCAGGAAATGTGATTGCTGTGTTAGTGTGATGGTGAAGTTGGACCA	631
Db	69	GCAGGTGGTCTCCGGGAATCGCTCACCGGCTGGCATCGCTGTGGAAAGTTCAACA	128
QY	632	TAAACCCCATACCTTTGCTGTGAATAGGCGCAATTGATCTGTATATTCAGACCTTCC	691
Db	129	CAACACACACCACTCTCTCCAAACAGCTCGAACATACCGGACCTTCAGACCTTCC	188
QY	692	TATATATGCCATATCCCAAAATTTTCAACCTCCCTCATCATATCTATATCAACATGCA	751
Db	189	GCTCTGGCGGTTTTCACCAAGCTTTCAACAACCTTTGGTGCGTCTGTACAGCGCAC	248
QY	752	AATGACCTATGATCGCGCTGCAGGTTTTTTGTATAGCTTTCAGACTGGAATTTATCC	811
Db	249	CTTGGCGTTTATGTCATATCAAGTTCTTGTCATGCTACAGACACTGGAATTTACCC	308
QY	812	TGCATTTGTAAGCCTTAGGCTCTATCTTTTATTTCTGTCTTTAAGGTGGTCTTCCAA	871
Db	309	GGTAGTGGAATTTGGACGATTAATCTTCTGTGCACTC--AATCGTGTCTCGATAC	365
QY	872	CAACAAAAGGTAATACAGAGAGTCAGGAATTTTAGGCTATGAGCTTCTTGACCTG	931
Db	366	GCAAAAGAGGTGGCGGACGCTGTGCTGAGATTCGCCGAGTTGGAGGTTCTGGGTTTG	425
QY	932	GTATTTCTTACTCTTTCTTCGCTTACCCAAATTTGGCTGAAAGGCTCATGTATTTGACCTC	991
Db	426	GTACCCCTGTGGTCTTCTTGCTGTCCGAATTTGGTGGAGAGGGTTGCTTTTGTCTTGC	485
QY	992	CTGTTTAGCAGTCGCGCGGCTTCCAATTTGGCAGTTTCAAGCTTGAATCACTTTGCTTAA	1051
Db	486	AAGCTTTGTATCAGGGGATTTACGATTTTCAGTTCTTGCTGCAACCACTTCTATCGC	545
QY	1052	TGTTTAACTGGTTTGCTTAGCGGTAAATGATTTGGTTTCAACGACGACAAAGGACGCT	1111
Db	546	TGTGTATGTTGGCCACCAAGAGGGAGACGACTGTTTGAAGGCAACAGCGGGCACT	605

QY 1112 CAACATACAGCTTCTCTCTGGTGGGATTTGATTCATGGTGGCTGGACATTTCAGATTGA 1171
 Db 606 TGATATTAAGTGTCTCCCGCTGGATGGATTTGGTTCCATGGTGGTGTGCAAGTTCCAGGTTGA 665
 QY 1172 GCATCATCTGTTTCCAGATGCTTAAGTGCACATTTCCAGGAAATCTACCCATTGTGAA 1231
 Db 666 ACACCATTTGTTTCTTGCTGTGCTGTGCTGCACATAAGATGGTCCGGCCGATTGTGCG 725
 QY 1232 CAACCTTTGCCAGAGCAT 1250
 Db 726 TGACCTTTGCCAGAGCAT 744

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559.4	38.0	1684	2	US-08-831-570-1 Sequence 1, Appl
2	559.4	38.0	1684	2	US-08-831-575-1 Sequence 1, Appl
3	559.4	38.0	1685	1	US-08-366-779-4 Sequence 4, Appl
4	559.4	38.0	1685	1	US-08-789-936-4 Sequence 4, Appl
5	559.4	38.0	1685	4	US-08-934-254-4 Sequence 26, Appl
6	377.8	25.7	1702	4	US-08-934-254-26 Sequence 4, Appl
7	122.6	8.3	291	4	US-09-313-294A-1966 Sequence 1966, Ap
8	93.4	6.3	266	4	US-09-313-294A-3256 Sequence 3256, Ap
9	58.6	4.0	1617	2	US-08-834-655-1 Sequence 1, Appl
10	58.6	4.0	1617	3	US-08-834-655-1 Sequence 1, Appl
11	58.6	4.0	1617	3	US-09-363-574-1 Sequence 1, Appl
12	58.6	4.0	1617	4	US-09-363-526-1 Sequence 1, Appl
13	57.4	3.9	1617	4	US-09-330-235-17 Sequence 17, Appl
14	57.4	3.9	449	4	US-09-439-261-38 Sequence 38, Appl
15	57.4	3.9	449	4	US-09-439-261-37 Sequence 37, Appl
16	57.4	3.9	655	4	US-09-439-261-3 Sequence 3, Appl
17	57.4	3.9	655	4	US-09-439-261-3 Sequence 3, Appl
18	57.4	3.9	864	4	US-09-439-261-12 Sequence 12, Appl
19	57.4	3.9	864	4	US-09-439-261-12 Sequence 13, Appl
20	57.4	3.9	1928	4	US-09-048-888-4 Sequence 4, Appl
21	55	3.7	2710	4	US-09-912-161-1 Sequence 1, Appl
22	54.2	3.7	473	4	US-09-439-261-37 Sequence 37, Appl
23	54.2	3.7	473	4	US-09-227-613-36 Sequence 36, Appl
24	54.2	3.7	1335	4	US-09-439-261-1 Sequence 1, Appl
25	54.2	3.7	1335	4	US-09-227-613-1 Sequence 1, Appl
26	49.2	3.3	1107	4	US-09-328-352-268 Sequence 268, App
27	48.8	3.3	1686	4	US-09-439-261-6 Sequence 6, Appl

28	48.8	3.3	1686	4	US-09-227-613-6 Sequence 6, Appl
29	48.8	3.3	1843	4	US-09-439-261-7 Sequence 7, Appl
30	48.8	3.3	1843	4	US-09-227-613-7 Sequence 7, Appl
31	48.8	3.3	2257	4	US-09-439-261-8 Sequence 8, Appl
32	48.8	3.3	2257	4	US-09-227-613-8 Sequence 8, Appl
33	48.4	3.3	7218	1	US-08-232-463-14 Sequence 14, Appl
34	43.6	3.0	1717	4	US-09-048-888-2 Sequence 2, Appl
35	42	2.9	347	4	US-09-702-705-355 Sequence 355, App
36	42	2.9	347	4	US-09-736-457-355 Sequence 355, App
37	38.2	2.6	295	4	US-09-313-294A-6637 Sequence 6637, Ap
38	35	2.4	1677	4	US-09-154-750A-74 Sequence 74, Appl
39	34.8	2.4	4350	4	US-09-295-593-37 Sequence 37, Appl
40	34.2	2.3	1884	1	US-08-307-382-3 Sequence 3, Appl
41	34.2	2.3	1884	1	US-08-366-779-3 Sequence 3, Appl
42	34.2	2.3	1884	1	US-08-478-727-3 Sequence 3, Appl
43	34.2	2.3	1884	1	US-08-473-508-3 Sequence 3, Appl
44	34.2	2.3	1884	1	US-08-789-936-3 Sequence 3, Appl
45	34.2	2.3	1884	4	US-08-934-254-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-831-570-1
Sequence 1, Application US/08831570
Patent No. 5959175
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,570
FILING DATE: 09-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 743-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1387
US-08-831-570-1
Query Match 38.0%; Score 559.4; DB 2; Length 1684;
Best Local Similarity 62.8%; Pred. No. 1.6e-164;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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QY 60 AAGAGACATTTGCAAGAGACCTTGCAAGCATAGCAACCAAGAGATTTATGATC 119
DB 58 AAGAAATACATTTCTAGATAGACTCAAGAACCAACATTAACCCGAGATCTATGATC 117
QY 120 TCTATCAAGGAAAGTTTACGATATCTCAAGTGACTAAAGACATCCCGGTGTGAG 179
DB 118 TCGATTCAGAGGAAAGCTATGATGTTTGGATGGGTGAAGACATCCAGGTCGAGC 177
QY 180 CTCGCATGTTAAGTTTGGCCGCAAGATGCTCATGCTGATCTGTTCCATCTT 239
DB 178 TTTCCCTTGAAGAGCTTGTGCTGCAAGAGTAACTGATGATTTGTTGATTCATCT 237
QY 240 GGCAGCTGCTGGCAATCTTGAAGAGTCTTACTGGTACTAGTTCAGTTCATCT 239
DB 238 GCCTCTACATGGAAGATCTTGAATTTTCACTGGGTATATCTTAAAGATTAATCT 237
QY 300 GTCTGAGATGTCAGAGACTACAGAAAGCTGCTCTGAGTTTCTAAAGATGGGTTG 359
DB 298 GTTCTGAGGTTTCTAAAGATTAAGAGAGCTTGTGATGTTTCTAAAGATGGGTTG 357
QY 360 TTCAAGACACAGGCAAGAGGCTCTACTGCTCAATCTTTTCGTGCTGTGTTGCT 419
DB 358 TATGACAAAAGGTCATATTAATTAATGTTGCAACTTTGCTTAAAGCAATGCTGTTGCT 417
QY 420 CTGAGTGTTCAGGCTGTTCTCTACTGCAAGAGACCTGGGCTCATCTTGTCTGTTG 479
DB 418 ATGAGTCTTATAGGGGTTTGTGTTGAGAGGCTTTTGTGATCATTTGTTTCTGGGTGT 477
QY 480 CTATGAGGATGCTATGCTCCAGAGTGTGGTGGGCAATGATCTTGTCTACTACAA 539
DB 478 TTGATGGGTTTCTTGGATTCAGAGGTGTTGATGGAATGATGCTGGGCAATTAATG 537
QY 540 GTATGCTTACCGTATGCTTAATGCTTTTCAATTCATGAGAAATGATGATGCT 539
DB 538 GTATGCTTATTCAGGCTTAATGATTAATGCTTAATGCTTAATGCTTAATGCTTAAT 537
QY 600 GGTGTTAGTGTGATGCTGGAAGTTGGAACCAATCAACCATCTTGTGCTGTAATAGC 659
DB 598 GGAATAGTATGTTGTTGTTGGAATGGAACCAATCAATCAATCAATGCTGTAATAGC 657
QY 660 GCCAATCTGATCTGATTAATCAAGACCTTCTAATTAATGCTCAATGCTCAATGCT 719
DB 658 CTGAATATGACCTGATTAATCAATATATATATATCTTGTGTTGCTTCAAGTTTCT 717
QY 720 AACTCCCTTATCATATCTATCAACATGCAAAATGATGCTGCTGCTGCTGCTGCT 779
DB 718 GGTTCACCTACCTCTCTATTAAGAAAGGTTGACTTTTGAATCTTATCAAGATTC 777
QY 780 TTTGTTAGCTTTCAGACTGGAATTTTATCTGCTGATTTGTAAGCTTGAAGCTTATCT 839
DB 778 TTTGTTAGTATCAACATTTGACATTTTACCTTATATGTTGCTGCTGCTGCTGCTGCT 837
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DB 838 TATGATCAATCTCTCAATATATGTTGTTGACCAAGAGAAAT--GTTGCTTATGAGTCAAG 894
QY 900 GAAATTTTAGGCTATGAGCTTTCTTACCTTGTGATTTCTACTCTCTTCTGCTGCTGCT 959
DB 895 GAACTTTTGAAGTCTGATGTTCTCTGATTTGTAACCGTGTGCTGTTTCTTGTGCTGCT 954
QY 960 AATTGCGCTGAAAGGCTATGATTTTACGTCCTGTTAGACGCGGGGTTCCAACT 1019
DB 955 AATTGGGGTGAAGAAATATGTTTGTATTTGCAAGTTTATCAAGTCAAGTGAAGTCAACAA 1014
QY 1020 TGGCAGTTCAAGTGAATCACTTGTCTTAATGTTTACATGCTGTTGCTGAGGATTAAT 1079
DB 1015 GTTCAGTTCCTTGAACCACTTCTTCAAGTGTATTAATGTTGAAGGCTTAAAGGAAAT 1074
QY 1080 GATTGTTTCAACAGACAGCAAGGCAAGGCTCAACATTAACAGCTTGTGCTGTTGAGGAT 1139
DB 1075 AATTGTTTGAAGAAACAAACGAGATGGGACATTTGCTGTTCTCTTGTGATGAT 1134

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QY 1140 TGGTTTACATGTTGCTGCTGCACTTTAGATTTGAGCATCATCTGTTTCCAAAGATGCTAAG 1199
DB 1135 TGGTTTCAATGTTGATTTGCAATTCAAATTTGAGCATCATTTGTTTCCAAAGATGCTAAG 1194
QY 1200 TGGCATTTCAGGAAATTTTCAACCATTTGTTGAAACAACTTTGCGAAGATTAATTTGTCC 1259
DB 1195 TGCACCTTAAGGAAATTTTCGCTGCTGATGATGATTTGCAAGAAACATTAATTTGCTT 1254
QY 1260 TATGAATGCTCACTCATGTTGGAGGCAATTAATGATTAATCTCAACCTGCTGCTGTTG 1319
DB 1255 TACATTTATGATCTTCTTCTTCCAAAGGCAATGAAATACACTGAAACATTTGAGGAACAA 1314
QY 1320 GCTATGAAGCTTAAGATGTTTACCAAGCCAGTTCCCAAGAACTGCTGGAAGCAATG 1379
DB 1315 GCATTCAGGCTATGAGATTAATACCAAGCCGCTCCGAAAGATTTGTTATGGGAAGCTCTT 1374
QY 1380 AACACTTTGGGGTGAACCTTAATTAACATCAAGTGTGCTTTCCGCTAAAGCTTCCAG 1439
DB 1375 CACACTCATGTTTAAATTAACCTTATGTTCAATGATTAATTTGAAGATTAATGATCTCTTA 1434
QY 1440 TCCCAATGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1469
DB 1435 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1464

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RESULT 2
US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 5977436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Li, Zhongren
; TITLE OF INVENTION: AN OLEOSIN 5' REGULATORY REGION FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; City: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,575
; FILING DATE: 09-Apr-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
; US-08-831-575-1
Query Match 38.0%; Score 559.4; DB 2; Length 1684;
Best Local Similarity 62.8%; Pred. No. 1,6e-164;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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QY	60	AAGAGC	ATTTGG	CAGCAG	ACCTTG	CAAGCA	GTAA	GCAAC	AGAGAT	TTTAT	GCAT	119									
Db	58	AAGAAAT	ATCATTA	CTCTCA	GTAACT	CAAGAC	CAAGAT	TAACCC	GGAGAT	CTAT	ATGATC	117									
QY	120	TCAT	CAAGG	AAAGTT	TAAGAT	ATCT	CAAGT	GAAGCT	TAAGAG	CAATCC	GGTGTAG	179									
Db	118	TCGAT	CAAGG	AAAGCT	TATGAT	GTTC	GGAT	TGGT	GAAGAA	GCAT	TCAGGTGG	177									
QY	180	CTCCAT	TGTAA	GTTTTGG	CCGCCA	AAATGT	CATGAT	TGCGTT	CATTGCT	TACAT	CTCT	239									
Db	178	TTTCC	TTGAAG	AGCTTG	CTGTG	TCMAAG	GTAACT	GTATG	CAATTTG	TGTGCA	ATTCATCT	237									
QY	240	GGCAT	CGTTGG	CAATAC	CTTGAC	AGTTCT	TTTACT	TGGGTACT	AGTTCA	AGATTA	CTCT	299									
Db	238	GCCCT	CAATG	GAAGAA	ACTTGTA	AGTTTTC	ACTGGGTAT	TATCTT	TAAGATTA	CTACT		297									
QY	300	GTC	TGAGAT	GTCC	AGACT	CAAGAA	GGCTCG	CTCGAT	TTTCT	TAAGATGG	TTTG	359									
Db	298	GTTC	TGAGGT	TTCT	AAAGAT	TTAT	TGGAAG	CTGTGT	TGATTTCT	TAAT	TGGTTTG	357									
QY	360	TTCA	AGAC	CAC	AGGGA	GGGTCA	CTGCTCA	ACCTTTTC	CGTGT	CTGTGT	TCCT	419									
Db	358	TATG	CAAAAA	AGGTCA	TATAT	GTTC	CAACTT	TGTCTT	TAATG	CAATGCT	TTTCT	417									
QY	420	CTGAG	GTTTAC	GGGTCT	CTACT	GC	CAAGAC	ACTGGG	CTCAT	CTTGTG	CTGTG	479									
Db	418	ATGAG	GTTTAT	GGGGTTT	TGTTTGT	GAGGGT	GTGTTT	GTGAT	CAATTTG	TTTCT	GGGTGT	477									
QY	480	CTAT	TGGGTA	TGCTAT	TGGCTC	CAAGTGT	TGGGTGGG	GCATGAT	CTTGTG	CACTAC	CA	539									
Db	478	TTGAT	TGGGGT	TTCTT	TGATTC	CAAGTGT	TGGAT	TGGAAT	GAATG	AGCTGG	CACTAT	537									
QY	540	GTTAT	TGCTTA	CCGTA	ATCAAT	TCGTCT	TTTTC	CAATCAT	TGCG	AGAAATG	ATGATCT	599									
Db	538	GTA	GTGCTG	ATTC	CAAGCT	TAT	TAAGTTAT	TGGGTA	TTTTTGT	CTGCAAA	TTGTCTT	CA	597								
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Db	598	GGAAT	TAAGTAT	TGGTTG	TGTG	GAAT	TGGAAC	CAAT	TAATG	CAATCAT	GATGCT	GT	TAATG	657							
QY	660	GCAAT	CTG	ATCC	GTAT	TTCAG	ACCTTCC	TATAT	TGCAAT	TCC	CAAAATTT	TC	719								
Db	658	CTTGA	ATATG	ACCTTG	ATTTAC	ATAT	TACCAT	CTTGTTG	TGTCTT	CAAGTT	TTTT		717								
QY	720	AAT	CCCTT	CAT	CAT	ATAT	CA	CACTG	CAAAATG	ACTAT	TGATCG	CGCTCC	AGTTT	779							
Db	718	GAT	CACTCA	CTCT	CATTTCT	AT	GAAAA	GGTGA	CTTTTGA	CTCT	TAT	CAAGAT	TTT	777							
QY	780	TTT	GTAG	CTTT	CAG	CACTG	CAATTTTAT	CTGTG	ATGTTA	GGCTT	AGGCT	CTAT	CTT	839							
Db	778	TTT	TAAGT	AT	CAACAT	TGGA	CAATTTTAT	ACCTTAT	TATG	TGTG	CTG	CAAGCT	CAAT	837							
QY	840	TTT	ATTC	GTCTTT	TAA	GTGTGTTT	TTTCA	CAACAA	AAAGG	GTAT	CAAGAA	GTG	AG	899							
Db	838	TAT	GTAC	AAATCT	CTCAT	ATATG	TGTGTG	ACAA	GAABAAT	---	GTGTCT	TA	GTAG	894							
QY	900	GAA	ATTTT	TAG	CTATG	CAGCTTTCT	TGA	CTTGT	TAATCT	CTACT	CTTCTG	CCCTA	CCC	959							
Db	895	GAC	CTCTG	GAATG	CTGAT	GTCTG	ATTTG	GTATCC	GGTCTG	TTGTTCT	TGTTG	TCCT		954							
QY	960	AAT	TGG	CCCTGA	AGG	GTAT	TTTCA	GTCTG	TCCTT	TGAG	CA	GTCCG	GGGT	CAAT	1019						
Db	955	AAT	TGGG	GTGA	AAAT	ATAT	GTGTTT	TTTGA	CAATTA	CTGAT	CACTG	GAATG	CA	CA	1014						
QY	1020	TGG	AGTT	CAGCT	TGAAT	CATTG	CTCT	TAT	GTTTTAC	CTG	GT	TTTGC	CT	TAG	CGTAT	1079					
Db	1015	GTT	CA	GTCTCT	CTTGA	CACTTCT	CTTCA	GTGTTT	AT	TG	GAAG	CCCTA	AA	GG	GAAT	1074					
QY	1080	GAT	TG	GTCTT	CA	CAAGCA	AAAGG	GCCT	CA	CAAT	TA	CAAGCT	CTT	GT	CTT	GGT	1139				
Db	1075	AAT	TG	GT	TTTGA	AA	CAAG	ATG	TGGA	CACT	TG	CAATTTCT	TT	GT	CT	CT	TTG	AT	GT	AT	1134

Qy	1140	TGGTTTCATGATGGCCGTCGACCTTTCACATTTAGAGCATCATCTGTTCCTCCAGGATGCTTAAG	1159
Db	1135	TGGTTTCATGATGGATTTGCATTTCCAAATTGAGACATATTGTGTTCCCAAGATGCTTGA	1154
Qy	1200	TGCCATTTTCAGGAAATATCTACCCATTTGTGACCAACTTTGCCAGAAACATAAATTTGTCC	1258
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Qy	1320	GCTATGGAAGCTAAGATGTTTACCAAGCCAGTTCCTCCAGAACATGTGCTGGGAAGCATATG	1379
Db	1315	GCATTTGACGGCTAGGGATATPAAACCAGCCGCTCCGAGAAATTTGTATGGGAAGCTCTT	1374
Qy	1380	AACACTTTGGGGTGAACCTTATNAAACATGAGTGCCTTTCCGTAAPAAAGTTCCAG	1439
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Qy	1440	TCCCAATGTTCTTTTTTTTTTTTTTTTTTT	1469
Db	1435	TGTTTGTCGTCCTGTCTTGTTCTTACTTGTT	1464

RESULT 3

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US-08-366-779-4
Sequence 4, Application US/08366779
Patent No. 5614393
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nucchio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Numbers, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 80C
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZVXX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-366-779-4
Query Match 38.0%; Score 559.4, DB 1, Length 1685
Best Local Similarity 62.8%; Pred. No. 1,6e-164;

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Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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QY 60 AAGAGACATTTGCGAAGACGCTGCAAGACATAGACACGAGATTTATGATC 119
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Db 59 AAGAAATACATTTACGATGAGTCAAGACACGATTAACCGAGATCTATGATC 118
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QY 120 TCTATCAAGGAAAGTTTACATATCTCAAGTGAATGAAGACATCCGGTGTGAG 179
   |||||
Db 119 TCGATTAAGGAAAGCTATGATGTTGGATTTGGATGAAGACATCCAGGTGGAGC 178
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QY 180 CTCCTCATTTGATAGTTTCCCGGCAAGATGCTCATGATGCTTATGCTTACATCT 239
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QY 240 GGCATGCTTGGCAATCTTGAAGGTTCTTACTGGTATCTAGTCAAGATTAATCT 299
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Db 1076 AATTGTTTAAAGAAACAAAGGATGAGCACTTGAATTTCTTCTCTGCTGATGAT 1135

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Db 1136 TGGTTTCATGTTGAGATTTGATTCATTTCCAAATTTGATGATCTTTTCCAGATGCTTAA 1195
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QY 1200 TGGCATTTCAGAAAATCTGACCATTTGTGAAACAACTTTGCGAAGATTAATTTGCTC 1259
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QY 1260 TATGAAATGCTTACATGTTGAGGAGCCATTAATATGATATCTTCCACCTGCTGCTG 1319
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Db 1256 TACAAATTTGATCTTTCTTCCAGGCGCAATGAATGACCTGCAACATTTGAGAACACA 1315
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QY 1320 GCTATGAGCTTAAAGATGTTTACCAAGCCAGTTCACCAAGACATGCTGCGAAGCAATG 1379
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Db 1316 GCAATGACGCTTGGATATTAACCAAGCCGCTCCGAAAGATTTGATGAGAGCTTCT 1375
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QY 1380 AACACTTTCGGGTGAACCTTATTAACATCACTGCTGCTTCTCCGTAAGACCTTCCAG 1439
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Db 1376 CACACTCATGTTAAATTAACCTTATGATGATGATGATGATGATGATGATGATGATGAT 1435
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QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1469
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Db 1436 TGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465
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RESULT 4
US-08-789-936-4
Sequence 4, Application US/08789936
Patent No. 5789220
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Arvut S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysalnet, Georges L.
APPLICANT: Nuberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789, 936
CLASSIFICATION: 435
FILING DATE: 28-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/366, 779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXX
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-789-936-4

Query Match 38.0%; Score 559.4; DB 1; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 1.6e-164;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

60 AAGAACACATTTGCGACAGACCTTGCAGACATTAAGCAACAGAGATTATGATC 119
 59 AAGAAATACATTACCTCAGATGAGATCAAGAACCAAGATTAACCCGAGATCTATGATC 118
 120 TCTATCAAGGAAAGATTATGATATCTCCAGATGAGACTTAAGAGATCCCGGTGAG 179
 119 TCCATTCAGAGGAAAGCCATATGATGTTGGATTGGATGAAGACCATCAGGTGGCAG 178
 180 CTCCTCATTTGATTTTGGCCGCAAGATGTCATGATGCTTATGCTTATGCTTATCCT 239
 179 TTTCCCTTGAAGGCTTCTGCTGCAAGAGTAACTGATGCTTTGTCATTCACCT 238
 240 GGCATGCTTGGCAATACCTTGCAGAGTCTTACTGAGTACGTTCAAGTTCACTCT 299
 239 GCCTTACATGAGAAATCTTGATTAAGTTTTCATGCGGATATATCTTAAAGATTACTCT 298
 300 GTCTCTGAGATGTCAGAGACTTACAGAGGCTGCTCTGAGTTTCTAAGATGGGTTTG 359
 299 GTTCTGAGGTTCTTAAAGATATAGGAAGCTTGTTGAGTTTCTAAATGGGTTTG 358
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 420 CTGAGTGTATGAGGTTCTCTCTACAGAGACCCGCGGCTGCTGCTGCTGTTG 479
 419 ATGAGTGTATGAGGTTTGTGTTGAGGCTGTTTGTGATACATTTGTTTCTGAGTGT 478
 480 CTAAAGGATATGCTATGCTCCAGAGTGTGGGTGGGAGATCTTGTCTACCA 539
 479 TTGATGCGGTTCTTGGATTCAGAGTGTGATTTGAGATGATGCTGGGCTTATATAG 538
 540 GTTATGCCATACCGTAACTTAATGCTTTTTCAAATCATTCAGAGAAATGATGCT 599
 539 GTAGTCTGATTCAGAGGCTTAAATGATTTATGGGATATTTGCTCAAAATGCTCTTGA 598
 600 GGATGATGCTGATGCTAGTGGAGTGGACATTAACCCATCTTGTGCTGATATAG 659
 599 GGAATATAGTATGCTGTTGGGAAATGGAACATTAATGACATATGCTGCTGAATAGC 658
 660 GCCAATCTGATCTGATATTCAGACCTTCTATATGCTCAATGCCCAAAATTTTC 719
 659 CTGAATATAGACCTGATTTACAAATATATACATTCCTGTTGTGTCTTCAAGTTTTC 718
 720 AACTCCCTTACATCACTACTCAACTGCAAAATGACTATGATGCGCTGCCAGTTT 779
 719 GGTTCACACCTCTCATTTCTATGAGAAAGTTGACTTTGACTTTATCAAGATTTC 778
 780 TTTGATGCTTACAGACCTGACATTTTATCCGATGTTAGCGTTAGCGCTATCTT 839
 779 TTTGATGATTAACAATGAGAAATTTTACCTATATGTTGCTCTAGGCTCAATATAG 838
 840 TTTATCTGCTTTTAAAGTGTGTTTTCACAAACAAAGGATATATACAGAACTAG 899
 839 TATGTCATCTCTCATATATGTTTGGACCAAGAAAT---CTGTCTATGAGTCTAG 895
 900 GAAATTTTAAAGCTTATGAGCTTCTGATGTTGATTTCTACTCTTCTGCTTACCC 959
 896 GAACTCTGGAGAGCTAGTGTCTGATTTGTTGACCCGTTGCTTCTTCTGTTGCTCT 955
 960 AATTGCGTGAAGGATATGATTTTCAAGTCTGTTAGCACTGCCGCTTCAACAT 1019
 956 AATTGGGGTGAAGAAATATGTTTGTATTTGCAAGTTTATCACTGATGCAAGATGCAACA 1015
 1020 TGGCAGTTACGCTTGAATCACTTGTCTTAAATGTTTACACTGTTGCTTACGCTGATAT 1079
 1016 GTTCAAGTTTCTCTTGAACCACTTCTCTCAAGTGTATATGTTGAAAGCTTAAAGGAAT 1075

QY 1080 GATGTTTACCAGACAGCAAGGGCAAGCTTCAATATACAGCTTGTGTTGGGAT 1139
 DB 1076 AATGGTTTGAACAACAAAGGATGAGACCTTGACATTTCTTCTCTTGATGAT 1135
 QY 1140 TGGTTTACATGCTGCTGCTGCTTTCAGATTTGATGATCATCTGTTTCCAGAGATGCTTAA 1199
 DB 1136 TGGTTTACATGCTGCTGCTGCTTTCAGATTTGATGATCATCTGTTTCCAGAGATGCTTAA 1195
 QY 1200 TGGCATTGAGAAATCTTCACTTGTGAACAACTTTGCGAGAGATATTTGCTC 1259
 DB 1196 TGCACCTTGAAGAAATCTGCTTACAGATGATGATGATGATGATGATGATGATGAT 1255
 QY 1260 TATGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1319
 DB 1256 TACATTTATGATCTTCTTCTTCCAGGCAATGATGATGATGATGATGATGATGATGAT 1315
 QY 1320 GCTATGAGCTTAAAGATTTTACCAAGCAAGTTCACCAAGATGCTGAGAGCAATG 1379
 DB 1316 GCATTTGAGGCTTAAAGATTTTACCAAGCGCTCCGAGAAATTTGATGAGAGCTT 1375
 QY 1380 AACCTTGGGTGAACCTTATMAACATCAAGTCTGTTCCGTAAGACTTCCAG 1439
 DB 1376 CACACTCATGTTAAATTAACCTTATGATGATGATGATGATGATGATGATGATGAT 1435
 QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1469
 DB 1436 TGTGTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465

RESULT 5
 US-08-934-254-4
 ; Sequence 4, Application US/08934254
 ; Patent No. 6355861

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

TITLE OF INVENTION: DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,254

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 8363ZYXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1685 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-934-254-4
 Query Match 38.0%; Score 559.4; DB 4; Length 1685;

Best Local Similarity 62.8%; Pred. No. 1,66-164;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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QY 60 AAGAGACATTTTCGACGAGACCTTGCAGAAATAGACACAGAGATTTATGATC 119
DB 59 AAGAAATACATTTACCTGATGAACTGAAACACAGATTAACCCGAGATCTATGATC 118
QY 120 TCTATCAAGGGAAGATTTACATATCTCCAAAGTGAATAAGAGATCCCGGTGTGAG 179
DB 119 TCGATTCAGAGGAAGAGCTATGATGTTTGGATTTGGGTGAAGAGCATCCAGGTGGAGC 178
QY 180 CTCCATTTGTTAAGTTTTCGCGCAAGATGCTAGATGCGTTCATGCTTACATCT 239
DB 179 TTTCCTTGAAGAGCTGTGCTGCTCAAGAGGTAATGATGATTTGTTGATTCATCT 238
QY 240 GGACATCTTGGCAATCTTGAAGATCTTCTTGAAGTCTGATCTTCAAGATTTACT 299
DB 239 GCTCTACATGGAAGATCTTGAATGATTTTCACTGGATATATCTTAAAGATTTACT 298
QY 300 GTCCTGAGATGTCAGAGACTAGACAGAGCTGCTCTGAGTTTCTAAGATGGATTG 359
DB 299 GTTCTGAGATTTCTAAGATTTAAGAGATTTGATGATTTTCTAAGATGGATTG 358
QY 360 TTCAAGACACGAGCAAGGGGCTACTGCTCAATCTTTTCTGCTGTGTGTGCT 419
DB 359 TATGACAAAAAGGCTCATATATGTTGCAACTTTGCTTATAGCAATGCTGTGCT 418
QY 420 CTGAGTGTTTTACGGGTCTCTACTGCAAGACACCTGGGCTACTTGTCTGTGTTG 479
DB 419 ATGAGTGTTTTATGGGGTGTGTGTGTGAGGGTCTTTTGTGCAATTTGTTTCTGGGTGT 478
QY 480 CTATAGGATGATGCTATGAGCTCCAGAGTGTGTGGGTGAGGATGATCTTGTACTACAA 539
DB 479 TTGATGGGGTTCCTTGTGATTCAGATGTTGATGATGATGATGATGATGATGATG 538
QY 540 GTTATGCTTAAACGTAAGCTTAACTGCTTTTCAATTCATGAGAAATGATGATGCT 599
DB 539 GTAGTGTCTGATTCAGAGCTTAAATGATTTATGGGTATTTTGTGCAAAATGCTTTCA 598
QY 600 GGTGTGATGTTGATGATGAGTGAAGTGAACATTAACACCATCTTGTCTGTAAATG 659
DB 599 GGAATAGATGATGATGATGAGTGAAGTGAACATTAACATCAATGCTGTAAATG 658
QY 660 GCAATCTGATCTGATATCTGATCAGACCTTCTAATTTGATGATGATGATGATGAT 719
DB 659 CTGATATATGATCTGATATCTGATCAGATTTCTGATGATGATGATGATGATGAT 718
QY 720 AACTGCTTACATGATCTATGACACTGCAAAATGATGATGATGATGATGATGATG 779
DB 719 GGTCTACTACCTCTCATTTCTATGAGAAAGTGAATTTGATGATGATGATGATGAT 778
QY 780 TTTGTAGCTTTGAGCACTGAGACATTTATCTGATGATGATGATGATGATGATGAT 839
DB 779 TTTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 838
QY 840 TTTATCTGCTTTTAAAGTGTGTTTCCAAACAAAGGATATCAAGAGATGATGATG 899
DB 839 TATGTACATCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
QY 900 GAAATTTTAAAGCTATGAGCTTTTGAATGATGATGATGATGATGATGATGATGAT 959
DB 896 GAACTCTTGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 955
QY 960 AATTGGCTTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
DB 956 AATTGGGATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
QY 1020 TGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1079
DB 1016 GTTCAATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1075
QY 1080 GATTGTTTCAAGACAGAAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1139

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DB 1076 AATTGTTGAGAAACAAACGATGGACATTTGATCTTGTCTCTGATGATGAT 1135
QY 1140 TGGTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1199
DB 1136 TGGTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195
QY 1200 TGGCATTTGAGAAATCTCAACCATTTGATGATGATGATGATGATGATGATGATG 1259
DB 1196 TGCATCTTGAAGAAATCTCGCCCTGATGATGATGATGATGATGATGATGATGATG 1255
QY 1260 TATGAATGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1319
DB 1256 TACAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1315
QY 1320 GCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1379
DB 1316 GATTCAGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1375
QY 1380 AACATTTGCGGTGAACCTTATTAACATCAAGTGTCTTCCGTAAGATTTCCAG 1439
DB 1376 CACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1435
QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1469
DB 1436 TGTGTGTCTTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGT 1465

```

RESULT 6
US-08-934-254-26
Sequence 26, Application US/08934254
Patent No. 6355861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406

US-08-934-254-26

Query Match 25.7%; Score 377.8; DB 4; Length 1702;
 Best Local Similarity 57.6%; Pred. No. 8.9e-108;
 Matches 717; Conservative 0; Mismatches 522; Indels 6; Gaps 2;

50 GGAGAGCCAAAGACATTTTCGACAGACCTTGCAGAACATTAAGCAACAGAGAG 109
 53 GGGCGAAGCTAGAGATATATACGGGGAGAGACTCCGGCCACACAGAGTCCGGCA 112
 110 TTTATGATCTCTATCAAGGAGAAAGTTTACATCTTCCAGTGAAGTAAAGCATCC 169
 113 TCTCTGATCTCCATCCAGGGCAAGGTTCTACGACTCTCGGTGGGGCGGAGACCC 172
 170 CGGTGTGAGCTCCCATTTGTTAGTTTTCGGGCGCAAGATGATGATGCTTCAATTC 229
 173 CGGGCGAGAGTCCCTCTCTCAGTCTGGGGCGGAGAGTACCGACGCTTCAATTC 232
 230 TTACATCTGAGCTGCTTGGCAATCTTGAAGGTTCTTACTG---GTAATACGT 286
 233 GATACACCGGGGACGGCGTGGGCGATCTGATCCGCTTTACCGGCTACTACTACT 292
 287 TCAAGATTAATCTGCTCTGAGATGTCAGAGACTACAGAGGCTGCTCTGAGTTTC 346
 293 CAAGGATTCGAAGTTCGAGATCTCAAGGACTACCGAGGCTTTGAACGAGATGTC 352
 347 TAAGATGGTGTGTAAGACACAGGCAAGGGGTCTACTGCTCAATCTTTTCGTC 406
 353 GCGGTCGGGATTTGAGAGAGAGGCGCCACATCATGTGAGCTTCTCGGCGTTGC 412
 407 TGTGTTGCTGCTAGTGTGTACAGGTGTTCTCTACTGCAAGAGACCTGGGCTCATCT 466
 413 GGTCAATGATGGCGGCAATCTCTACGCGCTGCTGGGCTGGAGTCCGCGAGTTACAT 472
 467 TGTCTGTGTTGCTATAGGATGCTATGCTTCAAGAGTGTGGGTGGGCGATATTC 526
 473 GCTCTCGGGGCACTCTGCTGGGCTTGTGATGATCAAGCGGCTATGTGGGCGATATTC 532
 527 TGTCTACTACAGATTAATGCTTAACGTAAGCTTAATGCTTTTCAATCATTTGAG 586
 533 CGGCGATTCAGAGTATGCAACCGGTGATCAACAGATACCGCACTCTACACAG 592
 587 AATGATGTTGCTGTTAGTGTGATGCTATGCTTCAAGAGTGTGGGTGGGCGATATTC 646
 593 CAACATCTTAACCGGATACGATCGGCTGTGAGAGTGGAGCCACACACACACCT 652
 647 TGTCTTAATAGCGCAATCTGATCTGATATTCAGACCTTCTTAATATTTGCAATATC 706
 653 CGCTGCAACAGCTCTGATAGAACCCGACCTCCAGCAATCCGCTATTTGCGCTTC 712
 707 CCCAAATTTTCACTCCCTTACATCATATCAACACTGCAAAATGACTATGATCG 766
 713 CACCCGACTTTCATCTCATCTCAGCTGCTTCTATGCGCGAGTCCGTAATTCAGCA 772
 767 CGCTGCAAGTTTGTGATGCTTTCAGACCTGCAATTTATCTGCAATGTTAGCGT 826
 773 AGTGGACGCTTCTATGCTACGACGACGACTGACCTACTACCGCTCATGATCTTCG 832
 827 TAGGCTATCTTTTATCTGCTTCTTAAAGTGTGTTTCCAAACAAAGGATATA 886
 833 CGAGTCAACCTTCTATCAGACCTTTTATGCTCTCAGACAGGCGGA---CGTCC 889
 887 CAAGAGAGTCAAGAAATTTTAGGCTATGAGCTTTCTGACTTGTATTTCTACTCT 946
 890 TGACCGGCTTAACTATAGGATCGGCTTCTGAGCTGTCTCCGCTCTTCGT 949
 947 TTTGCGCTAACCAATTTGCTGAAGGCTCATGATTTTCAAGCTCTGTTTACAGTCG 1006
 950 ATCTTGTCTCCGAACTGGCTTAAAGGTTTGGGTTGCTCTCATGACCTTTCGGTCA 1009
 1007 CGGATTCACATGAGCTGATGCTTGAATCACTTGTCTTAAATGTTTACAGTGTTC 1066
 1010 GGGGATTCAGCACTGCTCACTTCACTGCTCAACCACTTCTCGGGGAGCAATAGCTGG 1069

1067 GCCTAGCGGTATGATGTTGTTTACACGAGAGCAAAAGGCGACGCTCAACATACAGCTTC 1126
 1070 CCCAAGGGCGCAACTGTTTGAAGAGAGAGCAAGAGGAGATGATATACGTCGCC 1129
 1127 TGTGTGGGATTTGTTTCAATGTTGCTGCTGCACTTTCAGATGAGCATATCTGTTTC 1186
 1130 ACCGTGATGAGCTGTTTCTTTGTTGGGCTGCGAGTTCCAGTTGAGACACACTTGTCC 1189
 1187 AAGATGCTTAAGTGCATTTTACAGAAATCTACCCATTTGTAACAACTTTGCCAGAA 1246
 1190 TAGGCTCCGCGTGGGCACTTGAAGAGATTCGCGCTTGGCTGGGACTTGTGAAGA 1249
 1247 GCATATATTTGCTCTAAGAACTGCTACATGTTGGAGGCGCAATTA 1291
 1250 GACGGGATCCGTATAGAGCTTCGGGTTTGGAGCGACGCTTA 1294

RESULT 7

US-09-313-294A-1966
 ; Sequence 1966; Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalquid, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OR INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1966
 ; LENGTH: 291
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
 ; LOCATION: 256
 ; OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-1966

Query Match 8.3%; Score 122.6; DB 4; Length 291;
 Best Local Similarity 65.3%; Pred. No. 1.8e-28;
 Matches 179; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

940 TACTCTTTCTGCGCTACCCCAATGCGCTGAAAGGCTCATATTTACAGCTCTGTTAG 999
 7 TGTGTGCTTCTGCTGCTGCGGAAATGTTGGAGAGGCTCGGTTGTCTTTACGCTCA 66
 1000 CAGTCCGCGGTTTCCAACTTGGCAGTTGATGATCACTTGTCTTAAATGTTTACA 1059
 67 CCATGCGGGGATTTAGACAGCTGCAATTTGCTGTAACACTTCTGTCGAGCTATAG 126
 1060 CTGTTGCTTACCGGTAATGATGTTTCCACGAGCAAAAGGCGACGCTCAACATTA 1119
 127 TGGGGCAACCAAGGCAATGACTGTTTGAAGAGAGAGCGGAGGACGCTGACATCC 186
 1120 CAGCTTCTGCTGTTGGGATGTTTCAATGTTGCTGCTGATTTGATTTGATGATC 1179
 187 TGTGCTCTCTGATGATGATGTTTCAAGGCTGAGCTTCCAGATTGAGACCATTC 246
 1180 TGTTCACAGATGCTTAAGTCCATTTTCAGGA 1213
 247 TGTTCCTCCNCTACTAGTGCACCTCCGTA 280

RESULT 8

US-09-313-294A-3256
 ; Sequence 3256; Application US/09313294A
 ; Patent No. 6476212


```

? REFERENCE/DOCKET NUMBER: CGAB-201 USA
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 433-4150
? TELEFAX: (415) 433-8716
? TELEX: N/A
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1617 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: other nucleic acid
US-09-363-526-1

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Query Match	4.0%	Score 58.6	DB 4	Length 1617
Best Local Similarity	52.2%	Pred. No. 4.8e-08		
Matches 130	Conservative	0	Mismatches 119	Indels 0
			Gaps	0

[illegible]

```

RESULT 13
US-09-330-235-17
Sequence 17, Application US/09330235
Patent No. 6459018
GENERAL INFORMATION:
APPLICANT: Knutzon, Debbie
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
FILE REFERENCE: MOCO.156.00US
CURRENT APPLICATION NUMBER: US/09/330,235
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 1617
TYPE: DNA
ORGANISM: Mortierella alpina
US-09-330-235-17

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Query Match	4.0%	Score 58.6	DB 4	Length 1617
Best Local Similarity	52.2%	Pred. No.	4.8e-08	
Matches 130	Conservative	0	Mismatches 119	Indels 0
				Gaps 0

QY	453	ACCGGGCTATCTTTGGCTGTTGGTATGAGGTATGGCTCAAGAGTGTTGG	512
Db	518	ACCTCCCAACGTCGCTCGCGCTTTGGGTCGTCTCGACAGTCGCGAATGG	577
QY	513	GTGGGCGATGATCTTGTGCTACCAAGTATAGCTTAACCGTAACTTAATGCTTTT	572
Db	578	TTGGCTACGCACTTTTGGATCACCAGGCTCTTCAGAGCCGTTTCTGGGGTGATCTTTTC	637
QY	573	CAATCATTTGAGGAATGTGATTCGTGCTTAAGTGTGATGGTGAAGTTGGACAT	632

Db	638	GGCGCCTCTTGGGAGAGTGTCTGCACGAGGCTCTGTCTCTCTGTGGGAAAGACAAGCAC	637
Qy	633	AAACCCATCATTTTGCCTGTATATAGCGCAATCTGATCTGTATTTGACACCTTCT	632
Db	698	AACACTCACCAAGCGGCCCCCAACACTCCAGCGCAGAGATCCGACATTTCACACCACCT	757
Qy	693	ATAATGGC	701
Db	758	CTGTTGACC	766

```

RESULT 14
US-09-439-261-38
Sequence 38. Application US/09439261
Patent No. 6428990
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardeep
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-sheng
TITLE OR INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.P2
CURRENT APPLICATION NUMBER: US/09/439,261
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(5)
OTHER INFORMATION: k = g or t/u at position 5
NAME/KEY: misc_feature
LOCATION: (6)..(6)
OTHER INFORMATION: m = a or c at position 6
US-09-439-261-38

```

Query Match	3.9%	Score	57.4	DB 4	Length	445	
Best Local Similarity	58.5%	Pred. No.	5.4e-08				
Matches 100, Conservative	0	Mismatches	71	Indels	0	Gaps	0

QY	1080	GATTGGTTTACCAAGCAGACAAAGGGACGGCTCAATAGAGCTTGGCTTGGGGAT	113
	167	GACTGGGGTTTCCACCCAGCTCAGGGCCATGCAATGTGCACAGCTTCCTTCAATGAC	226
Db	1140	TGGTTTCATGGTGGCCCTGCACCTTTCAGATTGAGCATCATCTGTTTCCAGATGCGCTAAG	119
QY	227	TGGTCTAGTGACACCTTCACCTTCAGATTGAGCCATCTTTTTCACAGATGCTCGA	286
Db	1200	TGCAATTTCAGGAATCTCACCATTTGTGAACAACTTGGCAGAGCAT	1250
QY	287	CACAAATTACCAAGATGGCTCCCTCGTGTGCAGTCTTGTGTGCCAAGCAT	337

RESULT 15
US-09-227-613--37
Sequence 37, Application US/09227613A
Patent No. 6432684
GENERAL INFORMATION:
APPLICANT: MUKERJI, Pradip
APPLICANT: LEONARD, Amanda E.
APPLICANT: HUANG, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295, US, P1
CURRENT APPLICATION NUMBER: US/09/227,613A


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Db      79 GCGATTCAAGGAGGCTACAAAGCTCCGATTGGATTAAATCATCCCGAGGCGAC 138
Qy      180 CTCACATTTAGTTAGTTTGGCCGCAAGATGTCATGATCGCTTCAATTCCTTACCT 239
Db      139 ACGGATATCTCAATCTCGTGGTCAAGAGCTACCGATGCTTTCATCGATTTTCAATCC 198
Qy      240 GGCACCTGTTGGCAATACCTTGGACAGTCTTCTTACTAGGCTAGCTTCAAGATTAATCT 299
Db      199 GGAACCGCTTGGACACATCTCGACATCTTCAACCGGTTACACATCAGAGATTTCCAA 258
Qy      300 GTCTCTGAGATGTCAGAGACTACAGAAAGCTGCTCTGAGTTTCTTAAGATGGGTTTG 359
Db      259 GTCTCCGAGATCTACGCGATTTACCGTGTATGGCTGCGAGTTTGTAACTCGGCTTC 318
Qy      360 TTCAAGACACAGGCAAGGGGCTACTGCTCATCTTTTCTGCTGTGTTGTTGCT 419
Db      319 TTGCAAAACAAAGGTCACGTTACTCTTACACTTACGCTTCCGCGCAAGTTCTTC 378
Qy      420 CTGAGTGTTTAGGCTTCTCTACTGCAAGAGCAGCTGGGCTCATCTTGTCTGTTTG 479
Db      379 GGAATCTCTACGCTGTTTGGCTGTACTCCGCTTCTGCTTCAACAAATCGCCGCGG 438
Qy      480 CTAAATGGTATGCTATGCTCCAGAGTGTGGTGGGCGATGATTTCTGTCACTACCA 539
Db      439 CTCTCGGCTCTCTCTGATCCAGAGCGCTTACATAGTTCAGATTTCTGCTATTAAGT 498
Qy      540 GTTATGCTTACCGCTAGCTTAATGCTCTTTTCAATCATTCAGAGAAATGATGCT 599
Db      499 ATCATGTGCAACAAATCTTATTAACAATTCGCTACACTTCTCCGCTAATGCTCAC 558
Qy      600 GGTGTTAGTGTGATGATGGAAGTGGACATTAACACCATCTTGTGCTTAAATAG 659
Db      559 GGAATCTCAATGCGGTGGTGGAAATGACTCACAAATGCTCATATCTAGCTTGAACAG 618
Qy      660 GCCAATCTGATCTGATATTCAGACCTTCTTAAATTTGCCAATCCCAAAATTTTTC 719
Db      619 CTGATTTAGATCCAGATCTACAAACATCCCTGCTGCGCGCTCCCAAAATCTTTC 678
Qy      720 AACTCCCTTACATCACTATCACTGCAAAATGACCTATGATGCGCTGCAAGTTT 779
Db      679 TCCCTAATACCTCGAGATTTCTACGATCGAAATCAAGTTGATCAAGTGGGAATTC 738
Qy      780 TTTGTTAGCTTTTCAAGACTGACATTTTATCCGATGTTAAGCTTTAGGCTTATCTT 839
Db      739 TTAGATGATATCAACATTTACTTATTTATCCGATATGCTTTGAAAGATCAATCTTC 798
Qy      840 TTATATCTGCTTTTAAAGTGTGTTTCCAAACAAAGGATATATACAGAAAGTCAAG 899
Db      799 TTCAATCAACGTTTCTTGTGCTTCTCCAAACGTA--GTACCAATGCTGCTTAA 855
Qy      900 GAAATTTTAAAGCTATGACAGCTTTCTGACTGTGATTTCTTACTCTTTCTGCTTACC 959
Db      856 AACTTCCCGGAACTTAACTTCTTGTGACTGTGCTTCCCACTTACTCTCATGCTTACCA 915
Qy      960 AATTGACCTGAAAGGCTCATGTTTCAAGCTGCTGCTTGAAGCTGCGGGTTCCAAAT 1019
Db      916 AACTGACCTGAGAGATTTCTTCTGCTTCCAAAGCTTCAACGCTGCGGCTTCAAC 975
Qy      1020 TGGCAGTTAGCTTGAATCACTTGTCTTAAATGTTTAACTGGTGGCTAGCGGTAAAT 1079
Db      976 ATTCAATTTACGCTTAAACATTTGCTGTGATGCTTACGTTGGTCCACCGGTTAG 1035
Qy      1080 GATTTGTTTACAGAGACAAAGGCGCTCAACATTAACAGCTTCTGCTTGGTGGAT 1139
Db      1036 GACTGTTGAGAGAGAGGCGGAGCAATGATATCTTGTGATATATCAATGAT 1095
Qy      1140 TGGTTTCATGTTGCTGCACTTTCAGATTGAGCATCATCTGTTTCAAGAGTCTAG 1199
Db      1096 TGGTTCTTTGGTATTAACGTTTCAAGCTTGAACATATTTGTTCCCTGCTTACTCGT 1155
Qy      1200 TGGCATTTCAGAAATCTCACCATTTGTGAACAACTTGGCCAGAAAGATATTTGTCC 1259
Db      1156 TGGCATCTCCGAAAGTTTCTCGGTGTTCAAGAGCTTTGCAAGAAAGATATATCTTCCG 1215

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Qy      1260 TATGAACGTCTACCATGTTGGAGCGCAATAAATGATATCTTCCACCTGGGCTGTG 1319
Db      1216 TATGAGATGATGTCGTGGTTTAAAGCAATGTTGTTBACATTAACTTTGAAGACAGA 1275
Qy      1320 GCTATGAGAGCTAAGAGATTATCCAAAGCAGTTCCCAAGACATGCTTGGGAAGCATG 1379
Db      1276 GCTTATCAAGCTAAGAGAGCTGCTAATCCGGTGTGTTAAGAACTTGGTTGGAGCTTGG 1335
Qy      1380 AACACTTTGGGTGA 1394
Db      1336 AATACTCATGCTTAA 1350

RESULT 3
US-10-029-756-26
; Sequence 26, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-029-756-26

Query Match      25.7% Score 377.8; DB 14; Length 1702;
Best Local Similarity 57.6%; Pred. No. 4.8e-107;
Matches 717; Conservative 0; Mismatches 522; Indels 6; Gaps 2;

Qy      50 GGAAGAGCCAAAGAACATTTCCAGACAGACCTTGGCAAGATTAAGCAACGAGAGA 109
Db      53 GGGCGAAGCTAAGAGTATATCAACGCGGAGAGACCTCCGCGCACAAACAGTCCGGCA 112

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QY 110 TTATGATCTATCAAGGAAAAATTACATATCTCAAGTGAATAAGCATCC 169
 DB 113 TCTGTGATCTCATCAAGGCAAGCTCTACAGTGTCTTCGGTGGGCGAGCAACC 172
 QY 170 CGGTGTGAGCTCCATTTGTAAGTTTGGCGGCAAGATGCACTGATCGTTGATGC 229
 DB 173 CGGCGGGAAGTCCGCTCTCTCAGTCTGGCGGCAAGAGTCAACGACCTTCATTTGC 232
 QY 230 TTACCATCTGGGAGCTGGCAATCTTGAAGTTTCTTAACTG---GATCACT 286
 DB 233 GTACCAACCGGGGACGGCGTGGCGGCACTGAGTCCCTCTTCAACGGCTACTACTACT 292
 QY 287 TCAAGATTACTCTGTCTGAGATGTCACAGACTACAGAAAGGCTCGTCTGAGTTTC 346
 DB 293 CAAGACTTGAGAGTGTGAGATCTCCAGACTACCGAGGCTTTGAACAGATGTC 352
 QY 347 TAAGATGGTTTGTTCAGAACACCAAGCAAGGGGTCTACTCTCAATCTTTTTCGTGC 406
 DB 353 GCGGTCCGGGATCTTCAGAAAGAGGGCCACACATCATGTGACGTTCCGCGGTTCG 412
 QY 407 TGTGTTGTGCTCTGAGTGTTCACGGTGTCTCTACTGCAAGACACTGGGCTCATCT 466
 DB 413 GTGATGATGGCGCAATCGTCTACCGCGTGGCGTGGAGTCCGAGTTCACT 472
 QY 467 TTGCTCTGTTGCTAATGGGTATGCTATGAGCTCAGAGTGGTGGGGGAGTATTC 526
 DB 473 GCTGTGGGGGCACTGCTGGGCTTGTGTGATCTCAAGCCGCTGATGGGCACTGATC 532
 QY 527 TTGTCACTCAAGATTATGCTTAAACGTTAATCGTCTTTTCAATCATTTGAGG 586
 DB 533 CGGCACTTACCAAGTATGCTTAAACCGTTAATCGTCTTTTCAATCATTTGAGG 592
 QY 587 AATGTGATGCTGTGTGTATGTTGATGTGGAATTTGACATTAACCATCATCT 646
 DB 593 CAACATCTTACCGGAATGAGCAATGGTGTGGAATGGAACCCCAACGCCCACT 652
 QY 647 TGCCTGATATAGCGCAATCTGATCTGATATTCAGACACTTCTTAAATTTGCAATATC 706
 DB 653 CGCTGTGAAGAGCTGCACTGACACCCGCACTCCAGACATATCCGCTATATCCGCTTC 712
 QY 707 CCCAAATTTTCACTCCCTTACATCATATCATCACTGCAAAATGACATATGATGC 766
 DB 713 CACCCGACTCTTCACTCACTCACTCGTCTTCTATGCGGAGTCTGAAATTCAGCA 772
 QY 767 CGCTGCAGGTTTTTTTGTAGCTTTCAGCACTGACATTTTATCTCATTTTAACTT 826
 DB 773 AGTGGCAAGGTTCTTATGCTGCTACCACTGACACTGACCTTACCTGCTCATGATCTTCGG 832
 QY 827 TAGGCTCTATCTTTTATCTGTCTTTAAGTGTGTGTTTCAAAACAAAGGGTATA 886
 DB 833 CCGAGTCACTCTTCACTCACTGACCTTTTATGCTCTTCAACGAGGCGCA---CGTCC 889
 QY 887 CAAGAGAGTCAAGAAATTTTAAAGCTATGACGCTTTTGAATTTGATTTCTTACTCT 946
 DB 890 TGACCGGCTCTTAACTTAAATGAGTATCGGGTTTTCTGAGCGTGTTCGCGCTTCGT 949
 QY 947 TTTCTGCTTACCAATTTGCTGCTGAGAGGTCATGATTTTCACTCTTTTGAAGTGC 1006
 DB 950 ATCTTGTCTCCCAACGAGCTGAAAGGTTGCTGCTTCACTGCTTTTGGGCTCAC 1009
 QY 1007 CGGCTTCAACATTTGAGCTTCAAGCTTGAATCACTTTGCTTAAATTTTAACTGTTT 1066
 DB 1010 GGGGATCTCAAGCTTCAAGCTTCAAGCTTCTTCCGGGCAACATATCGGGCC 1069
 QY 1067 GCTTAAGCTTAAATGATTTGTTTCAACGACAGAAAGGCAAGCTCAACATCAAGCTTC 1126
 DB 1070 CCCCAAGGGGCAACAGTGTTCAGAGAGCAAGAAAGGAGCATGATATCAAGTCCC 1129
 QY 1127 TGTGTGTGGATTTGTTTATGTTGCTGCACTTCAATTTGAGATCATCTGTTTC 1186
 DB 1130 ACCGTGATGAGCTGTTCTTTTGTGGGTGCAAGTTCAGTGTGAGCAACATTTGTTCCC 1189

QY 1187 AAGATGCTTAACTGATGCTTCAAGAAATCTGCAATTTGCAACACTTTCAGAA 1246
 DB 1190 TAGGTCGGCGCGGTGAGAGCTTGAAGATTTGGCCCTTGTGGGACTTGTGAAGAA 1249
 QY 1247 GCATTAATTTGTCTTATGAATCTCTACATGTGGAGGCCAATAA 1291
 DB 1250 GCAAGGATGCTCGTATGAGTCTTGGGTTTGGAGCAAGCTTA 1294

RESULT 4
 US-09-770-149-494/C
 ; Sequence 494, Application US/09770149
 ; Patent No. US2002005963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goriach, Jörn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Mathew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Moesner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Krickler, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurlan, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2024 (PARA-013PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770,149
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FaSTSeq for Windows Version 4.0
 ; SEQ ID NO 494
 ; LENGTH: 657
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-770-149-494

Query Match 12.0%; Score 176.4; DB 9; Length 657;
 Best Local Similarity 59.9%; Pred. No. 3,7e-44;
 Matches 294; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 917 AGCTTTCTGACTGTGATTTCTTACTCTTTCTGCTTACCAATTTGGCTTAAAGGT 976
 DB 629 AGCTTTCTGACTGTGATTTCTTACTCTTTCTGCTTACCAATTTGGCTTAAAGGT 976
 QY 977 CATGATTTCACTCTCTGTTTACAGTCCGCGGTTCAACATTTGCAAGTTCAGCTTGA 1036
 DB 569 CTCTTCTGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTGA 510
 QY 1037 TCATTTGCTTCAATGTTTACACTGATTTGCTTACAGGATGATTTGTTTCAAGCA 1096
 DB 509 CCATTTGCTGCTGATGTCTACCTTGTCCACCCACCGGTAGGACTGTTTCAAGCA 450
 QY 1097 GACAAAGGCAAGCTTCAACATTAACAGCTTCTGCTGTGGATTTGATTTGATGAGCT 1156
 DB 449 AGCGGGGGAACATGATATCTTTGATGATATATGATTTGATTTGATTTGATTTGAT 390
 QY 1157 GCATTTGATGATGATATCTTTTCAAGAGTCCCTTAATGCTTTCAGAAAT 1216
 DB 389 ACGTTTCAAGCTTGAACATATTTGTTCCCTTACCTGTTGCTATCTCGGAAAGT 330
 QY 1217 CTCACCATTTGTAACAAACTTTGCCAAGACATTAATTTGTCTATGAACCTGCTACAT 1276

Db 329 TTCTCCGAGTTCAGAGAGCTTGGCAAGACATATCTCCGTATAGAGATGTCGTG 270
 QY 1277 GTGGAGGCGCAATAAATGTATATCCACCCGCGTGTGTGGCTATGGAAGCTAAGA 1336
 Db 269 GTTTGAGCAAAATGTGTGACCATTAACCTTTGAAGACGAGCTTATCAAGCTTGAAGA 210
 QY 1337 TGTACCAAGCCAGTTCACCAAGACATGTCTGGGAAGCAATGACACTTTCGGGTGAAC 1396
 Db 209 CGGCGCTAATCCGGTGTATAGAACTTGTGGGAAGCTTTGAATATCTCATGCTAAAT 150
 QY 1397 CTTATNAACA 1407
 Db 149 GATTTATATCA 139

RESULT 5
 US-09-770-444-39
 ; Sequence 39, Application US/09770444
 ; Patent No. US2002023280A1
 ; GENERAL INFORMATION:

APPLICANT: Gorlach, Jorn
 APPLICANT: An, Yong-Qiang
 APPLICANT: Hamilton, Carol M.
 APPLICANT: Price, Jennifer L.
 APPLICANT: Raines, Tracy M.
 APPLICANT: Yu, Yang
 APPLICANT: Rameaka, Joshua G.
 APPLICANT: Page, Amy
 APPLICANT: Matthew, Abraham V.
 APPLICANT: Ledford, Brooke L.
 APPLICANT: Moesener, Jeffrey P.
 APPLICANT: Haas, William David
 APPLICANT: Garcia, Carlos A.
 APPLICANT: Kricke, Maya
 APPLICANT: Slader, Ted
 APPLICANT: David, Keith R.
 APPLICANT: Allen, Keith
 APPLICANT: Hoffman, Neil
 APPLICANT: Hurban, Patrick
 TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 TITLE OF INVENTION: thaliana
 FILE REFERENCE: 2027 (PARA-016PRV)
 CURRENT APPLICATION NUMBER: US/09/770,444
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 60/178,502
 PRIOR FILING DATE: 2000-01-27
 NUMBER OF SEQ ID NOS: 999
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 39
 LENGTH: 476
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(476)
 OTHER INFORMATION: n = A,T,C or G
 US-09-770-444-39

Query Match 9.1%; Score 133.2; DB 9; Length 476;
 Best Local Similarity 55.4%; Pred. No. 1e-30;
 Matches 255; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 190 TAAATTTTGGCGGCAAGATGATGATGCTTCAATGCTTCAATCCTGGACGTCTT 249
 Db 16 TCATATCTGTTGTTCAAGAGCTCACCGATGCTTCAATCGATTTCAATCCGGAACGCTT 75
 QY 250 GGCATATCCTTGACAGATCTTTACTGGGTACTACGTTCAAGTTACTGTCGTGAA 309
 Db 76 GGACACATCTCGACATCTCTTCAACGGTTTACCAATCAAGATTTTCAAGTCTCGAAG 135
 QY 310 TGTCAAGACTACAGAGGCTGCTCTGAGTTTCTAAGATGAGGTTGTTCAAGAC 369

Db 136 TCTACGCGATTACCGCTGTATGCTGCCGAGTTCGTAACTCGTCTCTTGAAGA 195
 QY 370 CAGCAAGAGGGGTACTAGCTCAATCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 429
 Db 196 AAGGTACGTTACTCTCTACCTTACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 255
 QY 430 ACGGTGTCTCTACTGCAAGACACCTGGGCTCATCTTGTGTGTGTGTGTGTGTGTGTGT 489
 Db 256 ACGGT 315
 QY 490 TGTATGCTCAGAGT 549
 Db 316 TCTCTGATCCAGAGCGCTTACATAGGTCAGATCTGTGATATCATATCATGCA 375
 QY 550 ACCGTAGCTTATGCTCTTTTCAATATATGACAGAAATGATGATGATGATGATGATG 609
 Db 376 ACAAATCTTATACAGATTGCTCAGCTTCTCTNNGTAACTGTCTCACCGGAATCTCA 435
 QY 610 TTGCATGTGGAAGTTGACATTAACACCATCACTTGTG 649
 Db 436 TCGCGTGTGGAATGAGATCAAAATGCTATCATCTAGC 475

RESULT 6
 US-09-878-574-3260
 ; Sequence 3260, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Thompson, Michael D.
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants
 FILE REFERENCE: 38-21 (15401)B
 CURRENT APPLICATION NUMBER: US/09/878,574
 CURRENT FILING DATE: 2001-12-21
 PRIOR APPLICATION NUMBER: 09/333,535
 PRIOR FILING DATE: 1999-06-14
 NUMBER OF SEQ ID NOS: 15775
 SEQ ID NO 3260
 LENGTH: 287
 TYPE: DNA
 ORGANISM: Glycine max.
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(287)
 OTHER INFORMATION: unsure at all n locations
 OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-H6
 US-09-878-574-3260

Query Match 8.0%; Score 117; DB 10; Length 287;
 Best Local Similarity 62.9%; Pred. No. 9e-26;
 Matches 180; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 921 TTCTGACTGTGATTTCTTACTCTCTTCTGCGCTTACCAATGCGTGAAGGGGCTATG 980
 Db 2 TTTTGATTTGTGTTCCCTTATGATCTATCTATCTCCGCAATTTGGAGAGAGGGCTATG 61
 QY 981 TATTTACGTCCTGTTAGACATGCGCGGTTTCAACATTTGACAGTTCAGTTGATTCAC 1040
 Db 62 TTTGTTTGGCAGTTTGT 121
 QY 1041 TTTGCTTATATGTTTACATGTTGTGCTTACCGGTATGATTTGTTTACACGACACA 1100
 Db 122 TTGCGAGCAGATGTATGAGGGCCCAACCAATGCAATGACTGTGTGAGAAAGCAACT 181
 QY 1101 AAGGAGCGCTCAATACAGCTTCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1160
 Db 182 GGTGCAATTTGACATCTCTTGTCTTACATGATGATGATGATGATGATGATGATGATG 241
 QY 1161 TTTCAATTTGACATCTCTTGTCTTACATGATGATGATGATGATGATGATGATGATG 1206
 Db 242 TTCAACTTTGACATCTTGTCTTACATGATGATGATGATGATGATGATGATGATGATG 287

RESULT 7
US-09-924-035A-370/c
; Sequence 370, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo, Jm
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: Chaliana
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924, 035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-924-035A-370

Query Match 7.2%; Score 106.2; DB 10; Length 480;
Best Local Similarity 61.8%; Pred. No. 3.1e-22;
Matches 168; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 1136 GGATGGTTTCATGAGTGGCCCTGACCTTCAGATTGACATCATCTGTTCCAGAGATGCC 1195
DB 453 GGATGGTTTCATGAGTGGCCCTGACCTTCAGATTGACATCATCTGTTCCAGATGCC 394
QY 1196 TAAGTGCATTTGAGGAAATCTCACCCATTTGAGAACAACTTGCAGAGATATTT 1255
DB 393 TCGTGGCATCTCGGAAAGTTTCTCGGTTGTTCAAGACCTTGCAGAGATATCT 334
QY 1256 GTCTTATGAACCTGCTACATGTCGGGAGCCAAATTAATGTAATCTTCCCTGCTGC 1315
DB 333 TCCGTAAGAGATATGTCGTTGTTGAAGCAAAATGTTTACCATTAACACTTTGAAGAC 274
QY 1316 TGTGCTATGGAAGCTAAGATGTTACCAAGCCAGTCCCAAGAAATGTCGGGAGAC 1375
DB 273 AGCAGCTTATCAAGCTTGAAGACGTCGTTATCCGCTGTTAAGAACTTGGTTGGAGAC 214
QY 1376 AATGAACACTTTCGGGTGAACCTTATNAACA 1407
DB 213 TTGGAATATCATGAGCTAATTAATTAATCA 182

RESULT 8
US-09-878-574-9255
; Sequence 9255, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 9255
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102270H1
US-09-878-574-9255

Query Match 5.5%; Score 81.4; DB 10; Length 263;
Best Local Similarity 60.0%; Pred. No. 1.2e-14;

Matches 153; Conservative 0; Mismatches 101; Indels 1; Gaps 1;
QY 557 GCTTAATCGCTTTTCAATCATTCAGAGAAATGATGTCGAGTGTAGTGTGATG 616
DB 10 GCTGAGCCGGCTGAGCAAAATCTTTGTGGCAATTCAGTGCAGTGGATTAAGCATTCGATG 69
QY 617 GTGAAAGTTGAGCAATTAACCCATCTTGTGCTGTAATAGCCCAATCTGATCTGA 676
DB 70 GTGAAAGTTGAGCAATTAACCCATCTTGTGCTGTAATAGCCCAATCTGATCTGA 129
QY 677 TATTGAGCACTTCTTATTAATGAGCAATTCAGCAATTTTCACTCCCTTATCATCA 736
DB 130 T-TCCAGCAATACCTGCTCTTGTGCGTGTGACACGCTTCTTCAATCAATCAAACTTG 188
QY 737 CTATCAACTGCAAAATGACCTATGATGCGCTGCGAGGTTTGTGTTGATCTTGACA 796
DB 189 TTTCATGAGAGAAATTTGTTGTTGATTCATTTATTAAGTTTCTCATCAGTACAGCA 248
QY 797 CTGACATTTTATCC 811
DB 249 CTCACATTTCTACCC 263

RESULT 9
US-10-369-493-27824
; Sequence 27824, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27824
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27824

Query Match 4.7%; Score 69; DB 12; Length 1098;
Best Local Similarity 49.3%; Pred. No. 2.4e-10;
Matches 180; Conservative 0; Mismatches 185; Indels 0; Gaps 0;
QY 493 TATGCTCCAGAGTGTGGTGGGCGCATGCTTCTGTCACTACCAAGTTATGCCATACC 552
DB 179 TCTGCAACAGCTAGTCTTCACTGCCCATGAGCGCGGACCATGGCATCACCAACATT 238
QY 553 GTAAGCTTAATCGCTTTTCAATCATTCAGAGAAATGATGTCGAGTGTAGTGTG 612
DB 239 TCCATGTCATATGTCATTCGCGCATCATCTTCCGACTTCAATCGGTGTGCTAGCTAG 298
QY 613 CATGTGGAAGTTGAGCAATTAACCCATCTTGTGCTGTAATAGCCCAATCTGATC 672
DB 299 GTTGTGGAAGGCAACCAACAGTTCACCAATATCAACCAACAGCCCTGAGACAGATC 358
QY 673 CTGATATTCAGCACTTCTTATTAATGAGCAATATCCCAAAATTTTCACTCCCTTACAT 732
DB 359 CGGACATAGAACCTCCCTCTTCTTGGCAATTTCCATGCTTCTTCACTAATCTCGGT 418
QY 733 CATATATCAACATGCAAAATGACCTATGATGCGCTGCAAGTTTGTGTTAGCTTTC 792
DB 419 CCACATATCTATGACGCTGTCATGAGATGACATCTTTGCAAAATCTTCTGCTCCCTCC 478
QY 793 AGCACTGACATTTTATCTGCAATTTGTAAGCGTTAAGCTTATCTTTTATTTCTGCTT 852

RESULT 13
US-10-278-391-3
Sequence 3, Application US/10278391
Publication No. US20030159164A1
GENERAL INFORMATION:
APPLICANT: KOPCHIK, JOHN J.
KELDER, BRUCE
HUANG, YUNG-SHENG
KIRCHNER, STEPHEN J.
MUKERJI, PARADIP
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
PRODUCTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/278,391
APPLICATION NUMBER: US/10/278,391
FILING DATE: 23-Oct-2002
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/087,578
FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-03348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1374 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-278-391-3
Query Match 4.0%; Score 58.6; DB 13; Length 1374;
Best Local Similarity 52.2%; Pred. No. 5.1e-07;
Matches 130; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

453 ACCTGGGCTATCTTGGTGGTCTATAGGAGTATGCTATGAGGCTCCAGAGTGG 512
Db 448 ACCCTGGCCACAGCTCTCTGGCTGGCTTTGGGCTGTGTCGACGAGTGGAGTGG 507
QY 513 GTGGGGGATGATCTTGTCTACTACCAAGTTATGCTTACCGTAAAGCTTATCGCTTTT 572
Db 508 TTGGGTCACAGCTTTTGGATCACCAGGCTCTCCAGAGCGTTTCTGGGGTGAATCTTTTC 567
QY 573 CAATCATCTTCAGAAATGTGATGCTGTGTTAGTGTTCAGATGAGGAAGTTGACCAT 632
Db 568 GGGCGCTTCTTGGAGAGTGTCTGACAGGGCTTCTCGTCTGTGAGTGAAGACAAGCAC 627
QY 633 AACACCATGATCTTGGCTTATATAGGCGCAATCTGATCTATATTCAGACCTTCTT 632
Db 628 AACACTACACCGCCGCCCAAGTCTCAAGCGGAGATCCGACATTCAGACCCACCTT 687
QY 693 ATAAATGCC 701

Db 688 CTGTGACC 696
RESULT 14
US-10-191-513A-37
Sequence 37, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Paradip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295 US D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIORITY APPLICATION NUMBER: US 09/227,613
PRIORITY FILING DATE: 1999-01-08
PRIORITY APPLICATION NUMBER: PCT/US98/07422
PRIORITY FILING DATE: 1998-04-10
PRIORITY APPLICATION NUMBER: US 08/833,610
PRIORITY FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)...(5)
OTHER INFORMATION: k = g or t/u at position 5
NAME/KEY: misc feature
LOCATION: (6)...(6)
OTHER INFORMATION: m = a or c at position 6
US-10-191-513A-37
Query Match 3.9%; Score 57.4; DB 15; Length 449;
Best Local Similarity 58.5%; Pred. No. 5.9e-07;
Matches 100; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1080 GATTGGTTTCACAGAGCAAAAGGCGAGCTTCAACATTAAGCTTGTGGTGGAT 1139
Db 167 GACTGGGTTTCACCCAGCTCCAGGCGACATGCAATGTCACAAAGTGTGCTTCAATGAC 226
QY 1140 TGGTTTCATGAGTGGCTGCGCTTTCAGATTGAGCATCATCTGTTTCAAGATGCTTAAG 1199
Db 227 TGGTTTCATGAGCACTTCAACTTCCAGATTGAGCACAATCTTTTCCAGATGCTTGA 286
QY 1200 TGGCATTTGAGGAAATCTTCACCATTTGGAACAACCTTGGCAAGAGAT 1250
Db 287 CACAATTACCAACAAGTGGCTCCCTGTGAGTCTCTGTGTCAGCAT 337
RESULT 15
US-10-191-513A-3
Sequence 3, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Paradip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295 US D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIORITY APPLICATION NUMBER: US 09/227,613
PRIORITY FILING DATE: 1999-01-08

;
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-3

Query Match 3.9%; Score 57.4; DB 15; Length 655;
Best Local Similarity 58.5%; Pred. No. 7.5e-07;
Matches 100; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1080 GATTGTTTCCACCAGACAAAGGGCAGCTCACAATACAGCTTCTGCTTGGTGGAT 1139
DB 161 GACTGGGTTTCCACCAGCTCCAGGCCACATGCAATGCCAAGCTGCTTCATGAC 220
QY 1140 TGGTTTCATGATGAGCTGCACTTTCAGATTGAGCATCATCTGTTCCAGAGATGCTTAG 1199
DB 221 TGGTTTCATGAGACCTTCAACTTCAGATTGAGACCATCTTTTCCACGATGCTTGA 280
QY 1200 TGCATTTTCAGGAAATCTCACCATTGTGAACAAACTTTGCCAGAGCAT 1250
DB 281 CACAATTACCAAGTGGCTCCCTGTGTCAGTCTTGTGTGCCAAGCAT 331

Search completed: January 1, 2004, 05:18:54
Job time : 370.894 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 : Search time 41.2461 Seconds
(without alignments)
1724.030 Million cell updates/sec

Title: US-09-857-524B-2
Perfect score: 2470
Sequence: 1 MEEPKKHISQADLAKHKQPG.....KDYTKFVPRKMWVEMANTFG 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A.GeneSeq.19Jun03:*

- 1: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2470	100.0	448	21	AAV71551
2	1465.5	59.3	448	17	AAV71551
3	1465.5	59.3	448	19	AAV71551
4	1465.5	59.3	448	20	AAV71551
5	1465.5	59.3	448	21	AAV71551
6	1465.5	59.3	448	21	AAV71551
7	1459.5	59.1	448	23	AAV71551
8	1459.5	59.1	448	24	AAV71551
9	1451.5	58.8	446	20	AAV71551

10	1446.5	58.6	448	24	ABG73417
11	1407.5	57.0	449	21	AAV29290
12	1395.5	56.5	449	21	AAV51333
13	1391.5	56.3	458	21	AAV51348
14	1372.5	55.6	449	21	AAV51392
15	1372.5	55.6	449	21	AAV51392
16	1372.5	55.6	449	21	AAV51392
17	1372.5	55.6	449	21	AAV51392
18	1372.5	55.6	449	21	AAV51392
19	1372.5	55.6	449	21	AAV51392
20	1372.5	55.6	449	21	AAV51392
21	1372.5	55.6	449	21	AAV51392
22	1372.5	55.6	449	21	AAV51392
23	1372.5	55.6	449	21	AAV51392
24	1372.5	55.6	449	21	AAV51392
25	1372.5	55.6	449	21	AAV51392
26	1372.5	55.6	449	21	AAV51392
27	1372.5	55.6	449	21	AAV51392
28	1372.5	55.6	449	21	AAV51392
29	1372.5	55.6	449	21	AAV51392
30	1372.5	55.6	449	21	AAV51392
31	1372.5	55.6	449	21	AAV51392
32	1372.5	55.6	449	21	AAV51392
33	1372.5	55.6	449	21	AAV51392
34	1372.5	55.6	449	21	AAV51392
35	1372.5	55.6	449	21	AAV51392
36	1372.5	55.6	449	21	AAV51392
37	1372.5	55.6	449	21	AAV51392
38	1372.5	55.6	449	21	AAV51392
39	1372.5	55.6	449	21	AAV51392
40	1372.5	55.6	449	21	AAV51392
41	1372.5	55.6	449	21	AAV51392
42	1372.5	55.6	449	21	AAV51392
43	1372.5	55.6	449	21	AAV51392
44	1372.5	55.6	449	21	AAV51392
45	1372.5	55.6	449	21	AAV51392

ALIGNMENTS

RESULT 1	AAV71551	standard; protein; 448 AA.
ID	AAV71551	
AC	AAV71551	
XX	12-OCT-2000	(first entry)
XX	Florida bitterbush	delta-6 fatty acid desaturase.
XX	Florida bitterbush	delta-6 fatty acid desaturase; tartaric acid;
XX	transgenic plant; fatty acid	membrane-bound desaturase.
XX	Picramnia pentandra.	
XX	WO200032790-A2.	
XX	08-JUN-2000.	
XX	02-DEC-1999.	99WO-US28589.
XX	03-DEC-1998.	98US-0110784.
XX	(DUPO) DU PONT DE NEMOURS & CO B I.	
XX	Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;	
XX	WPI, 2000-412336/35.	
XX	N-PSDB; AAD01349.	
XX	Polynucleotide encoding delta-6 desaturase enzyme useful for producing	
XX	transgenic plants and for producing antibodies specific to which is	

PT useful for screening cDNA expression libraries -
 XX
 PS Claim 10; Page 40-41; 57pp; English.

CC The present sequence is a delta-6 fatty acid desaturase protein sequence
 CC from clone pps-pk0011.d5:115 isolated from Florida bitterbush developing
 CC seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the
 CC formation of tauric acid, a fatty acid that has a triple bond at the
 CC delta-6 carbon. The present sequence is useful for producing
 CC transgenic plants having altered levels of delta-6 desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.

XX Sequence 448 AA;

Query Match 100.0%; Score 2470; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 3.4e-253;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEEPKKHSQADLAKHQPGLMISIKGYDYSKMTKEHPGGLPLSPAGQDVTDAFI 60
 DB 1 MEEPKKHSQADLAKHQPGLMISIKGYDYSKMTKEHPGGLPLSPAGQDVTDAFI 60
 QY 61 AHPGTAQYLDREFFGYGYQDYVSSEMSKDYRLVSEFSMGLFKTPGKGVCSIFPVS 120
 DB 61 AHPGTAQYLDREFFGYGYQDYVSSEMSKDYRLVSEFSMGLFKTPGKGVCSIFPVS 120
 QY 121 VLPSALSYGVLYCKSTVAHLCSGLMGMLVLSQGWVGHDSCHYQVMEKRLNRLFOIIAG 180
 DB 121 VLPSALSYGVLYCKSTVAHLCSGLMGMLVLSQGWVGHDSCHYQVMEKRLNRLFOIIAG 180
 QY 181 NVLAGSVVAMWKLDNTHHFAKNSANLDPDIOHPLIAISPKFPNSLTSTYHNCMTYDR 240
 DB 181 NVLAGSVVAMWKLDNTHHFAKNSANLDPDIOHPLIAISPKFPNSLTSTYHNCMTYDR 240
 QY 241 AARFVSFOHMTFPPALSLVRLYFILSPKVFSENNKRYKRSEILIGVAFLTWISLL 300
 DB 241 AARFVSFOHMTFPPALSLVRLYFILSPKVFSENNKRYKRSEILIGVAFLTWISLL 300
 QY 301 SRLPNMERVMTFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTITAS 360
 DB 301 SRLPNMERVMTFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTITAS 360
 QY 361 AAMDWFHGLHFOIENHLFPRMPKCHFRKISPIVYKLCQKHNLSYETATWMEANKVYST 420
 DB 361 AAMDWFHGLHFOIENHLFPRMPKCHFRKISPIVYKLCQKHNLSYETATWMEANKVYST 420
 QY 421 LRAVAMEAKDVTKVPKGMVMEANTFG 448
 DB 421 LRAVAMEAKDVTKVPKGMVMEANTFG 448

RESULT 2

ID AAR98455 standard; Protein: 448 AA.

AC AAR98455;
 DT 15-SEP-1996 (first entry)
 XX Borage delta-6-desaturase.
 DE
 XX Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KM polyunsaturated fatty acid; octadecatetraenoic acid;
 KM chilling resistance; oilseed.
 XX
 OS Borage officinalis.
 XX
 FH Key
 FT Region

Location/Qualifiers
 156..163
 FT /label= lipid_box

FT Region 196..200
 FT /label= Metal_box-1
 FT Region 372..377
 FT /label= Metal_box-2

XX WO9621022-A2.
 XX
 PD 11-JUL-1996.

XX 28-DEC-1995; 95MO-IB01167.

XX 30-DEC-1994; 94US-0366779.

PA (RHON) RHONE POULENC AGROCHIMIE.

XX Freyessinet GL, Nuccio M, Numborg AN, Reddy AS, Thomas TL;

XX WPI; 1996-333997/33.

DR N-PSDB; AAT30395.

PT Transgenic plants comprising the borage delta-6-desaturase gene -
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling

PS Claim 3; Page 52-53; 75pp; English.

CC Borage delta-6-desaturase (AAR98455) catalyses the conversion of
 CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
 CC deduced from that of the delta-6-desaturase gene (AAT30395) isolated
 CC from a borage membrane-bound polysomal library. The sequence is
 CC distinct from that of Synchocystis delta-6-desaturase (AAR98456).
 CC Expression of the desaturase in transgenic plants, esp. sunflower,
 CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
 CC increased GLA prodn. Alteration of the plant membrane lipids as a
 CC result of expression of the desaturase may also result in increased
 CC resistance to chilling.

XX Sequence 448 AA;

Query Match 59.3%; Score 1465.5; DB 17; Length 448;
 Best Local Similarity 55.4%; Pred. No. 1.7e-146;
 Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

QY 5 KKHISQADLAKHQPGLMISIKGYDYSKMTKEHPGGLPLSPAGQDVTDAFIAYHP 64
 DB 6 KKHISQADLAKHQPGLMISIKGYDYSKMTKEHPGGLPLSPAGQDVTDAFIAYHP 64
 QY 65 GTAMQYLDREFFGYGYQDYVSSEMSKDYRLVSEFSMGLFKTPGKGVCSIFPVSUFA 124
 DB 65 GTAMQYLDREFFGYGYQDYVSSEMSKDYRLVSEFSMGLFKTPGKGVCSIFPVSUFA 124
 QY 125 LSYGVLYCKSTVAHLCSGLMGMLVLSQGWVGHDSCHYQVMEKRLNRLFOIIAGNYIA 184
 DB 125 LSYGVLYCKSTVAHLCSGLMGMLVLSQGWVGHDSCHYQVMEKRLNRLFOIIAGNYIA 184
 QY 185 GVSVAAMWKLDNTHHFAKNSANLDPDIOHPLIAISPKFPNSLTSTYHNCMTYDAPF 244
 DB 185 GVSVAAMWKLDNTHHFAKNSANLDPDIOHPLIAISPKFPNSLTSTYHNCMTYDAPF 244
 QY 245 FVSFOHMTFPPALSLVRLYFILSPKVFSENNKRYKRSEILIGVAFLTWISLLSRP 304
 DB 245 FVSFOHMTFPPALSLVRLYFILSPKVFSENNKRYKRSEILIGVAFLTWISLLSRP 304
 QY 305 NMPERVMTFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTITASAWD 364
 DB 305 NMPERVMTFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTITASAWD 364
 QY 365 WFRGGLHFOIENHLFPRMPKCHFRKISPIVYKLCQKHNLSYETATWMEANKVYSTLRAV 424
 DB 365 WFRGGLHFOIENHLFPRMPKCHFRKISPIVYKLCQKHNLSYETATWMEANKVYSTLRAV 424
 QY 425 AAMEAKDVTKVPKGMVMEANTFG 448
 DB 425 AAMEAKDVTKVPKGMVMEANTFG 448

Db 425 ALQARDITKPLPKNLVWEALHTHG 448

RESULT 3
AAW67471
ID AAW67471 standard; Protein; 448 AA.

AC AAW67471;
XX
XX
DT 02-MAR-1999 (first entry)
XX
DE Borage delta-6 desaturase protein.
XX
XX Upstream region; regulatory region; sunflower; albumin; seed; expression;
KM lipid metabolism; delta-6 desaturase; transgenic plant.
XX
XX Borage officinalis.
XX
FH Key Location/Qualifiers
FT 40..44
FT /note= "cytochrome b5 haem-binding motif"
FT Domain 156..163
FT /note= "His-rich metal binding motif"
FT Domain 196..200
FT /note= "His-rich metal binding motif"
FT Domain 373..377
FT /note= "His-rich metal binding motif"
XX
XX WO9845460-A1.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98WO-US07178.
XX
XX 09-APR-1997; 97US-0831570.
XX
XX (RHON) RHONE-POULENC AGROCHIMIE.
XX
XX Beremand PD, Nunberg AN, Thomas TL;
XX
XX WPI; 1998-583201/49.
XX
XX N-PSDB; AAV34398.
XX
XX
XX New sunflower albumin 5' regulatory region - useful for directing
PT altered lipid metabolism in plant seeds
XX
XX
XX Example 2; Fig 1; 38pp; English.
XX
XX This sequence corresponds to the borage (Borage officinalis) delta-6
CC desaturase enzyme. The encoding lipid metabolism gene is an example
CC of a heterologous gene which can be expressed at high levels in a
CC seed-specific manner in transgenic plants, when placed under control
CC of the sunflower albumin gene 5' regulatory region (AAV34397).
XX
XX
SQ Sequence 448 AA;

Query Match 59.3%; Score 1465.5; DB 19; Length 448;
Best Local Similarity 55.4%; Pred. No. 1.7e-146;
Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

QY 5 KKHISQADIAKHKPODLMWISIKGVYDLSKWKHPGGLPLSPFAGDOVTDAPFAVHP 64
DB 6 KKITDELKNDKPDGLMWSIQKAYDSDWKDHPGGSFLKSLAGQEVTDAPFAVHP 65
QY 65 GTAMQYLDFEFTGYVQDVSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFESVLA 124
DB 66 AATWKULDFEFTGYVQDVSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFESVLA 125
QY 125 LSYVGLYCKSTAAHLCSGILMGLMQSGVGHDSCHYVMMNRKLNRLFOIIAGNVIA 184
DB 126 MSYVGLYCEGVVHLFSGCLMGFLWISQGMIGHDAGHYVVDSSLNFKMGIFANCLIS 185
QY 185 GVSVAWMKLDHNTNHFACNSANLDPDIOHLPIAISPFPNSLTSYHNCKMTYDRAAR 244

Db 186 GISIGWKKNNHNAHIAACNSLEYDPLQYIPELVVSSKEFGSLTSHFYEKRLFPDSLSP 245
QY 245 FVSFOHTEYYPALLSLRLYLFLISFKVVSNNKRVYKRSOELIGVAPLWVSLLSRLP 304
DB 246 FVSFOHTEYYPALLSLRLYLFLISFKVVSNNKRVYKRSOELIGVAPLWVSLLSRLP 304
QY 305 NMPERVMYFTSCIAVAGFQMOFSLNHPASVNYTGLPSGNDWPHOOTKTLNTASAMWD 364
DB 305 NMGERIMFYIASLSVGMQOVQFSLNHPSSVYVGPKNMNEKOTDGLDLSCEPMD 364
QY 365 WFGGLHFOIEHLEFPRMPKCHFRKISPIVNLCOQHNLSYETATWEMANKVYSTLRV 424
DB 365 WFGGLHFOIEHLEFPRMPKCHFRKISPIVNLCOQHNLSYETATWEMANKVYSTLRV 424
QY 425 AMBAKDVTKPVPKRWVEMANTFG 448
DB 425 ALQARDITKPLPKNLVWEALHTHG 448

RESULT 4
AAW98130
ID AAW98130 standard; Protein; 448 AA.

AC AAW98130;
XX
XX 21-JUN-1999 (first entry)
XX
XX Borage delta-6 desaturase.
XX
XX Delta-6 desaturase; borage; oleosin; Acs21; promoter;
KM transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
XX gamma-linolenic acid; octadecatretenic acid.
XX
XX Borage officinalis.
XX
XX
XX Key Location/Qualifiers
FH 40..44
FT Binding-site /note= "cytochrome b5 haem-binding motif"
FT Binding-site 156..163
FT /note= "metal binding, histidine-rich motif"
FT Binding-site 196..200
FT /note= "metal binding, histidine-rich motif"
FT Binding-site 373..377
FT /note= "metal binding, histidine-rich motif"
XX
XX
XX WO9845461-A1.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98WO-US07179.
XX
XX 09-APR-1997; 97US-0831575.
XX
XX (RHON) RHONE-POULENC AGROCHIMIE.
XX
XX Li Z, Thomas TL;
XX
XX WPI; 1999-180333/15.
XX
XX N-PSDB; AAX24917.
XX
XX Nucleic acid containing oleosin 5'-regulatory region - useful for
PT modulating fatty acid synthesis and lipid metabolism in plants,
XX particularly to increase content of gamma-linolenic acid
XX
XX Example 2; Page 61; 101pp; English.
XX
XX The present sequence is borage delta-6 desaturase, an enzyme that
CC catalyses the conversion of linolenic acid to gamma-linolenic acid
CC (GLA). Delta-6 desaturase cDNA (see AAX24917) was isolated from a
CC borage membrane-bound polysomal cDNA library using a partial clone,
CC obtained from an EST database search, as probe. The borage delta-6
CC desaturase nucleic acid can be operably linked to the seed-specific

CC 5' regulatory region (see AAX24916) of the Arabidopsis thaliana
CC oleosin At5g1 gene in claimed expression cassettes of the invention.
CC Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton,
CC peanut, oilseed rape or Arabidopsis are obtained that show increased
CC levels of GUA or octadecatetraenoic acid. The levels of desirable
CC fatty acids in oilseed crops can be manipulated to provide seed
CC oils of use in human health and industrial applications.

XX Sequence 448 AA;

Query Match 59.3%; Score 1465.5; DB 20; Length 448;

Best Local Similarity 55.4%; Pred. No. 1.7e-146;

Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

DB 5 KKHISADLAKHQPDDLMISIKGYDLSKWKHPGGLPLSPAGDVTDAFIAYHP 64
DB 6 KKITDELKNDKPDLMISIQKAYDSDWKDHPGSPPLKSLAGDVTDAFVAFHP 65
QY 65 GRAMQYLDREFTGYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFSVLFA 124
DB 66 ASYWKALDKFTGYLYLKDYSVSESKDYRLVSEFSKMGLEKTPGKGVCSIFSVLFA 125
QY 125 LSVYGYLYCKSTWALCSGLMGMLWLGSGWGHDSCHQVMPNKLRLFOIIAGNVIA 184
DB 126 MSYGYLYLFCGVLVHLFSGCLMGFLWLGSGWGHDSCHQVMPNKLRLFOIIAGNVIA 185
QY 185 GSVAMWKLDHNTHTHACNSANLDPDLOHPIAISPKFNSLTSYHNCKMTYDRAAR 244
DB 186 GSGIGWKNHNAHNAACNSLEVDPLQYIPLVSSKFPGLSHPEKRLTFDLSR 245
QY 245 FVSFOHTEFYPALLSVRLYLFLSPKVFNSNKRKYKSOEILGYAAFLTWYSLRLP 304
DB 246 FVSFOHTEFYPALLSVRLYLFLSPKVFNSNKRKYKSOEILGYAAFLTWYSLRLP 304
QY 305 NMPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHQTGTLTITASAMD 364
DB 305 NMPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHQTGTLTITASAMD 364
QY 365 WFRGGLHFOLEHNLFRPMKCHFRKISPIVNLCKHNLSTETATWANKMYSTLRAY 424
DB 365 WFRGGLHFOLEHNLFRPMKCHFRKISPIVNLCKHNLSTETATWANKMYSTLRAY 424
QY 425 AMEAKDVTKVPKNNWMEAMNTFG 448
DB 425 ALQARDITKPLPKNLMEALHTHG 448

RESULT 5

ID AAY71554 standard; Protein; 450 AA.

AC AAY71554;

DT 12-OCT-2000 (first entry)

DE Soybean sphingolipid desaturase #2.

KW Soybean sphingolipid desaturase; membrane-bound desaturase;
KM transgenic plant; fatty acid.

OS Glycine max.

PN WO200032790-A2.

PD 08-JUN-2000.

PF 02-DEC-1999; 99MO-US28589.

PR 03-DEC-1998; 98US-0110784.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;

XX WPI; 2000-412336/35.

DR N-PSDB; AAD01352.

XX

PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing

transgenic plants and for producing antibodies specific to which is

useful for screening cDNA expression libraries

PS Claim 10; Page 47-48; 57pp; English.

CC The present sequence is a sphingolipid desaturase

CC from clone sgl.pk0017.b4.15 isolated from soybean seedling cDNA

CC library, seq. The present sequence is useful for producing

transgenic plants having altered levels of sphingolipid desaturase which

in turn would alter the fatty acid composition. The enzyme is also useful

for producing polyclonal or monoclonal antibodies. The polynucleotide

is useful as primer or probe for screening cDNA libraries to

isolate desired full-length cDNA clones.

XX Sequence 450 AA;

Query Match 59.3%; Score 1465.5; DB 21; Length 450;

Best Local Similarity 55.4%; Pred. No. 1.8e-146;

Matches 248; Conservative 90; Mismatches 109; Indels 1; Gaps 1;

QY 1 MESPKHISQADLAKHQPDDLMISIKGYDLSKWKHPGGLPLSPAGDVTDAFI 60
DB 4 VEKPKKITSSEELKGNKGGDLMLISIQKAYNSDVKHFGDVTISNLADGVTDAFI 63
QY 61 AYHGTAMQYLDREFTGYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFVS 120
DB 64 AYHGTAMQYLDREFTGYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFVS 123
QY 121 VFLSVGYLYCKSTWALCSGLMGMLWLGSGWGHDSCHQVMPNKLRLFOIIAG 180
DB 124 VFLSVGYLYCKSTWALCSGLMGMLWLGSGWGHDSCHQVMPNKLRLFOIIAG 183
QY 181 NVIASVVAWMLKDHNTHTHACNSANLDPDLOHPIAISPKFNSLTSYHNCKMTYDR 240
DB 184 NVIASVVAWMLKDHNTHTHACNSANLDPDLOHPIAISPKFNSLTSYHNCKMTYDR 243
QY 241 AARFVSFOHTEFYPALLSVRLYLFLSPKVFNSNKRKYKSOEILGYAAFLTWYSL 300
DB 244 IARFLCYGHFFPYPCVAVNLVYQITLLFESRRK-VQDALNLMGLVFTWPLV 302
QY 301 SRIENPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHQTGTLT 360
DB 303 SRIENPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHQTGTLT 362
QY 361 AMWDWFGHGLHFOLEHNLFRPMKCHFRKISPIVNLCKHNLSTETATWANKMYST 420
DB 363 SSMDWFGHGLHFOLEHNLFRPMKCHFRKISPIVNLCKHNLSTETATWANKMYST 422
QY 421 LRAVAMEAKDVTKVPKNNWMEAMNTFG 448
DB 423 LRAVAMEAKDVTKVPKNNWMEAMNTFG 450

RESULT 6

ID AAY51349 standard; Protein; 448 AA.

AC AAY51349;

DT 27-APR-2000 (first entry)

DE Sunflower HADES protein.

KW Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;

KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;

KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;

KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;

KM pharmaceutical; food; chemical raw material.

[illegible]

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Db      365  WFHGGTGFQIEHHHLPFKMPKPRCNLEKISBPYIELECKGNLPFNVASFSKANEMLTTLTANT 422
OY      425  AMEAKDVTKPYPKVMWEANMFG 448
      |::|::|::|::|::|::|
Db      425  ALQARDITKPLPKNLVWEALHTHG 448

RESULT 7
AAU79830      AAU79830 standard; Protein; 448 AA.
XX
XX AC      AAU79830;
XX
XX      15-JUL-2002 (first entry)
XX
XX      Borago officinalis delta6-desaturase.
XX
XX      delta6-desaturase; sunflower; soybean; maize; tobacco;
XX      peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
XX      chilling tolerance; borage.
XX
XX      Borago officinalis.
XX
XX      Key      Location/Qualifiers
XX      FT      156..163
XX      FT      /label=Lipid_box
XX      FT      196..200
XX      FT      /label=Metal_box_1
XX      FT      372..377
XX      FT      /label=Metal_box_2
XX
XX      US6355861-B1.
XX
XX      12-MAR-2002.
XX
XX      19-SEP-1997; 97US-0934254.
XX
XX      13-OCT-1992; 92US-0959952.
XX      10-OCT-1991; 91US-0774475.
XX      08-JAN-1992; 92US-0817919.
XX      14-SEP-1994; 94US-0307382.
XX      28-JAN-1997; 97US-0789936.
XX
XX      (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX      Thomas TL;
XX
XX      WPI; 2002-380944/41.
XX      N-PSDB; ABK49502.
XX
XX      Novel nucleic acid encoding evening primrose delta6-desaturase which
XX      converts linoleic acid to gamma linolenic acid useful for producing
XX      gamma linolenic acid in transgenic plant or bacteria -
XX
XX      Example 9; Column 31-34; 53pp; English.
XX
XX      The invention describes an isolated nucleic acid encoding an evening
XX      primrose Delta6-desaturase. The nucleic acid and a vector expressing the
XX      nucleic acid are useful for producing a plant such as sunflower, soybean,
XX      maize, tobacco, peanut, carrot or oil seed rape plant, with increased
XX      gamma linolenic acid (GLA) content, and also for inducing or increasing
XX      production of GLA in a bacteria or plant deficient, lacking in or
XX      producing low levels of GLA. The nucleic acid is also useful for inducing
XX      chilling tolerance in plants. This is the amino acid sequence of the
XX      borage delta6 desaturase involved in the production of gamma linoleic
XX      acid.
XX
XX      Sequence 448 AA;
XX
Query Match 59.1%; Score 1459.5; DB 23; Length 448;
Best Local Similarity 55.2%; Pred. No. 7.6e-146;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

```

Qy	5	KKHSIADALAKHPOGDLWISIKGAYDISKWTKEHPGGEPLPSFAQODVTDFAIYHP	64
	6	KKIITSDELKMDKPPEDLWISIQKAYDSBVWYKHPPGGSFPLKSLAQEYTDFAVAFHP	65
Qy	65	GTAMOVYLDRFETGYVYVODYSVSEMSKDYRLVSEFSXMGLEFKTPGKYVCSIFPVSVLFA	124
Db	66	ASTWKMULDKEFTGYLKYDYSVEVSKDYRKLVFEESKMGKLYDKKHIMFATLCEIAMLFA	125
Qy	125	LSYGVGLVYCKSTWNAHCSGLMLGMLTOSGMWGHDSCHYQWMPRKINRLFOIITAGNVIA	184
Db	126	MSYGVGLVFCBGVULVHLPSCGLMGFLMTOSGMIGHAGHYMVVSDRLNKKEGIFPAANCLS	185
Qy	185	GVSVAWAKLDHNTHTHFCANSANLDPDIQHLPIIASPREFNLSTSYANHCWATYDRAARF	244
Db	186	GISIGMWMKNHNAHIAONSLEVDPLQYIIPLVYSSKFPQSLTSHFEKRLTJDSLSRF	245
Qy	245	FUSFQWHTTRYPALLSVRLYLFILSEKVVFSNNKRYKYSQELIYGAAPLWYSLLSRLP	304
Db	246	FVSYQHTTEYPIIMCARLMMYVQSL-IMLLTTRNYSYSAOBLTGLVFSIYPLVWSCLP	304
Qy	305	NMBERVWYFSCIAVAFQHMOPSLNHFASNYVTGLPBGNDMFHOQTGLNTITASAMWD	364
Db	305	NMBERIMFVYASLSVGMQOVFSLNHBESSYVYKRPKNWTFEKQDTGTIDJISCPHMD	364
Qy	365	WPHGSLHFOIENHLFPRMPKCHFRKISPIVNTLCOJANLSEYATATWMEANRMVSTLRAV	424
Db	365	WPHGSGOFOIENHLFPMKPRCMLRKISPYVIELCKKCNLPUYVYASFSAKNEMTJRLTJLNT	424
Qy	425	AMEAKDVTPKVPKNNWMEANMTEG	448
Db	425	ALQARDITKPLPKNLWEAKLHTHG	448

RESULT 8	
ABG73095	
ID	ABG73095 standard; Protein; 448 AA.
AC	ABG73095;
DT	17-APR-2003 (first entry)
DE	Borage delta-6-desaturase #1.
XX	
KM	delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
KW	maltze; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA,
KM	octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
borage.	
XX	
OS	Borage officinalis.
XX	
Key	Location/Qualifiers
FM	Misc-difference 370
FT	/note= "Encoded by TTG"
XX	
PN	US2002108147-A1.
XX	
PD	08-AUG-2002.
XX	
PF	21-DEC-2001; 2001US-0029756.
XX	
PR	13-OCT-1992; 92US-0959952.
PR	19-SEP-1997; 97US-0934254.
PR	10-OCT-1991; 91US-0774475.
PR	08-JAN-1992; 92US-0817919.
PR	14-SEP-1994; 94US-0307382.
PR	28-JAN-1997; 97US-0789936.
PA	(THOM) THOMAS T L.
XX	
PI	Thomas TL;
XX	
XX	
DR	WPI, 2003-066659/06.
DR	N-PSDB; ABX15366.

XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatrienoic acid production in plant -
 XX
 PS
 XX Example 9; Fig 5B; 55pp; English.

CC The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GLA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GLA content from the plant
CC cell, for inducing or increasing production of GLA in an organism lacking
CC in or producing low levels of GLA and for inducing production of
CC octadecatrienoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecatrienoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GLA substrate. This sequence represents
CC a borage delta-6-desaturase polypeptide.

SQ Sequence 448 AA;

Query Match	59.1%	Score 1459.5	DB 24	Length 448
Best Local Similarity	55.2%	Pred. No. 7.6e-146		
Matches 245	Conservative 90	Mismatches 108	Indels 1	Gaps 1

```
Oy      5 KKHISQADLAKHKORGDWMIISKGVYDISKWTKEHFGSELPLLSFAGODVTDAPIAYHP   64
        ||:: : : |||||::| : | : ||| | | | | | | | | | | | | | | | | |
Db      6 KKYSINDELKNHKDPRGDLWISIQGKAVDSVDWKDHPPGSFPLSLSGAEVTDFAVAFHR   65
```

Accession	Protein	Length	Score	E-value	Ident	Mismatches	Gaps	Positives	Negatives
Dd	ASTMKNLDRKFFTCYILKQDYSVEVKDVRKLVFEESKMGKGLDYKKGHIMFATLCIAMLFA	66	125	1.0e-10	12	1	0	12	1
Qy	LSVYGVLYCKSTWAHLCSGLMGMLMLDSGVVGHDSCHYQVMPNRKLNRLFOIITAGNVIA	125	184	1.0e-10	18	1	0	18	1
Dd	MSVYGVLPFGVYLNLHFSGLMGFMIMDSGMVGHDSCHYQVMPNRKLNRLFOIITAGNVIA	126	185	1.0e-10	19	1	0	19	1
Qy	GVSVAWAKLDHNTNHNACNSANLDDIDHLPILAIISPEFNSLSIYNHNCMTYDRAARF	185	244	1.0e-10	24	1	0	24	1
Dd	GISIGWKKNNHNAHIAACNSLSEYDDLOIYIPFLVSSKFESLSIHYEKRKLTFDSLSRF	186	245	1.0e-10	25	1	0	25	1
Qy	FVSEFHMTFYPALLSRYLYFLTSPKRVFNSNNKRYKRSOEILGAAFLTWYSLLSRLP	245	304	1.0e-10	30	1	0	30	1
Dd	FVSIQHTMTEPPIICARLNMVQSL-IMLLTKRNVSYRAOBLDCLVFSIWTYPLVSLCP	246	304	1.0e-10	31	1	0	31	1
Qy	NMBEIRVWYFTSCIAVAGFOHMQFSLNHNASNYVTGLPESGNMFPHQOTKGTILITASAWMD	305	364	1.0e-10	36	1	0	36	1
Dd	NMBEIRIMFVIAISLSTVGMQVOFSLNHTSSSVYGVKPGNNWFKKQDGTIDISCPPMMD	305	364	1.0e-10	37	1	0	37	1
Qy	WFGHGLHFOIENHLFPRMPKCFPRKISIPVLNLCOKNLSYETATIMMEANKVYSLIRAV	365	424	1.0e-10	42	1	0	42	1
Dd	WFGGSGQFOIENHLFPRMPKRCMLRKISIPVIELCKGNLPPYVASFSKXANEMTLRTLRNT	365	424	1.0e-10	43	1	0	43	1
Qy	AMEAKDVTKEVPRKGMWMEAMNTEG	425	448	1.0e-10	44	1	0	44	1
Dd	ALQARDITKPLPKNLVWEALHTHG	425	448	1.0e-10	45	1	0	45	1

KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN WO9846765-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; 98WO-US07422.
 PR 11-APR-1997; 97US-0833610.
 PA (ABRO) ABBOTT LAB.
 PA (CALC) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI; 1999-009334/01.
 XX New nucleic acid encoding deltas and other desaturase enzymes -
 PT useful in production of oils of increased arachidonic acid content,
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 XX Disclosure; pages 96-98; 153pp; English.
 XX The present sequence represents a fatty acid delta-6 desaturase enzyme.
 CC The specification describes methods for desaturating a fatty acid and
 CC for producing a desaturated fatty acid by expressing increased levels of
 CC a desaturase. The present desaturase is an enzyme which introduces a
 CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
 CC molecule. The enzyme can be used for desaturating fatty acids. The
 CC enzyme can be used to produce polyunsaturated fatty acids, which can
 CC be used for treating malnutrition, in pharmaceutical compositions,
 CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
 CC be used for treating e.g. restenosis after angioplasty, inflammation,
 CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
 CC or reduce blood pressure. They can also be used to inhibit platelet
 CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
 CC proliferation of vessel wall smooth muscle and fibrous tissue.
 CC reduce or prevent gastro-intestinal bleeding and other side effects
 CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
 CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
 CC and chronic fatigue after viral infections, treat AIDS, multiple
 CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
 CC disorders.
 CC
 SO Sequence 446 AA;
 Query Match 58.8%; Score 1451.5; DB 20; Length 446;
 Best Local Similarity 55.2%; Pred. No. 5.3e-145;
 Matches 244; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

DB 246 FVSQGWTFYPIPCARLMMYQSL-IMLTGRNVSYRAQELGCLVFSIWPPLVSCLP 304
 QY 305 NMPERVMYPTSLCAVAGPQHMQPSLNHFASNNYTG.PSGNDMEFHQTKTLNTAAMPD 364
 DB 305 NNGERIMFVIALSVGMQOVPSLNHFSSVYVGKPKNNWFEKQTDITLIDSCPPMND 364
 QY 365 WFGGLHFOIEHHLPFPMKCHFRKISPIVNTKLCQGNLSYETATWMEANKVYSTLRAY 424
 DB 365 WFGGLHFOIEHHLPFPMKCHFRKISPIVNTKLCQGNLSYETATWMEANKVYSTLRAY 424
 QY 425 AMEADVTYKVPKNNWMEAMNT 446
 DB 425 ALQARDITKPLPKNLVMEALHT 446
 RESULT 10
 ABG73417
 ID ABG73417 standard; Protein; 448 AA.
 XX
 AC ABG73417;
 DT 16-APR-2003 (first entry)
 XX
 DE Borage delta-6-desaturase #2.
 XX
 KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
 KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KW octadecetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 XX borage.
 OS Borage officinalis.
 XX
 XX US2002108147-A1.
 XX
 XX 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001US-0029756.
 XX
 PR 13-OCT-1992; 92US-0959952.
 PR 19-SEP-1997; 97US-0934254.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 PA (THOM/) THOMAS T L.
 XX
 PI Thomas TL;
 XX
 DR WPI; 2003-06659/06.
 XX
 PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecetraenoic acid production in plant -
 XX
 XX Example 15; Fig 11; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC a borage delta-6-desaturase polypeptide.

Sequence 448 AA;
Query Match 58 64; Score 1446.5; DB 24; Length 448;
Best Local Similarity 54.38; Pred. No. 1.8e-144;
Matches 241; Conservative 94; Mismatches 108; Indels 1; Gaps 1;
QY 5 KKHISADLAKHOPGDLWISIKKVDISKWTEHFGELPLISFAGQVDTAFIAYHP 64
D 6 KKITDELKNNHKKPGLWISIQKAYDSDWKDHGGSFPLKSLAGQVDTAFVAFHP 65
QY 65 GTAMQVYDRFFFTGYVODIVSENSKDYRLVSEBSFMGLFKTPGKGVCSIFPVYLF 124
D 66 ASTMKLIDKFEFTGYLLDYKDVSEVSKDYRLVFEFSKMGLYDKKHIMFATLCFIAMLF 125
QY 125 LSYGVYLYCKSTMAHLCSSGLMGLMLOGMGVGHDSCHYVMPNRKRLFOIAGVIA 164
D 126 MSYGVYLYFCGVLVHLSGCLMGLMLOGMGVGHDSCHYVMPNRKRLFOIAGVIA 165
QY 185 GVSVAWVKLDHNTTHFACNSANLDPDIQHLPIAISPFNSLTSYYHNCMTYDRAARF 244
D 186 GIGIGWKKMNNHNAHIACNLEVDPLQYIPLVSSKFFGSLTSHFEKRLIFDSLSRF 245
QY 245 FVSFGWTFYRALLSVRLYFILSKVYFSNNKRVYRSGEILGYAFLTWYSLLSRLP 304
D 246 FVSFGWTFYRALLSVRLYFILSKVYFSNNKRVYRSGEILGYAFLTWYSLLSRLP 304
QY 305 NMPERWVYFSCLAIVAGFQHMOSLNHFASNNVTGLPSGMDWPHOQTKTLNTASAWMD 364
D 305 NMPERWVYFSCLAIVAGFQHMOSLNHFASNNVTGLPSGMDWPHOQTKTLNTASAWMD 364
QY 365 WFGGGLHFOIEHLFPRMPKCHFRKISPIYVNLCOKNLSYETATWMEANKVYSTLR 424
D 365 WFGGGLHFOIEHLFPRMPKCHFRKISPIYVNLCOKNLSYETATWMEANKVYSTLR 424
QY 425 AMEAKDVTXVPKXMTWEANNTFG 448
D 425 ALQARDITKPLKVLWEALHTHG 448

RESULT 11
AAG29290 standard; Protein; 449 AA.
XX AAG29290;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 34824.
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 18-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 20-JUL-1999; 99US-0144352.

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 PR 20-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 28-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147392.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
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 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
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 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 08-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
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 PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159637.
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 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 57.0%; Score 1407.5; DB 21; Length 449;
 Best Local Similarity 54.5%; Pred. No. 2.5e-140;
 Matches 242; Conservative 82; Mismatches 119; Indels 1; Gaps 1;

QY 5 KKHISQADLAKHKQPDLMISIKGVYDISKMTKEHPGEBLPLSPAGDVTDAFLAYHP 64
 DB 7 KRYVTSSEDLKKNKPPDLMISIQKYYDVSDWKSHPGGEAAILNLAGDVTDAFLAYHP 66
 QY 65 GTAMQYLDREFFGYVYQDVSVSEMSKDYRRLVSEFSKMLFKTRPGYVCSIFGVLPFA 124
 DB 67 GTAMHLEKRLHNGYHVRDHSVSDSKYRRLVLAERFSKRLGFPDKKGVTLTYLLCVGMFLA 126
 QY 125 LSYVGVLYCKSTWAMHLCSGILMGMLLQSGWYGHDSCHYQVMPNRKLNRLFOIAGNVIA 184
 DB 127 AVLYGVLACTSIWAMHLSAVILGLMIQSAVYGHDSGHYTVISTKRCNKLIQLSGNCUT 186
 QY 185 GVSVAWKKLDHNTTHFACNSANLDPDIQHLPTIALSPKFPNSILTSYHNCMTYDPAARF 244
 DB 187 GISIAWKKWTHNAHNLACNSLDHDPDLOHPIPIFAVSTKFPNSWTSRFGKLTFFDLARF 246
 QY 245 FVSPQWTEYFPALLSVRLYFLTILSPKVPNSNKKRYVKRSEOLIGYAPLITWYSLLSRLP 304
 DB 247 LLSYQWTFPVPWCGRINLFTQTFLLPS-KKHVEDRLNLTAGILVFTWFLVSLP 305
 QY 305 NMPERVMYFTSCLAVAGFOHMOFSLNHFASNYVTGLPSGNDWFHQOTKGLNTITASAMWD 364
 DB 306 NMQERPIFYVSPFAVTAIQHVOFCNLHFADYVTGPPNDMEKOTAGTLDISCRSPMD 365
 QY 365 WPHGGLHFOIEHLFPRMKCFHRKISPIVVKLCQKHNLSEYETATWEMANKVYSTLRAY 424
 DB 366 WFFGGLQFQLEHNLFPRLPRCHLRTVSPVKEICKKHNLPRSLSWEMANVMTIRLKN 425
 QY 425 AMEAKDVTKEPVKRWEMAMNTFG 448
 DB 426 AIQARDATNPVLDKNLMEAVNTHG 449

RESULT 12

AA51333 standard; Protein; 449 AA.

AC AA51333;

DT 27-APR-2000 (first entry)

DE B. napus sidl protein.

KW Sphingolipid desaturase; sidl; sphingobase; ceramide; capnoid;
 transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 tolerance; resistance; soil salinity; ion stress; toxicity; drought;

KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material.
 XX Brassica napus.
 OS DE19828850-A1.
 PN 30-DEC-1999.
 PD 27-JUN-1998; 98DE-1028850.
 XX 27-JUN-1998; 98DE-1028850.
 PF 27-JUN-1998; 98DE-1028850.
 XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 PA Heinz E, Zaehlinger U, Schmidt H, Sperling P;
 PI MPI; 2000-127549/12.
 DR N-PSDB; AA244832.
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 PS Claim 8; Fig 2; 62pp; German.
 XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents the Brassica napus sphingolipid
 CC desaturase. Sld1 protein described in the method of the invention.
 CC
 SQ Sequence 449 AA;

Query Match 56.5%; Score 1395.5; DB 21; Length 449;
 Best Local Similarity 54.1%; Pred. No. 4.8e-139;
 Matches 240; Conservative 85; Mismatches 118; Indels 1; Gaps 1;

QY 5 KKHISQADIAKHKOPGDLWISIKKYDYSKWKHEHGGELPLLSFAGODVDTAFIAYHP 64
 DB 7 KRITSDDLKKNHOPGDLWISIKKYDYSKWKHEHGGELPLLSFAGODVDTAFIAYHP 66
 QY 65 GTAMQYLDREFTGYVYVODYSVSEMSKDYRRLVSEFSKMGFKPTKPGKGVCSIFVSVLFA 124
 DB 67 GTAMRHLEMLNHNHYVYVODYSVSEMSKDYRRLVSEFSKMGFKPTKPGKGVCSIFVSVLFA 126
 QY 125 LSYGVLYCKSTNAHLCSGLMGMWLOSQVGHDSCHYVWPKRKLNRFOIIAGNVLA 184
 DB 127 AAVYGVVACTSIWAHLISAVLLGLWISQVYVGHDSCHYVWPKRKLNRFOIIAGNVLA 186
 QY 185 GVSVAWVKLDHNTNHNHACNSANDPDIOHPIITAISSPKFNSLTSYHNCMKMYDRAARF 244
 DB 187 GISIAWVKMTNHNHNSCNSLDHDPDIQHPVLAIVSKFKSNTSRPYGKGLTFDPLARF 246
 QY 245 FVSFQHTFYPALLSVRLYLFIISPKVVSNNKRYKRSQELIGYAAFLTWSILLRRLP 304
 DB 247 LISYQHSFPIPCVGRINLFIQTLILHS-RRYVPRRAINTGILVFWWFLVLSFLP 305
 QY 305 NMPERWYTFSCIAVAGFQHWQSLNHNHNSVYTGILPSGNDWHTQOTGLTINTASAMWD 364
 DB 306 NMOERITFVFLMAVVAIOHVOCLNHFADVYTGPNNGDMWFKOTAGTGLDISCRSYMD 365

QY 365 WFGHGLHFOIEHNLPRMPKCHFRKISPIVYNKLCQKHNLSEYETATWEANKVYSTLRRAV 424
 DB 366 WFFGGLQFOLEHNLPRMPKCHFRKISPIVYNKLCQKHNLSEYETATWEANKVYSTLRRAV 425
 QY 425 AMEAKVYTKFVPPKXMYWEAMNTFG 448
 DB 426 AVQARDVTNPVLENLMLREALNTHG 449

RESULT 13
 AA51348
 ID AA51348 standard; Protein; 458 AA.
 XX
 AC AA51348;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE Sphingolipid desaturase protein.
 XX
 KM Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material.
 XX
 OS Unidentified.
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
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 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 PI Heinz E, Zaehlinger U, Schmidt H, Sperling P;
 DR MPI; 2000-127549/12.
 DR N-PSDB; AA244851.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 PS Disclosure; Fig 15; 62pp; German.
 XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a sphingolipid desaturase protein
 CC described in the method of the invention.
 CC
 SQ Sequence 458 AA;

Query Match 56.3%; Score 1391.5; DB 21; Length 458;
 Best Local Similarity 52.7%; Pred. No. 1.3e-138;
 Matches 224; Conservative 90; Mismatches 119; Indels 1; Gaps 1;

QY 5 KKHISQADIAKHKOPGDLWISIKKYDYSKWKHEHGGELPLLSFAGODVDTAFIAYHP 64
 DB 7 KRITSDDLKKNHOPGDLWISIKKYDYSKWKHEHGGELPLLSFAGODVDTAFIAYHP 66

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
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PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
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PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 28-JUL-1999; 99US-0145951.
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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.

Search completed: January 1, 2004, 06:36:51
Job time : 43.2461 secs

PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
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PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 55.6%; Score 1372.5; DB 21; Length 449;
Best Local Similarity 51.7%; Pred. No. 1.3e-136;
Matches 231; Conservative 95; Mismatches 120; Indels 1; Gaps 1;

QY 2 EEPKKHISQADLAKHOPGDMISIKGVYDISKWTKEHPGELPLISFAGQDVTDAFIA 61
DB 4 ETEKKYITNEDLKKHNSGDLMTAIOGKYVNSDWMIKTHPGDVTIILVGDVTDAFIA 63
QY 62 YHGTAMQVYDRFTGYVODYSVSEMSKDYRRLVSEFSKMGPKTPGKGVYCSIFPVSV 121
DB 64 FHPGTAMHLDHLFTGTHIRDFOVSEVSRDYRRMALEFRKLGLENKGAVTLTYLAFVAA 123
QY 122 LFALSYGVLYCKSTWHLCSGLMGLMLOSGWGHDSCHYOVMYRKLRLFOIAGN 181
DB 124 MFLGVLYGVLAGTSVFAHQIAAALLGLMLOSAVIGHDSGHYVIMSKSYNRFAGLLSGN 183
QY 182 VIAGSVANMKLDHNTTHFAKNSANLDDPIQHLPIAISPKFPNSLTSYHNCMTYDRA 241
DB 184 CLTGISIAWKKWTHNAHLACNSLDYDPIQHPVFAVSTKFFSLTSRFDKLTDPDV 243
QY 242 ARPFVSPQWTFYBALSLVLYPIISFKVYPSNNKRYRSGEILGYAFLTWYSLLS 301
DB 244 ARFLVSIQHFTYYPVWCFFGRINLFIOFLLFS-KREVDPDALNPAIIVFWTFPLVS 302
QY 302 RLBNWPERVWYFTSCLAIVAGFOHMFSLNHFASNVYTGSLPSGNDWFHOQTKTLNITAS 361
DB 303 CLBNWPERFFVFTSFTVTLQHIQFTLNFPADVYGPPTGSDWPFKQAACTIDISCRS 362
QY 362 WMDWFGHGLFQIEHHIFPPMPKCHFRKISPIYNKLCQKINLSYETATMEANKMYVSTL 421
DB 363 YMDWFGGLQFOLEHHIFPRLPRCHLRKVSPPVQELCKKNLPIYSMSWFEANVLTINTL 422
QY 422 RAVAMEAKDYTKRVPKMYMEANTFG 448
DB 423 KTAAYQARDVANPVXNLVWEALNTHG 449

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 16.8616 Seconds
(without alignments)
2555.128 Million cell updates/sec

Title: US-09-857-524B-2
Perfect score: 2470
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1407.5	57.0	449	2 A84900	hypothetical prote
2	1395.5	56.5	449	2 T50555	delta-8 sphingolip
3	1391.5	56.3	458	2 S68358	delta-8 sphingolip
4	1372.5	55.6	449	2 T47950	delta-8 sphingolip
5	622	25.2	523	2 JC7556	linoleoyl-CoA desa
6	454	18.4	444	2 T13155	linoleoyl-CoA desa
7	449	18.2	444	2 UG0180	delta-6 fatty acid
8	449	18.2	473	1 T26280	linoleoyl-CoA desa
9	385	15.6	447	1 T43319	delta-5 fatty acid
10	371.5	15.0	454	2 H88791	protein T13P2.1 f
11	257	10.4	345	2 T36617	probable Delta6 fa
12	220	8.9	359	2 S35157	Delta6 fatty acid
13	183	7.4	368	2 S54609	linoleoyl-CoA desa
14	173	7.0	359	2 S52650	omega-3 fatty acid
15	166.5	6.7	384	1 S54484	probable fatty aci
16	161	6.5	387	2 T07687	omega-6 desaturase
17	159.5	6.5	135	2 A86390	hypothetical prote
18	157	6.4	137	2 S46307	cytochrome b5 - r1
19	152.5	6.2	134	2 T52469	cytochrome b5 (imp
20	152.5	6.2	147	2 S67453	probable heme bind
21	152	6.2	438	2 T15039	omega-3 fatty acid
22	151	6.1	370	2 B83034	conserved hypochet
23	148.5	6.0	120	2 S63052	cytochrome b5 - ye
24	148	6.0	139	2 S46306	cytochrome b5 - co
25	146.5	5.9	134	2 T00796	cytochrome b5 At2g
26	145	5.9	121	2 H96631	probable Cytochrom
27	144.5	5.9	140	2 T52468	cytochrome b5 (imp
28	143	5.8	427	2 G70590	probable deaA3 pro
29	142.5	5.8	135	2 T09946	cytochrome b5 - bc

30	142.5	5.8	890	2 T11805	nitrate reductase
31	142.5	5.8	900	2 S47029	nitrate reductase
32	142	5.7	881	2 S25445	nitrate reductase
33	141.5	5.7	352	2 B69901	fatty-acid desatur
34	141.5	5.7	453	1 JQ2339	omega-3 fatty acid
35	141.5	5.7	904	1 RDNTNT	nitrate reductase
36	140.5	5.7	446	1 JQ2336	omega-3 fatty acid
37	140.5	5.7	591	1 CBBY2	L-lactate dehydrog
38	140.5	5.7	904	1 RDNTNS	nitrate reductase
39	139.5	5.6	134	2 T14454	cytochrome b5 - w1
40	139.5	5.6	135	2 S49200	cytochrome b5 - co
41	139	5.6	132	2 E84905	probable cytochrom
42	139	5.6	380	2 JQ2338	omega-3 fatty acid
43	138.5	5.6	359	2 AG2005	omega-3 fatty acid
44	137.5	5.6	129	2 T41083	probable cytochrom
45	137.5	5.6	431	2 T07685	omega-3 fatty acid

ALIGNMENTS

RESULT 1
A84900
hypothetical protein At2g46210 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 02-Feb-2001
C/Accession: A84900
R/Jin, X.; Kaul, S.; Rounsley, S.D.; Shua, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eues, D.; Niernman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MID:20083487; PMID:10617197
A/Accession: A84900
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-449 <STO>
A/Cross-references: GB:AF002093; NID:93702328; PIDN:AAC6285.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g46210
A/Map position: 2

Query Match	Score	57.0%	DB 2;	Length	449;
Best Local Similarity	54.5%	Pred	No. 12e-110;		
Matches	242;	Conservative	82;	Mismatches	119;
				Indels	1;
				Gaps	1;
Qy	5	KKHISQADLAKHKOPDLMISIKGVYDISKTKHFGGELPLSPAGODVDTAFAYHP	64		
Db	7	KHYVISEDLKKNKPKDLMISIQGVYDVSMDVKSHRGGEMALINLAGDVTDAFYAHP	66		
Qy	65	GTAMQYLDKFFPGYVYVDSVSEMSKDYRLVSEPSKMGCLPRTGKGVYCSIFVSVLPA	124		
Db	67	GTAMHLEKLNHGYHVDHVSVDSDYRLVLAEFKRGCLPDKKGHVTLTYTLTCVGMMA	126		
Qy	125	LSVYGVLYCKSTMAHLCGMLMGMLGSGVCHDSCHQWMPNRLNLFQIIAANVLA	184		
Db	127	AVLYGVLYCTSIWAHLISAVLLGLMTQSAVYGHDSGHTVSTKCNKLQILSNCLL	186		
Qy	185	GVSVAWMLKDNHTTHPACNSANLDPDIOHLPITLSPKFNSTLYSHNCKMYDPAARF	244		
Db	187	GSISAWMKWTHNAHNAICNSLDHDPLOHLPFAVSTKFNMTSFRYRKLPFDPLARF	246		
Qy	245	FVSPQHWTFYPLALLSVRLYPLFLSPKVVNSNNKRVYKSGEILGTAAPLTYWSLSLSRLP	304		
Db	247	LISYQHWTFYPMVCGRINLFIQTFLFLRS-KRHVPDRALNTAGLIVFTWTFPLVSLP	305		
Qy	305	NNPERVMYFTSLCAVAGPQHQFSLNHPASNYVTGIPSGNDWFHOQTKTLNTTASAMPD	364		
Db	306	NNOERTIFVFSFAVYALDHVQPCLNHPADAVYTGPNNDWPEKOTACTLIDISCRSPMD	365		
Qy	365	WFGGGLHFOIEHNLFPKPKCHFRKISPIVNLKCOGHNLSYSTATATWMEANKVYSTRAV	424		
Db	366	WFGGLQFQLEHNLFPRLRPRCHLRITVSPVVKELCKKGNLPYSLSWMEANVTIRTLKNA	425		

Qy 425 AMEAKDVTKEPVKMMWEAMNTFG 448
 Db 426 AIOARDTNPVLKNLMEAVNTHG 449

RESULT 2

delta-8 sphingolipid desaturase (imported) - rape

C/Species: Brassica napus (rape)
 C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
 C/Accession: T50555

R/Speering, P.; Zaehneringer, U.; Heinz, E.

J. Biol. Chem. 273, 28590-28596, 1998

A/Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome

A/Reference number: Z22986; MUID:99003197; PMID:9786850

A/Accession: T50555

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-449 <SPE>

A/Cross-references: EMBL:AJ224160; PIDN:CA11857.1

A/Experimental source: cultivar Drakkar

C/Genetics:

Query Match 56.5%; Score 1395.5; DB 2; Length 449;
 Best Local Similarity 54.1%; Pred. No. 1.2e-109;
 Matches 240; Conservative 85; Mismatches 118; Indels 1; Gaps 1;

Qy 5 KKHISOADLAKHQPGLMWSIKGKYDYSKTEHPGGLPLLSFAGODVDTAFIAYHP 64
 Db 7 KRFTSDLKKHNPGLMWSIKGKYDYSKTEHPGGLPLLSFAGODVDTAFIAYHP 66

Qy 65 GTAMQVLDREFTGYVVDYVSSEMSKDYRLVSEFSKMGLEFKTPGKGVYCSIFVSVLFA 124
 Db 67 GTAMRHLENNHNGYHVDHVDSDYRRLAERFSGKGLFDKKGHTLVTLTCVAAMLA 126

Qy 125 LSYVGVLYCKSTWMLHCSGLMGLMLOSQVGVHDSCHYOVMRKLNLRLFOIAGNVIA 184
 Db 127 AVVYGVVACTSIYHMLSAVILGLMLOSQVGVHDSCHYOVMRKLNLRLFOIAGNVIA 186

Qy 185 GVSVAWMLKLDHNTTHFACNSANLDPDIOLHPIAISPKFNSLTSYHNCMTYDRAARF 244
 Db 187 GISIAWMLKTHNAHNSLSDHDPDLOHPIAVLSKFKFSMTSRYYGRQLTFDPLARF 246

Qy 245 FVSGQHTFYPALISVRLYLFIISFKVPSNNKRYRSGEILGYAFLTWYSLLSRLP 304
 Db 247 LLSYQHSFYPIMCVGRINLFIOTLLILFS-RRVPPRALNIGILVFWTFPLVSLP 305

Qy 305 NMPERVYFTSCLAVAGFQHMOPSLNHPASNVYTGPSGNDWFHQOTKGLTINTASAMWD 364
 Db 306 NMOERILFVFLSNVAVIIOHVQFLNHPADVYTGPPGNDWFHQOTKGLTINTASAMWD 365

Qy 365 WFGHGLFQIEHNLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYSTLRAY 424
 Db 366 WFGGLFQIEHNLFPRLPCHLRGSPVYQELCKKGNLPLRSLSWMEANVTILRTIRKA 425

Qy 425 AMEAKDVTKEPVKMMWEAMNTFG 448
 Db 426 AVQARDVTNPVLKNLMEAVNTHG 449

RESULT 3

delta-8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower

C/Species: Helianthus annuus (common sunflower)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000

C/Accession: S68358

R/Speering, P.; Schmidt, H.; Heinz, E.

Eur. J. Biochem. 232, 798-805, 1995

A/Title: A cytochrome-b(5)-containing fusion protein similar to plant acyl lipid desatur

A/Reference number: S68358; MUID:96028121; PMID:7588718

A/Accession: S68358

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-458 <SPE>

A/Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1; PID:g1040729

C/Superfamily: cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein; oxidoreductase

F16-90/Domain: cytochrome b5 core homology <CB5>

F51,74/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 56.3%; Score 1391.5; DB 2; Length 458;
 Best Local Similarity 52.7%; Pred. No. 2.7e-109;
 Matches 234; Conservative 90; Mismatches 119; Indels 1; Gaps 1;

Qy 5 KKHISOADLAKHQPGLMWSIKGKYDYSKTEHPGGLPLLSFAGODVDTAFIAYHP 64
 Db 16 KKHITSELKKNPNDLWSIKGKYDYSKTEHPGGLPLLSFAGODVDTAFIAYHP 75

Qy 65 GTAMQVLDREFTGYVVDYVSSEMSKDYRLVSEFSKMGLEFKTPGKGVYCSIFVSVLFA 124
 Db 76 GTAMKHLDKLFYGVHDKYQVSDISRDYRLASEFAKGFBEKKGHVYSLCFVSLLS 135

Qy 125 LSYVGVLYCKSTWMLHCSGLMGLMLOSQVGVHDSCHYOVMRKLNLRLFOIAGNVIA 184
 Db 136 ACYGVLYSGSFVHMLSGAILGLAMWQIAYLGDHGHQVMATRMNNKFAFIQNCIT 195

Qy 185 GVSVAWMLKLDHNTTHFACNSANLDPDIOLHPIAISPKFNSLTSYHNCMTYDRAARF 244
 Db 196 GISIAWMLKTHNAHNSLSDHDPDLOHPIAVLSKFKFSMTSRYYGRQLTFDPLARF 255

Qy 245 FVSGQHTFYPALISVRLYLFIISFKVPSNNKRYRSGEILGYAFLTWYSLLSRLP 304
 Db 256 FVSGYHLYYPIVCARVNLVYQITILLISKR-IDRGNIIGTLIFWTFPLVSLP 314

Qy 305 NMPERVYFTSCLAVAGFQHMOPSLNHPASNVYTGPSGNDWFHQOTKGLTINTASAMWD 364
 Db 315 NMPERAVFVLSVPCVGIQHOIPLNHPGSDVYVGPKNWFEKQTRGIDDIAGSMD 374

Qy 365 WFGHGLFQIEHNLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYSTLRAY 424
 Db 375 WFGGLFQIEHNLFPRLPCHLRGSPVYQELCKKGNLPLRSLSWMEANVTILRTIRKA 434

Qy 425 AMEAKDVTKEPVKMMWEAMNTFG 448
 Db 435 ALOARDTNPAPQNLMEAVNTHG 458

RESULT 4

delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana

N/Alternate names: protein F2A19.180

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000

C/Accession: T47950; T51848

R/De Haan, M.; Maarse, A.C.; Grievell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Que

submitted to the Protein Sequence Database, January 2000

A/Reference number: Z24480

A/Accession: T47950

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-449 <DEH>

A/Cross-references: EMBL:AJ32962; PIDN:CA871088.1

A/Experimental source: cultivar Columbia; BAC clone F2A19

R/Speering, P.; Zaehneringer, U.; Heinz, E.

J. Biol. Chem. 273, 28590-28596, 1998

A/Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome

A/Reference number: Z22986; MUID:99003197; PMID:9786850

A/Accession: T51848

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-449 <SPE>

A/Cross-references: EMBL:AJ224161; PIDN:CA11858.1

A/Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots

A:Gene: slidi
 A:Map position: 3
 A:Note: P2A19.180
 C:Function:
 A:Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated, PMID:99003197]
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 55.6%; Score 1372.5; DB 2; Length 449;
 Best Local Similarity 51.7%; Pred. No. 1e-107;
 Matches 221; Conservative 95; Mismatches 120; Indels 1; Gaps 1;

QY 2 EEPKRIHQADLAKHOPGDLWISIKKYVYISKWKTEHGEGLPLLSFAGQDVTDAFIA 61
 DB 4 ETEKKTITMEDLKKHKSGLMIAIQKQYVSDWIKTHPGDVTILNLVGQDVTDAFIA 63
 QY 62 YHFGTMOVLDRFPGTYVODVSSEMSKDYRLVSEFSKMGFKTKPGKGVCSIFVSV 121
 DB 64 FHFGTAMHLDHLEFTYHNRDFQVSEVSRDVRMAAEFRGLGFENKGVHTLYTLIAFVA 123
 QY 122 LFLALSYGVLYCKSTWALHCSGLMGMLNLSQGVGHDSCHYOVMPNRKLNRLFOIAGN 181
 DB 124 MFLGVLYGVLYCTSVRAHQIAALGLMLIQSAVIGHDSGHYVIMSKSYNRPAQLSGN 183
 QY 182 VIAGVSVAMWKLDPNTHHFACNSANLDPDIOHLPIIASEFPNSLTSYYHNCMTYDA 241
 DB 184 CLGISIAWKKWTHNAHLACNSLDVDPLOHLPVFAVSTKFPSSLJTSRFDKLTFFDPV 243
 QY 242 ARPFVSFOHMTFYPALLSVRLYLFIISFKVFSNNKRVYKRSOELIGYAAFLTWYSLIS 301
 DB 244 ARFLVSYOHFTYYPVWCFCGRINLFIOTFLFLFS-KREVDPALNPFAGILVFWTFPLVS 302
 QY 302 RLDPNPERVWYFPTSCLAVAGFQHMOPSLNHPASNVYTGLPBGNDWFHOQTKGLNTASA 361
 DB 303 CLPNWEREPFPTSTVTAHQIOTLNFADVYVGPSTGDMWEKQAGTIDISCBS 362
 QY 362 WMDPFGHGLFOIENHLFPRMPKCHFRKISPIVNLKCOQHNLSEYETATWENAKMYSTL 421
 DB 363 YMDPFGGLOFOIENHLFRLPRCHLRKISPVVDELCKGNLHYRSMSEANVLTINTL 422
 QY 422 RAVAMEAKDVTKVPKPMWEANMTTG 448
 DB 423 KTAAYQARDVANPVNKLWEALNTHG 449

RESULT 5

QY 11010501-CoA desaturase (EC 1.14.19.3) - Mucor rouxii
 JCT556
 N:Alternate names: delta6-desaturase
 C:Species: Mucor rouxii
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
 C:Accession: JCT556
 R:Laoteng, K.; Manontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
 Biochem. Biophys. Res. Commun. 279, 17-22, 2000
 A:Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desaturase
 A:Reference number: JCT556; PMID: 20563795; PMID:11112411
 A:Accession: JCT556
 A:Molecule type: DNA
 A:Residues: 1-523 <LAO>
 A:Cross-references: GB:AF290983
 A:Experimental source: strain ATCC 24905
 C:Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformation
 C:Keywords: oxidoreductase; transformation

Query Match 25.2%; Score 622; DB 2; Length 523;
 Best Local Similarity 29.7%; Pred. No. 1.9e-44;
 Matches 146; Conservative 76; Mismatches 191; Indels 78; Gaps 9;

QY 20 GDMWISIKGVYDISKWKTEHGEGLPLLSFAGQDVTDAFIAHFGTAMYL----- 71
 DB 34 GDSVLYEQKVVYVNNFMAGPGSEALRSALGRDVTDEIRTMHPQVVEKLTINLYCTGD 93
 QY 72 -----DRPFT-----GYVQDYVS-----EMSKD-- 91

DB 94 YMPDVIRPASKMOHFTFKPKEDKPYLTATWEGGTFVQAYDAIDOLAKHSHDLIKAV 153
 QY 92 -----YRLVSEFSKMGFKTKPGKGVCSIF-----FVSEPALSVYGV 131
 DB 154 LOKDLNGDOIIRAYRKLAEELYAKGLF-----CNWKYAREGCRYTLFLFLSMFTL 206
 QY 132 YCKSTWALHCSGLMGMLNLSQGVGHDSCHYOVMPNRKLNRLFOIAGNVIAGVSAW 191
 DB 207 KQETHTWMAAGAAPAMFPHQLVFTAHDSGHNEIGKSIDHIVIGIILNFIQGLSLGMW 266
 QY 192 KLDNTHHFACNSANLDPDIOHLPIIASEFPNSLTSYYHNCMTYDAARFVSFOH 251
 DB 267 KQNHVHNLVTNHPBHDPIQHPFMAITTKFPNNIYSTYKRVLPFDAAREFVHQH 326
 QY 252 TFPYALLSVRLYLFIISFKVFSNNKRVYKRSOELIGYAAFLTWYSLLSRLPNPERVW 311
 DB 327 LYVLLISFGRFNLHLSFYVLT-CNVVTRTLDELGITFFVWPSLSLTLPMTNIRIA 385
 QY 312 YFTSCLAVAGFQHMOPSLNHPASNVYTGLPBGNDWFHOQTKGLNTASAMWDFHGLH 371
 DB 386 YIMVSYMLFPLHYQITLSHFGMSTEDRGP-EPPAKMLRTTMDVDCPEHMDPFGHQL 444
 QY 372 FOIENHLFPRMPKCHFRKISPIVNLKCOQHNLSEYETATWENAKMYSTLRAVAMEAKDV 431
 DB 445 YQAVHHLFRLPRHNLRCVPLVKKFCDEVGLHYVWYNSFGVYLTGLTKSVADQVGM 504
 QY 432 TKPVRGM-VW 441
 DB 505 NEVAKSNAEIW 515

RESULT 6

QY 11010501-CoA desaturase (EC 1.14.19.3) [validated] - human
 T13155
 N:Alternate names: Delta6 fatty acid desaturase; protein DKFZP586C20.1
 C:Species: Homo sapiens (man)
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
 C:Accession: T13155; T08765
 R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
 J. Biol. Chem. 274, 471-477, 1999
 A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
 A:Reference number: Z1612; PMID:99085046; PMID:9867867
 A:Accession: T13155
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-444 <CHO>
 A:Cross-references: EMBL:AF136799; NID:94406527; PID:94406528; PIDN:AAD20018.1
 R:Mambutti, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z16471
 A:Accession: T08765
 A:Molecule type: mRNA
 A:Residues: 'RTGG', 138-428, 'D', 430, 'W', 432-444 <WAM>
 A:Cross-references: EMBL:AL050118
 A:Experimental source: adult uterus; clone DKFZP586C201
 A:Genetics: GDB:PADSD6
 A:Gene: GDB:PADSD6
 A:Cross-references: GDB:9956652
 A:Note: DKFZP586C201.1
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: cytochrome; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty
 F;18-94/Domain: cytochrome b5 core homology <CB5>
 F;53/76/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 18.4%; Score 454; DB 2; Length 444;
 Best Local Similarity 28.7%; Pred. No. 2.1e-30;
 Matches 124; Conservative 65; Mismatches 185; Indels 58; Gaps 13;

QY 9 SQADLAKHOPGDLWISIKKYVYISKWKTEHGEGLPLLSFAGQDVTDAFIAHFGTAM 68
 DB 22 SWEIEQKHNLRTDRMLVLDKRYVNTTKMSIOHPGGGRVIGHVAGBDATDAFRAFH----- 77
 QY 69 QYLDREFGTYYV-----QDYSV-SEMSKDYRLVSEFSKMGFKTKPGKGV 113

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Db      78 ---DLFVGKFLRLIGELAPESPQDHGKSKITFEDPALAKTAEDMWLFXTN----- 129
Qy      114 CSIFF-----VSVFALSYVGLYCKSTV-AHLCSGLMGMLOSQVNGHDSCHYQM 166
Db      130 -HVFLLLLAHITALESIAMFTVFGNGYIPPLITAFVATSOAQAGWLQHDYGHLSYV 188
Qy      167 PNRKRLRLFOIAGNVIAQSVAMWKLDPHTHFPACNSANLDDIDQHLPIAISPKFNS 226
Db      189 RRPKNHLVHKPFIYGLKGSANMNNRHFQHAKRPIFKDDVNNLHVFLG---EW 244
Qy      227 LTSYHNCMTYDRAARFVVSFOHMTFY---PALLSVRLYLFLSKVFSN-NKRVYK 281
Db      245 QPIREYKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 299
Qy      282 RSGEILGIAFLTWYSLLSLRLPNRBRVWYFTSCIAVAGFQHWQSLNHPASNYTGLP 341
Db      300 VSYIIFFTYIPFYGLGLT-----FLNFRFLSHMFV-WYQWNIHVEI--DOE 350
Qy      342 SGNDWFHOOTKFTLNTASAMWDPHGLHFOIENHLPMPKCHFRKTSPIVNLCKQH 401
Db      351 AYRDWSSQITATCNVBOSEFNDWFGHLMFOIEHHLFPMRNNLHKIAPLVKSLCAKH 410
Qy      402 NLSYETATWMEA 413
Db      411 GIEYQEKPLLR 422

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RESULT 7

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JG0180
Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C/Accession: JG0180
R:Aki, T.; Shimada, Y.; Inagaki, K.; Hishashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des
A:Reference number: JG0180, NUID:99160394, PMID:10049752
A:Accession: JG0180
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <AKI>
A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BAW5496.1; PID:94514722
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
F:18-94/Domain: cytochrome b5 core homology <CB5>
F:53-76/Binding site: heme iron (His) (axial ligands) #status predicted

```

Query Match 18.2%; Score 449; DB 2; Length 444;

Best Local Similarity 26.1%; Pred. No. 5.7e-30; Indels 78; Gaps 13;

Matches 120; Conservative 75; Mismatches 186;

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Qy      1 MEEPKHISQADLAKKQPDLMISIKGVYDISKWTKEHPGELPLSPAGQVTDAPL 60
Db      14 LQAPMPTFMWESIQKINLRTDRWLVIDRKVYNTKMSQRHPGHRVYIGHYSGSDATDAFR 73
Qy      61 AHNPGANQYLDREFFGYVQDYVS-----SEMSKYRLVSEFSKMGFL 105
Db      74 AFI-----LDDDFGKFLKPLLIGELAPESPQLDRKSSQITTEDFRLAKTAEDMWLF 126
Qy      106 KTPGKGVCSIFSVSLFALSYVGLYCKSTV-AHLCSGLMGMLOSQVNGHDSCHYQ 164
Db      127 KTNHLEFLLLSHIIYMESEIATILSYFGNGYIPYITAFVATSOAQAGWLQHDYGHLS 186
Qy      165 VMPNRKRLRLFOIAGNVIAQSVAMWKLDPHTHFPACNSANLDDIDQHLPIAISPKFNS 224
Db      187 VYKKSIMNHIHVHFKVIGLKGASANMNNRHFQHAKRPIFKDDVNNLHVFLG---W 244
Qy      225 NSLTSTYHNCKMTYDRAARFVVSFOHMTFY---PALLSVRLYLFLSKVFSN-NKRVYK 278
Db      245 QPLE---YGRKKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 293
Qy      279 -----YKRSQELGIAFLTWYSLLSLRLPNRBRVWYFTSCIAVAGFQ 323

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Db      294 VDLAMASVYARPFYTYIPFYGLGLVPLNFRFLSH-----WFLV----- 335
Qy      324 HMOFSLNHPASNYTGLPBGNDWFHOOTKFTLNTASAMWDPHGLHFOIENHLPMPK 363
Db      336 -WYQWNIHVEI--DLIDYRDWFSQSLATCNVBOSEFNDWFGHLMFOIEHHLFPMR 392
Qy      384 KCHFRKTSPIVNLCKQHLSYETATWMEANNNVYETLR 422
Db      393 RNNLHKIAPLVKSLCAKHGIEYQEKPLLRALDIYSSLK 431

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RESULT 8

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T26280
linoleyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - Caenorhabditis elegans
N:Alternate names: Delta6 fatty acid desaturase
C:Species: Caenorhabditis elegans
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 03-Jun-2002
C/Accession: T26280; T37238
R:Swindburne, J.; Alnough, R.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z20188
A:Accession: T26280
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-473 <WIL>
A:Cross-references: EMBL:Z70271; PIDN:CA94233.1; GSPDB:GN00022; CESP:W08D2.4
A:Experimental source: clone W08D2
R:Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A:Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by he-er
A:Reference number: Z21637, NUID:98149727, PMID:9480865
A:Accession: T37238
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-38,69-430,'V',432-473 <NAP>
A:Cross-references: EMBL:AF031477; NID:93088519; PIDN:AA015586.1; PID:93088520
C:Genetics:
A:Gene: CESP:W08D2.4
A:Map position: 4
A:Intons: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
A:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

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Query Match 18.2%; Score 449; DB 1; Length 473;

Best Local Similarity 28.2%; Pred. No. 6.1e-30; Indels 100; Gaps 18;

Matches 138; Conservative 65; Mismatches 187;

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Qy      17 KQPGDLMISIKG-VYDISKWTKEHPG-----ELPLS----- 49
Db      5 KNASGLRMKVDGKMWLYSELYKKHPGAVIEQYSIPLNKNIETRGITTRGSSNALDI 64
Qy      50 ---FAGQDVTDPIAYHPGTAMQY-----LDRFTGYVQDY 83
Db      65 LVFYRNSDATNHFAPHESSQAYVKQLDLKKGHEDEFLKQLEKRLDKVDINVSAYDV 124
Qy      84 SVSEMSKYRLVSEFSKMGFL-----GLFKTEGKYCYCIFPVSULFALSYVC-VLYKSS 135
Db      125 SVAQERK---WVESFEKRLKRLHDDGLMKANE---TYFLPKAISTSIAMFAFYLY 175
Qy      136 TNAHLCSGLMGMLOSQVNGHDSCHYQVMPNRKRLRLFOIAGNVIAQSVAMWKLDPH 195
Db      176 LGWYITSAQLLALAQQFQWLTHERFHOPTKRNPLNDITSLFNGFLQGFSDWKKDKH 235
Qy      196 NTHHFPACNSANLDDIDQHLPIAISPKFNSLTSYHNCMTYDRAARFVVSFOHMTFY 255
Db      236 NTHHATNVIDHDGIDIALPLAFATP---GDLCKY---KASFEKALIKTIVPYOHLYFTA 288
Qy      256 ALISVRLYLFLSKVFSN-NKRVYKRSQE-----ILGTAAPLTWYSLLSLRLPNMP 307
Db      289 MFLMRFSWTGQSVQVQFKENQMEYKYORANFWEQATIVGHAWV-FYQLFL--LPTWP 345
Qy      308 ERVMTYTSCLAVAG--FQHWQSLNHPASNYTGLPBG---NDWFOOTKFTLNTASA 361

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Db      346 LRAVAYIISQMGGLIAH-VTFENNSVDKY---PANSRIINFAALOILFTTRNMT PSP 401
Qy      362 MWDMFPGHGFQFOEHLFPMPKCHFRKXSPIYNKLCQKHNSYERATWMEANKMYSTLT 421
Db      402 FIDMLMGSLNYQIEHHLFPTMPRCNLNACMKYKWKCKENNLPLYLVDDYFGVAMNLQOL 461
Qy      422 RAVA--MEAK 429
Db      462 KMAHEHIQAK 471

RESULT 9
T43319
Deltas fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T43319; T24875
R:Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
FEBS Lett. 439, 215-218, 1998
A:Title: Functional identification of a fatty acid deltas desaturase gene from Caenorhab
A:Reference number: Z22422; MUID:99059458; PMID:9845325
A:Accession: T43319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-447 <MIC>
A:Cross-references: EMBL:AF078796; NID:g4003522; PIDN:AA095143.1; PID:g4003523
R:Swindburne, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24875
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197; VSHFNN, 198-447 <MIL>
A:Cross-references: EMBL:Z81122; PIDN:CA03352.1; GSPDB:GN00022; CESP:T13F2.1
A:Experimental source: clone T13F2
C:Genetics:
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match      15.6%; Score 385; DB 1; Length 447;
Best Local Similarity 25.0%; Pred. No. 1.4e-24;
Matches 115; Conservative 74; Mismatches 199; Indels 72; Gaps 14;

Qy      23 WISIKGVYDISKMT-KEHPGELPLLSFAGODVTDALFAYHGT--AMQYLDREFTGY 79
Db      12 FIKIDKMQOIDDVAVLRSHPGS-AITTYKNMDATVFTHTFGSKKAYQWLTELKKECP 70
Qy      80 VQDYSVSEMSKDYRLVSEFSKGLF-----KTPKGYV--CSIFP 118
Db      71 TQEPRLPIDKDPIDKIDVNV-MGTFNISEKSAQINKSFDTLRMRVRAEGLMDGSPLEY 129
Qy      119 V-----SVLFALSVGLVCKSTWMLCSGLMGLMLOSQWGHDSCHYQVMPNKK 170
Db      130 IKKILETITLIFA-----FLYQHTYLPALIMGVAMQOLGWLHFAHQLFKNXY 183
Qy      171 LNRLFOIAGNVYAGVAMWKLNDHTNHFACNSANLDPDIQHLPIALISPKFNFSLTSY 230
Db      184 YNDLASVFGNPLQVSHFNNGFSGGWKEQHNHAAATNVVGRDGLDLP-----FYATVAH 236
Qy      231 YHNCKMTYRRAARFVFSQ---HMTFYPALLSVRLYLFIISFKVVSNNKRVYKRSQEI 286
Db      237 LNN---YSQDSVWVTLFRMOHVHTFMLPFLRLSMLOSIIFVSQMPHTYVDYRNAT 292
Qy      287 ---LGYAFLTWYSLLSRLPMPERVNYFTSCLAVAG-----FOHWQPSLNHFAFN 335
Db      293 YEOVGSLHWANSLGQLYFLPDMSTRIMFVLVSHLVGGLSLHVTFFNYSVEKPAIASN 352
Qy      336 VYTGLPDSGNDWFHQQTGTLNITASAMWDFHGLHFOIEHLFPMPKCHFRKXSPIYN 395

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Db      353 IM-----SNVACIQIMTTRNNRPGRFIDMLWGSLNYQIEHHLFPTMPRHNLNTVMPLVK 406
Qy      396 KLCQKHNSYERATWMEANKMYSTLTBAVAMEAKDYTKPV 435
Db      407 EFAAANGLPYWDYFTGFWLEIEQFRINAVAAKLTCKI 446

RESULT 10
H88791
protein T13F2.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H88791
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88791
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:chr_IV; PIDN:CA03352.1; PID:g3879828; GSPDB:GN00022; CESP:T13F2.1
C:Genetics:
A:Gene: T13F2.1
A:Map position: 4
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match      15.0%; Score 371.5; DB 2; Length 454;
Best Local Similarity 24.6%; Pred. No. 1.9e-23;
Matches 115; Conservative 74; Mismatches 199; Indels 79; Gaps 15;

Qy      23 WISIKGVYDISKMT-KEHPGELPLLSFAGODVTDALFAYHGT--AMQYLDREFTGY 79
Db      12 FIKIDKMQOIDDVAVLRSHPGS-AITTYKNMDATVFTHTFGSKKAYQWLTELKKECP 70
Qy      80 VQDYSVSEMSKDYRLVSEFSKGLF-----KTPKGYV--CSIFP 118
Db      71 TQEPRLPIDKDPIDKIDVNV-MGTFNISEKSAQINKSFDTLRMRVRAEGLMDGSPLEY 129
Qy      119 V-----SVLFALSVGLVCKSTWMLCSGLMGLMLOSQWGHDSCHYQVMPNKK 170
Db      130 IKKILETITLIFA-----FLYQHTYLPALIMGVAMQOLGWLHFAHQLFKNXY 183
Qy      171 LNRLFOIAGNVYA-----GVSVAWKLNDHTNHFACNSANLDPDIQHLPIALISPKF 223
Db      184 YNDLASVFGNPLQVSHFNNGFSGGWKEQHNHAAATNVVGRDGLDLP-----F 236
Qy      224 FNSLSYHNCKMTYDRARFVFSQ---HMTFYPALLSVRLYLFIISFKVVSNNKRV 279
Db      237 YATVMEHLNN---YSQDSVWVTLFRMOHVHTFMLPFLRLSMLOSIIFVSQMPHTYVD 292
Qy      280 YKRSQEI---LGYAFLTWYSLLSRLPMPERVNYFTSCLAVAG-----FOHWQPS 328
Db      293 YRNATIEQVGLSLHWANSLGQLYFLPDMSTRIMFVLVSHLVGGLSLHVTFFNYSVE 352
Qy      329 LNHFASNVYTGLPDSGNDWFHQQTGTLNITASAMWDFHGLHFOIEHLFPMPKCHFR 388
Db      353 KPALSSNIM-----SNVACIQIMTTRNNRPGRFIDMLWGSLNYQIEHHLFPTMPRHNLN 406
Qy      389 KSPIYNKLCQKHNSYERATWMEANKMYSTLTBAVAMEAKDYTKPV 435
Db      407 TMAPLVKEFAAANGLPYWDYFTGFWLEIEQFRINAVAAKLTCKI 453

RESULT 11
T36617
probable Delta6 fatty acid desaturase (EC 1.14.99.-) SC35.42c [similarity] - Streptomyces
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T36617
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.

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submitted to the EMBL Data Library, June 1999

A:Reference number: Z21610

A:Accession: T36617

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-345 <OLI>

A:Cross-references: EMBL:AL078610; PIDN:CA844385.1; GSPDB:GN0070; SCOEDB:SCH35.42c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCH35.42c

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 10.4%; Score 257; DB 2; Length 345;

Best Local Similarity 26.0%; Pred. No. 6, 1e-14;

Matches 94; Conservative 62; Mismatches 161; Indels 44; Gaps 14;

QY 91 DYRLVSESKGLF-KTPGKGYCSIFVSV--LFLASYGVLYCKSTVAHLCSGLMG 147

DB 16 DPARLSKRVADAGILGRPG---YTLRTAVTGLVAGMAAFVLGASWMTLAIAPLA 72

QY 148 MMLQSGWVGDSCHVOVMNRKLNRLFOIAGNVLAGSVAMWKDHNTHFACNSANL 207

DB 73 VMGGQVALVADMAHVRFRRRRSELSGRAGSI-GMSGWMQDRTTHANPNTEDL 131

QY 208 DPDIQHLPIAISPKFNSLTSYHNCMTYDRAARFVSPQHTFPYALLSVRLYFIL 267

DB 132 DPDIQF-DLVSPDQARATG-----LPRLGKQAFLEPFLITLEGFNHVA 179

QY 268 SFYVPSNNKRVYKRSQ---ILGYAFLTWYSLLSRLPMBRWYFTSCLAAGFQH 324

DB 180 SGRAM--ANRLKRRALDGLALLHCA--VYLTALFVLP--PGMAIAF--LAVHQLCF 230

QY 325 WQSLNHFANVTGLP-----SGNDWFHOQTKGLNTITASAWMDWHGHLHQLIEHILF 379

DB 231 GVLGSAFAFN-HKMPILTADRPDLRQVLTLSRVNGCLFTDLALGGLNHQIEHILF 289

QY 380 PRAPKCHFRKISPIVNLCKOKHLSYETATMWEANKVYSTLVAAMEADVTKPYPKM 439

DB 290 PSMPSPRLKARAIVRRCYCDLGVDAFETGLVASYRLALSLH-----DAGTPLRRT 342

QY 440 V 440

DB 343 V 343

RESULT 12

S35157 Delta6 fatty acid desaturase (BC 1.14.99.-) [imported] - *Synechocystis* sp.

C:Species: *Synechocystis* sp.

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000

C:Accession: S35157; S76243

R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

Plant Mol. Biol. 22, 293-300, 1993

A:Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium *Synechocystis* sp.

A:Reference number: S35157; MUID:93283633; PMID:8389613

A:Accession: S35157

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <RSD>

A:Cross-references: GB:L11421; NID:9349562; PIDN:AAA27286.1; PID:9349563

R:Keneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76243

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <KAN>

A:Cross-references: EMBL:D90914; GB:AB001339; NID:91653477; PIDN:BA18502.1; PID:d101923

A:Experimental source: PCC 6803

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.9%; Score 220; DB 2; Length 359;

Best Local Similarity 24.0%; Pred. No. 8, 3e-11;

Matches 96; Conservative 54; Mismatches 148; Indels 102; Gaps 20;

QY 90 KQYRRLVSE-----PSKMGKTPGKGVCSIFVSVLRLASYGVLYCKSTVAHLCSG- 143

DB 13 RGRFRVLNQVADYFAHEHGLTQRDNPSMTLKLII-----VLMFSAAPFLFAP 62

QY 144 ----LLMGMLIQ-----SCWGHDSCHVOVMNRKLNRLFOIAGNVLAGSVAMWK 192

DB 63 VIFPVYLLSCMYALALAAFSFVYGDHANNVYSSPHINRYLGMYTDFV--GLSSFLWR 120

QY 193 LDHN-THHFACNSANLDPDIQHLPIAISPKFNSLTSYHNCMTYDRAARFVSPQHT 251

DB 121 YRHNVLHHYTYNLGHVDEIHGDGVRKSP--QEHVGIYR-----FOQFYTW 166

QY 252 TFPYALLSVRLYFLISFVPSNNKRVYKRSQ-----ELGYAFLTW--YS 297

DB 167 GLY---LFIPIYFELDYVLV--NKGKXHDHKKIPFQPLBLASLIGIK--LLMLGYVG 219

QY 298 LLISRLPMBE---RWYFTSCLAAGFQHMQPSLNPASNVYTGLPSC-----NDM 346

DB 220 LPLALGFSIPEVLIGASVYTMVYGVCTI---FMLAHVLSTEFLEPDGSGAIDEM 275

QY 347 FHOQTKGLNTI--TASAMMDWPHGGLHFOIEHILFRMPKCHFRKISPIVNLCKOKHLSY 405

DB 276 ALCQITTFANFANNPFMMFCGLNHQVTHILFPIGCHIHVPLENITIKDVCQERGER 335

QY 406 EPTATWEANKVYSTLRVAMEAKDVTKPYPKMNV--EAM 444

DB 336 K-----YPTFKAA-----IASVYRLLEAM 355

RESULT 13

S54809

linoleoyl-CoA desaturase (BC 1.14.19.3) - *Spirulina platensis*

N:Alternate names: Delta6-desaturase

C:Species: *Spirulina platensis*

C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 03-Jun-2002

C:Accession: S54809

R:Tasaka, Y.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54809

A:Accession: S54809

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-368 <TAS>

A:Cross-references: EMBL:X87094; NID:9809109; PIDN:CA60573.1; PID:9809110

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 7.4%; Score 183; DB 2; Length 368;

Best Local Similarity 22.1%; Pred. No. 1, 1e-07;

Matches 77; Conservative 47; Mismatches 100; Indels 124; Gaps 16;

QY 132 YCKSTVAHLCSGLMGMLQSGWVGHDSCHVOVMNRKLNRLFOIAGNVLAGSVAMW 191

DB 96 YSKYQWVNYLSGLT-----HDA-----IGVSSYLTM 120

QY 192 KLDHNT-HHFACNSANLDPDIQHLPIAISPKFNSLTSYHNCMTYDRAARFVSPQHT 250

DB 121 KFHNVLHHYTYNLGHVDEIHGDDELVRMS-----SMFY--RWYHRYQH 163

QY 251 W-----TFYPALLSVRLYLF-----ILSFYVPSNNKRVYK 282

DB 164 WFIWYVYRPIRYWYSADVQTMFKQYDHDEIIPSPTWIDIALTLAFKA----- 212

QY 283 SQEILGYAFL-----TWYSLISRLPMBRWYFT-----SCLAVAGFQHMQPSLNP 333

DB 213 ---FQVAVFLIPIAVGSSPLEAVI---GASIVYTHGLVACV-----FMLAHYI 257

QY 334 SNVY-----TGLPSGNDWPHOQTKGLNTITA-SAMMDWPHGGLHFOIEHILFRMPKCHFR 368

Db 258 EPAFLDPLDLHIDDEWALAQVKTIVDFAPNNPIIMWYGVGLNQTIVHLLFPHICHHP 317

QY 389 KISPIVNLCKQKINLSYET-ATMEANKVYSLTRAVANEAKVTPV 435
 Db 318 KAPILAEVCEBEGVYVAHQTFGALANYSWLKQMSINPE--TKAI 363

RESULT 14

S52650 omega-3 fatty acid desaturase (EC 1.14.99.-) - *Synechocystis* sp. (strain PCC6803)

N/Alternate names: delta 15 desaturase
 C/Species: *Synechocystis* sp.

A/Variety: PCC 6803

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C/Accession: S52650; S75843
 R/Sakamoto, T.; Los, D.A.; Higasashi, S.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.

Plant Mol. Biol. 26, 249-263, 1994

A/Title: Cloning of omega-3 desaturase from cyanobacteria and its use in altering the de

A/Reference number: S52649; PMID:9503596; PMID:7524725

A/Accession: S52650

A/Molecule type: DNA

A/Residues: 1-359 <SAK>

A/Cross-references: GB:D13780; NID:G600596; PIDN:BA02924.1; PID:G600598

A/Note: the authors translated the initiation codon GTG for residue 1 as Val

R/Kaneke, T.; Sato, S.; Kotorani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

8.

A/Reference number: S74322; PMID:97061201; PMID:8905231

A/Accession: S75843

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-359 <KAN>

A/Cross-references: EMBL:D90913; GB:AB001339; NID:G1653348; PIDN:BA16302.1; PID:G165338

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Genetics:

A/Start codon: GTG

C/Superfamily: omega-3 fatty acid desaturase

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 7.0%; Score 173; DB 2; Length 359;

Best Local Similarity 22.6%; Pred. No. 7.5e-07; Matches 84; Conservative 43; Mismatches 129; Indels 116; Gaps 20;

QY 117 FPAVSLFALSVGVLYCKSTWHLCSGLMGLMLQSG--W----VGHDSCHYQVMPNR 169

Db 47 FFLDVGILAGFYALA-----AYLDGWFYPIFMLIGTLFWGLFVVGHDGCHGSPSKK 100

QY 170 KLNRLFOIILAGNIVAGSVAMWKLNDHTTHFACNSANLDPDIOHLPIAISPFENSLTS 229

Db 101 TLNNWIGHLSHTPIL-VPYHGMWIRISHRTH--ANTGNIIDDESMYP--VSECKYQMA- 153

QY 230 YHNCMTQDRAARFVFSQHWTFYPALLSVRLYLFLISFKVVSNNKRYKRSQELIG 289

Db 154 -----WEEKLR-----FLPLIAYPIYLF-----RSPNRQG- 181

QY 290 AAFLLTWYSLLSRLPNWP-----ERVVYFTSCLAVA-----GFOHMFSS- 328

Db 182 SHF-----MPSGLRPEKKAVALSTFALAAVFGFLGFLFMQFGWMLFLKFYVA 231

QY 329 -----LHNFASNVYTGDP--SGNDWFHQQTGTLNITAS--AMMDWFHGL 370

Db 232 PVLVFWVMDLVTFLLHTEENI-----FWYRGDMYF--LKGALSTIDRDGFINPIHDI 285

QY 371 HFOIEHNLFRMPKCHFRK-----ISPIVNLCKQKINLSYETATMEANKVYSLTRAVAN 426

Db 286 GTIVAAHHTFSNMHHYKILRRATEAIKPLIGBYR-----YSDPEIWOAFKPSYAWACHFVNP 340

QY 427 EAKDVTKPVPKN 438

Db 341 QGSGVYVYQSPSN 352

RESULT 15

S54484 probable fatty acid hydroxylase (EC 1.14.15.-) YMR272c - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: protein YMR156.14c

C/Species: *Saccharomyces cerevisiae*

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Apr-2002

C/Accession: S54484

R/Lye, G.; Churchev, C.M.

submitted to the EMBL Data Library, May 1995

A/Reference number: S54014

A/Accession: S54484

A/Molecule type: DNA

A/Residues: 1-384 <LYE>

A/Cross-references: EMBL:Z49260; NID:G809081; PID:G809095; GSPDB:GN00013; MIPS:YMR272c

A/Experimental source: strain AB972

C/Genetics:

A/Genes: SGD:SCS7; MIPS:YMR272c

A/Cross-references: SGD:S0004885

A/Map position: 13R

C/Superfamily: yeast probable membrane protein YMR272c; cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein; oxidoreductase; transmembrane protein

F/3-89/Domain: cytochrome b5 core homology <CB5>

F/200-216/Domain: transmembrane #status predicted <TM1>

F/223-239/Domain: transmembrane #status predicted <TM2>

F/287-303/Domain: transmembrane #status predicted <TM3>

F/57-72/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.7%; Score 166.5; DB 1; Length 384;

Best Local Similarity 21.2%; Pred. No. 2.9e-06; Matches 96; Conservative 67; Mismatches 141; Indels 149; Gaps 25;

QY 9 SQADIAKHQKQPDLLISIKG-KVYDISKTKENPGCELPPLSPAQDVT----DAFIAYH 63

Db 13 SKKTVQEHNTADVTCWYQNRKIVDTVRFLSHPGDBSILDYAGKDITKIMKDSVHSH 72

QY 64 PGTAMQYL-DRFRTYVYVDYVSSEMSKDYRRLVSEFSMGFLKTPKGVYSIFVSVL 122

Db 73 SDAVEILDEDEVLIGLATDEBA-----RLTKNKHVEVQLSADGTETPSTTFVKEL 126

QY 123 FA-----LSV---YGVLYCKSTWHLCSGLMGLM---MLQSGWVG--HDSCHYQVMPNRKL 171

Db 127 PAEKLSTATDYSNDYKKGKFLDLNRPILMOQLBRDFKDFVDDQIHRPRH-----GKGS 182

QY 172 NRLFOIILAGNIVAGVS-VAMWKLNDHTTHFACNSANLDPDIOHLPII---AISPFENS 226

Db 183 APLF-----GNFLEPLTKTAMVV-----PVAMLPVVVYHMGVALKNMQ 222

QY 227 LTSYHNCMTQDRAARFVFSQHWTFYPALLSVRLYLFLISFKVVSNNKRYKRSQEI 286

Db 223 LPAFLFC-----VGVPVWT-----LLEYGILHRLFHF----- 250

QY 287 LGYAAFLTWYSLLSRLPNW-PEVWVYFTSCLAVAGFQHQGSLNHFASNVYTGLPQSGND 345

Db 251 -----DDMLPESINAFATHLLGLGCHHY-----LPM--D 277

QY 346 WFHQQTGTLNITASA-----WMDN--FHGILHFOI-----EHLHFRMPKCHFR 388

Db 278 KYRLVMPFTLPIVILCAPFKLVFALLPLYWAAAGAGGIFGVYVDECHFF-----LHHS 332

QY 389 KISPIVNLCKQKINLSYET-----TATME 412

Db 333 KLPPFRKLKXYHLHHYKNYQLGFGVTSWFWD 365

Search completed: January 1, 2004, 06:39:39
 Job time : 18.8616 secs

RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=9820296; PubMed=9559540;
 RA Dunn T.M., Haak D., Monaghan E., Beeler T.J.;
 RT "Synthesis of monohydroxylated inositolphosphorylceramide (IPC-C) in
 RT Saccharomyces cerevisiae requires Scs7p, a protein with both a
 RT cytochrome b5-like domain and a hydroxylase/desaturase domain.";
 RL Yeast 14:311-321(1998).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=98019193; PubMed=9353282;
 RA Mitchell A.G., Martin C.E.;
 RT "Fahp, a Saccharomyces cerevisiae cytochrome b5 fusion protein, and
 RT its Arabidopsis thaliana homolog that lacks the cytochrome b5 domain
 RT both function in the alpha-hydroxylation of sphingolipid-associated
 RT very long chain fatty acids.";
 RL J. Biol. Chem. 272:28281-28288(1997).
 CC -1- FUNCTION: INVOLVED IN THE ALPHA-HYDROXYLATION OF SPHINGOLIPID-
 CC ASSOCIATED VERY LONG CHAIN FATTY ACIDS. HYDROXYLATES THE C26-FATTY
 CC ACID OF INOSITOLPHOSPHORYLCERAMIDE-B (IPC-B) TO FORM IPC-C.
 CC -1- COFACTOR: IRON (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
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 CC -----
 DR EMBL: Z49260; CA89255.1; -.
 DR PIR: S54484; S54484.
 DR HSSP: P04166; 1EUE.
 DR SGD: S0004885; SC57.
 DR GO: GO:0005783; C:cytoplasmic reticulum; IMP.
 DR GO: GO:0016491; F:oxidoreductase activity; IMP.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR006087; Sterol_desat.
 DR Pfam: PF04116; FA_hydroxylase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR PRINTS: PRO0363; CYTOCHROMEBS.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KM Oxidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
 KM Transmembrane; Endoplasmic reticulum; Heme.
 FT DOMAIN 1 90
 FT TRANSMEM 197 217 HEME-BINDING.
 FT TRANSMEM 223 243 POTENTIAL.
 FT TRANSMEM 298 318 POTENTIAL.
 FT TRANSMEM 353 373 POTENTIAL.
 FT METAL 45 45 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 70 70 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 384 AA; 44881 MW; DF4BA5F2E0BA2218 CRC64;
 Query Match 6.7%; Score 166.5; DB 1; Length 384;
 Best Local Similarity 21.2%; Pred. No. 3e-06;
 Matches 96; Conservative 67; Mismatches 141; Indels 149; Gaps 25;
 QY 9 SQADLAHKQPGDWLSIKG-KVYDISKTKHKGELPLLSFAGQDVT---DAFLAVH 63
 DB 13 SKTVQEHNTANDCWVTVYQNRKITVDYTRFLSEHSGDESLDYAKGDIETIMQSDVHEH 72
 QY 64 PGTAKQYL-DRFTGYVVDYVSSEMSKDYRRVLSESKGKLFKTKGKYGCIFPVSVL 122
 DB 73 SDSAYELDEYVILGYLATDEEA-----RLTNKHKVEYVLSADGTEFDSTTVKEL 126
 QY 123 FA---LSV---YGVLYCKSTWALHCSGLMGML---WLGSGWVG--HDSCHYGVMPRK 171

DB 127 PAEEKSLATDYSDNYKKHFLDLNRLMLQILRSDPKDFVVDQIHRRHY-----GKGS 182
 QY 172 NNLFOIAGNVAGVS-VAMWKLIDNTHHFAQNSANLDPDIGHPLI-----AISPFFNS 226
 DB 183 ADLF---GNFLEPLIKTAMWV-----PVMLEPVVYTHMGVALKNMQ 222
 QY 227 LTSYHNCMTVDRAARFVSFOHWTFPALISVRLYLFLSKVVFSSNNKVKRSQBI 286
 DB 223 LFACFLFC-----VGFWVT---LEYGHRFLRFLP----- 250
 QY 287 LGYAAFLTWYSLLSLRLPWA-PERYMYFTSCIAVAFQWQFSLNHNFASTVTGLPSGD 345
 DB 346 WFGQTKGLNITASA-----WMDV--FHGGLHFOI---EHLFPMPKCHFR 388
 QY 251 -----DMLPESNIAFATHPLHLGCHRY-----LPM--D 277
 DB 278 KRLVMPFLFVILCAPFYKLVALLPLVWAAGRAGLFGVYCYDECHP-----LHNS 332
 QY 389 KISPIVNLK-----CQGNLSYE-----TATWME 412
 DB 333 KLPPFRKLLKXHLNHYKNYQLGFGVTSWPF 365
 RESULT 4
 ID PD61 SOYBN STANDARD; PRT; 387 AA.
 AC P48630;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1
 DE (EC 1.14.19.-).
 GN PAD2-1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eumetidae I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxId=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=96151506; PubMed=8587990;
 RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;
 RT "Developmental and growth temperature regulation of two different
 RT microsomal omega-6 desaturase genes in soybeans.";
 RL Plant Physiol. 110:311-319(1996).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC -----
 DR EMBL: L43920; AAB00859.1; -.
 DR PIR: T07687; T07687.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;

KM Transmembrane.
 FT TRANSMEM 54 74 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 121 141 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 227 247 POTENTIAL.
 FT TRANSMEM 251 271 POTENTIAL.
 FT DOMAIN 109 113 HISTIDINE BOX-1.
 FT DOMAIN 145 149 HISTIDINE BOX-2.
 FT DOMAIN 319 323 HISTIDINE BOX-3.
 SQ SEQUENCE 387 AA; 44662 MW; 49068805C21A1C31 CRC64;
 Query Match 6.5%; Score 161; DB 1; Length 387;
 Best Local Similarity 25.4%; Pred. No. 8.4e-06;
 Matches 86; Conservative 48; Mismatches 139; Indels 66; Gaps 19;
 QY 118 FSVYVYDLSFAFYIATYTFHLLPQPSLIAMPYVWLGCLLTGVVIAHECGHAFS 117
 DB 167 PNKRLNLPQIAGNVAGSVAMWKLDNTHFHACNSANLDPDIOHLPIAISPKFENS 226
 DB 118 KYQWVDVVGGLTHSTLL-VPEYSWKSHRRH--SNTGSLDRDVEVP---KPKSKVA 170
 QY 227 LTSYHNCKMTYDRAAFVFSFQ-HMTFYPAL-LSVLYLFLIS---FKVFSNNKRY 280
 DB 171 WFSKYLNNPL--GRAVSLVLTITGCMYLAFNVSGRPYDSFASHYHPAYISNRRL 228
 QY 281 KRSEILGYAFLTWYSLLSLRPNBERV---MYFTSLAVAGF-----OHMQFSL 329
 DB 229 IYVSDV---ALFSTVYSLY--RVATLKLWLVCVYGPPLIIVGVLTITVYLOHTHFAL 283
 QY 330 NHPASNYTGLPSCNDFPHOQTKLTNITASAMWD-----FHGSLHFOLEHLLFRMP 383
 DB 284 PHYDSEW-----DWL---KGL---ATMDRYSGLINKVFHITDTVAHHLFSTMP 329
 QY 384 KCHFRK----ISPIVNLCKHNLSEYETATWMEANKMY 418
 DB 330 HYHMEATNAIKPILEGVYQPDPIFYKALMREARECLY 368
 RESULT 5
 CYB5 ORYSA STANDARD; PRT; 137 AA.
 ID CYB5 ORYSA AC PA9100;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 NC EMBL TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Callus;
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stohart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting."
 RL Plant Mol. Biol. 25:527-537(1994).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: X75670; CAA53366.1; -.
 CC F1R; S46307; S46307.
 CC DR HSSP; P00171; IEHB.
 CC DR Gramene; P49100; -.
 CC DR InterPro; IPR001199; Cyt B5.
 CC DR Pfam; PF00173; heme 1; 1.
 CC DR ProDom; PD000612; Cyt B5; 1.
 CC DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 CC DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 CC KM Electron transport; Transmembrane; Heme; Iron; Microsome.
 FT TRANSMEM 108 128 POTENTIAL.
 FT METAL 41 41 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 137 AA; 15296 MW; 4260C963B60FDA CRC64;
 Query Match 6.4%; Score 157; DB 1; Length 137;
 Best Local Similarity 32.1%; Pred. No. 5.5e-06;
 Matches 45; Conservative 22; Mismatches 53; Indels 20; Gaps 5;
 QY 5 KKHISQADLAKHKQPDLMISIKGVYDISKMTKEHSGELPLSPAGDVTDAF-IAVH 63
 DB 6 KKYTLEEVAKHNSKDDCLLIGKYYNYSKFLSDHPGDDVLSTGKDATDDEFDVG 65
 QY 64 PGFAMGYLDRFTFGYVVDYVSSEMSKDVRLVSEBSKNGLFETPKGYGCSIFPSV-- 121
 DB 66 TTTARMMDE---YVVGIDITSTIPARTKTVPPKPHYNQDTPF-----FIKTIQ 114
 QY 122 -LFLSVGV-----LYCKS 135
 DB 115 FLVPLAILGLAVAIRYTS 134
 RESULT 6
 CYB5 RHIST STANDARD; PRT; 131 AA.
 ID CYB5 RHIST AC 09HFTV;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Rhizopus stolonifer (Rhizopus nigricans).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Rhizopus.
 NC EMBL TaxID=4846;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21414663; PubMed=11523811;
 RA Kunic B., Tuan G., Brekvar K., Pompon D.;
 RT "Functional cloning, based on acrole resistance in Saccharomyces
 RT cerevisiae, and characterization of Rhizopus nigricans redox carriers
 RT that are differentially involved in the P450-dependent response to
 RT progesterone stress."
 RL Mol. Genet. Genomics 265:930-940(2001).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: AF290427; AAC23835.1; -.
 CC DR HSSP; P04166; IEUE.
 CC DR InterPro; IPR001199; Cyt B5.
 CC DR Pfam; PF00173; heme 1; 1.
 CC DR PRINTS; PR00363; CYTOCHROME B5.

DR ProDom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
 KM Electron transport; Heme; Iron; Membrane.
 FT METAL 38 38 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 62 62 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 131 AA; 14651 MW; 5890741307682F0 CRC64;
 Query Match 6.2%; Score 153; DB 1; Length 131;
 Best Local Similarity 34.8%; Pred. No. 1.1e-05;
 Matches 46; Conservative 19; Mismatches 51; Indels 16; Gaps 5;
 QY 6 KHISQADLAKHKOPGDLWISIKGVYDISKTKTEHFGELPLSPAGQVTDPAFIAY-HP 64
 DB 4 KIFSLDEVSFKTKSDLMVVIHKKVYDIFRFVVEHFGESVIVDEGSKATKTEAFEDIGHS 63
 QY 65 GRAMQVLDREFFTGYVODYSVSFMS--KDYRLVSEFSKXKLEFKTGKGVYCSIFPVSVL 122
 DB 64 DEAREMELVEYLIG-----SLDEASRTKEYNVNV--IRAGELPEEKKGSLRI-----IL 110
 QY 123 FALSIVGVLYCK 134
 DB 111 PALATIGALVYK 122
 RESULT 7
 CY51_ARATH STANDARD; PRT; 134 AA.
 ID Q42342; Q9SB05;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5 isoform 1.
 GN AYG533560 OR MNC6.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsie.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=9087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned P1 and PAC clones.";
 RL DNA Res. 5:297-308(1998).
 RN [3]
 RP SEQUENCE OF 1-113 FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Cooke R., Laurie M., Raynal M., Delseny M.;
 RU Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (by similarity).
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE, BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL; AB007801; BAA74839.1; -;
 DR EMBL; AB015476; BAB09732.1; -;
 DR EMBL; F20001; CAA23377.1; -;
 DR PIR; T52469; T52469.
 DR HSSP; P00171; 1EH8.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME5.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
 KM Electron transport; Transmembrane; Heme; Iron; Microsome;
 KW Multigene family.
 FT TRANSMEM 107 127
 FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 1 3 MSS->ARA (IN REF. 3).
 SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60F7C873FD CRC64;
 Query Match 6.2%; Score 152.5; DB 1; Length 134;
 Best Local Similarity 38.5%; Pred. No. 1.2e-05;
 Matches 30; Conservative 17; Mismatches 30; Indels 1; Gaps 1;
 QY 1 MEEPKHISQADLAKHKOPGDLWISIKGVYDISKTKTEHFGELPLSPAGQVTDPAF- 59
 DB 1 MSSDRKVLSPFEVSKNKTCKDMLISGVYDVFPMDDHPCGDDEVILSTGKDATNDFE 60
 QY 60 IAVHPTAWQVLDREFFTG 77
 DB 61 DVGSHDTARDMDKXFFIG 78
 RESULT 8
 YDAA_SCHPO STANDARD; PRT; 147 AA.
 ID Q10352;
 AC Q10352;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein C1P12.10c in chromosome I.
 GN SPAC1P12.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
 RA Holtroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagele K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch B.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolchert G., Aert R., Robben J., Grymponrez B.,
 RA Welycens I., Vanscraels B., Rieger M., Schaefer M., Weller-Auer S.,
 RA Gabel C., Fuchs W., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinhardt R., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Galliard C., Talladé V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Berto J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovsky G.V., Usery D., Barrell B.G., Nure F.,
RT "The genome sequence of *Schistosoma mansoni* pome.";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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CC EMBL; 269944; CAA93814.1; -
CC PIR; S67453; S67453.
CC HSSP; P00175; 1LTD.
CC GeneDB Sprobe: SPAC1F12.10C; -
CC InterPro: IPR001199; Cyt_B5.
CC Pfam; PF00173; heme_1; 1.
CC PRINTS; PR00363; CYTOCHROME_B5.
CC ProDom; PD000612; Cyt B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS50255; CYTOCHROME_B5_2; 1.
CC Hypothetical protein; Heme.
CC METAL 106 106 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC METAL 129 129 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC SEQUENCE 147 AA; 16667 MW; E874859F52E1AF1D CRC64;

Query Match 6.2%; Score 152.5; DB 1; Length 147;
Best Local Similarity 39.0%; Pred. No. 1.4e-05;
Matches 30; Conservative 16; Mismatches 24; Indels 7; Gaps 2;

QY 8 ISQADLAKHKQPGDLMISIKGVYDISKWTKEHPGGLPLSPAGQDVTAFIYHPGTA 67
DB 74 VTKBELAKHKTKEDCWAIGKYNVSAYLPYHAGCKRILDVAGRATYIFMKFH---A 130
QY 68 W---QYIDRFFFTGYV 80
DB 131 WVNBEALTKTSFVGFLV 147

RESULT 9:
CYB5_BOROF STANDARD; PRT; 132 AA.
ID CYB5_BOROF STANDARD; PRT; 132 AA.
AC 004354;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
OS *Borago officinalis* (Bourrache) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Jamids; Boraginaceae; Borage.
OC NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268723; PubMed=9108131;
RA Savanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G.,
RA Christie W.W., Sherry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta-6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; U79011; AAC49701.1; -
CC HSSP; P00171; 1CYO.
CC InterPro: IPR001199; Cyt_B5.
CC Pfam; PF00173; heme_1; 1.
CC PRINTS; PR00363; CYTOCHROME_B5.
CC ProDom; PD000612; Cyt B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS50255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS50255; CYTOCHROME_B5_2; 1.
CC Kew Electron transport; Transmembrane; Heme; Iron; Microsome.
CC TRANSMEM 104 124 POTENTIAL.
CC FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC SEQUENCE 132 AA; 14556 MW; 96EF72A06F2E8C5B CRC64;

Query Match 6.1%; Score 151.5; DB 1; Length 132;
Best Local Similarity 41.1%; Pred. No. 1.5e-05;
Matches 30; Conservative 15; Mismatches 27; Indels 1; Gaps 1;

QY 6 KHISQADLAKHKQPGDLMISIKGVYDISKWTKEHPGGLPLSPAGQDVTAFIY-HP 64
DB 3 KFTLLEVAQHNNSKQCMILINGKVDVTFEDHPGSDVLSTATGKADTFEDIGHS 62
QY 65 GTAMQYIDRFFFTGY 77
DB 63 SSAKAMLDREYVG 75

RESULT 10:
CYB5_YEAST STANDARD; PRT; 120 AA.
ID CYB5_YEAST STANDARD; PRT; 120 AA.
AC P40312;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
GN CYB5 OR YNL111C OR N1949.
OS *Saccharomyces cerevisiae* (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycaceae.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL100;
RX MEDLINE=94237477; PubMed=8181746;
RA Tuan G., Eginat J.-C., Rougeulle C., Cullin C., Pompon D.,
RT "Cloning and characterization of a yeast cytochrome b5-encoding gene
RT which suppresses ketoconazole hypersensitivity in a NADPH-P-450
RT reductase-deficient strain.";
RL Gene 142:123-127(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97245296; PubMed=9090055;
RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
RA Pallavicini A., Lanfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
RT *Saccharomyces cerevisiae* reveals an unusually high number of
RT overlapping open reading frames.";
RL Yeast 13:261-266(1997).
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases. It plays a role in
CC fatty-acid desaturation and is also involved in several steps of
CC the sterol biosynthesis pathway, particularly in the 4-
CC demethylation of the 4,4'-dimethyl zymosterol.
CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 DR EMBL: L22494; AAA67468.1; -
 DR EMBL: 269382; CAA93396.1; -
 DR EMBL: 271387; CAA95990.1; -
 DR PIR: S63052; S63052.
 DR HSSP: P04166; 1EUE.
 DR SGD: S0005055; CYB5.
 DR GO: GO:0005792; C:microsome; IDA.
 DR GO: GO:0016126; P:steroid biosynthesis; IDA.
 DR InterPro: IPR001199; Cyt_B5.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR ProDom: PD000612; Cyt_B5_1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR KEGG: K01199; Cytochrome b5; Heme; Iron; Microsome.
 DR TRANSMEM: 98 118
 FT METAL 37 37 POTENTIAL.
 FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 17 17 E -> Q (IN REF. 1).
 FT SEQUENCE 120 AA; 13297 MW; 598BF26730CA019 CRC64;
 SQ
 Query Match 6.0%; Score 148.5; DB 1; Length 120;
 Best Local Similarity 30.8%; Pred. No. 2.3e-05;
 Matches 40; Conservative 23; Mismatches 50; Indels 17; Gaps 5;
 QY 4 PKKHISQADLAKHKOPGDLWISIKGVYDISKWTKEHPGGLPLLSFAGQDVTDATAY- 62
 DB 2 PKKY-SYGEVAENHNGENFWIIDDKRYDVSQPKDHPGDELIMLGQDATESFVDIG 60
 QY 63 HPGTAQVYDRFTFTGYVQDYSVSEMSKDYRLVSEPSKMKLFTPKGKGVCSIFPVSVL 122
 DB 61 HSDEAL-----RLKLGKLYIGD-----VDKTSERVSVEKVSSTSEMSKSGTF-----LVVYL 105
 QY 123 FALSYGVGLY 132
 DB 106 LALLMLGVAY 115
 RESULT 11
 CYB5_TOBAC STANDARD; PRT; 136 AA.
 ID ID CYB5_TOBAC
 AC P49058;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxId=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=leaf;
 RA MEDLINE=94325476; PubMed=8049375;
 RT Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting";
 RL Plant Mol. Biol. 25:527-537(1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN

CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
 CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
 CC -1- SUBCELLULAR LOCATION: MICROSOmal MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
 CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
 CC LEVELS IN THE LEAF.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X71441; CAA50575.1; ALT_INIT.
 DR EMBL: X68140; CAA48240.1; -
 DR HSSP: P04166; 1BSM.
 DR InterPro: IPR001199; Cyt_B5.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5_1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR KEGG: K01199; Cytochrome b5; Heme; Iron; Microsome;
 DR TRANSMEM: 107 127
 FT METAL 40 40 POTENTIAL.
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 10 11 LA -> EF (IN REF. 1; CAA48240).
 FT CONFLICT 105 105 MISSING (IN REF. 1; CAA48240).
 FT SEQUENCE 136 AA; 14979 MW; DACE9EA695B2835F CRC64;
 SQ
 Query Match 6.0%; Score 148; DB 1; Length 136;
 Best Local Similarity 28.5%; Pred. No. 2.9e-05;
 Matches 41; Conservative 21; Mismatches 42; Indels 40; Gaps 5;
 QY 6 KHISQADLAKHKOPGDLWISIKGVYDISKWTKEHPGGLPLLSFAGQDVTDATAY- 64
 DB 6 KYFTLAIVSQHNNADQWLVISGVYDVKPLFDHHDGDBVLISATGKATDQFEDVGH 65
 QY 65 GTAWQYLDLRFPTG-----YYVDYSVSEMSKDYRLVSEF-SKMKL 104
 DB 66 SSARMLDDEVYVGDIDSATIPRTKTYTPPNOPHYNDKT-----SEFVVKLQ 113
 QY 105 FKTGKGVYCSIFVSVLPALSY 128
 DB 114 FLVP-----LIIIGVAFGIRFY 130
 RESULT 12
 CY52_ARATH STANDARD; PRT; 134 AA.
 ID ID CY52_ARATH
 AC Q48845;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable cytochrome b5 isoform 2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Rounleay S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Frazer C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, bound to the
 CC cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AC003974; AAC04491.1; -
 CC PIR: T00796; T00796.
 CC HSSP: P04166; 1B5M.
 CC InterPro: IPR001199; Cyt_B5.
 CC Pfam: PF00173; heme_1.1.
 CC PRINTS: PR00363; CYTOCHROME_B5.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS00255; CYTOCHROME_B5_2; 1.
 CC KEGG: Electon transport; Transmembrane; Heme; Iron; Microsome;
 CC Multigene family.
 CC TRANSMEM: 107 127 POTENTIAL.
 CC FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 134 AA; 15016 MW; B405F5430F5716C1 CRC64;
 CC -----
 CC Query Match 5.9%; Score 146.5; DB 1; Length 134;
 CC Best Local Similarity 35.9%; Pred. No. 3.8e-05;
 CC Matches 28; Conservative 22; Mismatches 27; Indels 1; Gaps 1;
 CC
 CC QY 1 MESPKNHISADLAKKPGDLMISIKGVYDISKTKHPGGLPLSPAGDVTDAF-59
 CC DB 1 MDEBAKIFITSEVSEHQAHCWIVNGKYVNTKFLDPHGADVLSTGQADIDDFG-60
 CC QY 60 IAYHPTAMQYLDREFTG 77
 CC DB 61 DVGHSESAREMEQYVVG 78
 CC
 CC RESULT 13
 CC CYB5_CUSRE STANDARD; PRT; 135 AA.
 CC ID P49097;
 CC AC P49097;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Cytochrome b5.
 CC OS Cuscuta reflexa (Southern Asian dodder).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; lamiales; Solanales; Convolvulaceae; Cuscuta.
 CC NCBI_TaxID=4129;
 CC (1)
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=95047507; PubMed=7959021;
 CC RA Subramaniam K., Manadevan S.;
 CC RT "The cDNA sequence of cytochrome b5 associated with cytokinin-induced
 CC RT haustoria formation in Cuscuta reflexa.";
 CC RL Gene 149:375-376(1994).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron

CC carrier for several membrane bound oxygenases.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, bound to the
 CC cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: L22209; AAA62621.1; -
 CC PIR: T09946; T09946.
 CC HSSP: P04166; 1EUR.
 CC InterPro: IPR001199; Cyt_B5.
 CC Pfam: PF00173; heme_1.1.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS00255; CYTOCHROME_B5_2; 1.
 CC KEGG: Electron transport; Transmembrane; Heme; Iron; Microsome.
 CC TRANSMEM: 106 126 POTENTIAL.
 CC FT METAL 39 39 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 63 63 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 135 AA; 14745 MW; CFF21C952981F5DA CRC64;
 CC -----
 CC Query Match 5.8%; Score 142.5; DB 1; Length 135;
 CC Best Local Similarity 41.1%; Pred. No. 8.2e-05;
 CC Matches 30; Conservative 12; Mismatches 30; Indels 1; Gaps 1;
 CC
 CC QY 6 KHISQADLAKKPGDLMISIKGVYDISKTKHPGGLPLSPAGDVTDAF-HP 64
 CC DB 5 KYTSLAEVSEHQAHCWIVNGKYVNTKFLDPHGADVLSTGQADIDDFG-64
 CC QY 65 GTAMQYLDREFTG 77
 CC DB 65 SSARAMDMEMCVG 77
 CC
 CC RESULT 14
 CC NIA2_PHAVU STANDARD; PRT; 890 AA.
 CC ID P39866;
 CC AC P39866;
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR-2).
 CC GN NIA2 OR NR2.
 CC OS Phaseolus vulgaris (Kidney bean) (French bean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae; Phaseolus.
 CC NCBI_TaxID=1885;
 CC (1)
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=cv. Saxa;
 CC RA Jensen P.E., Hoff T., Stummann B.M., Henningsen K.W.;
 CC RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
 CC AND ONE MOLYBDENUM ATOM.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 40.2085 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-2
Perfect score: 2470
Sequence: 1 MEEPKGHSQADLAKKQPG.....KDVTKPVPKNWWEANTRFG 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP_rvtrus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1543	62.5	446	10 Q9ZTY9	Q9ZTY9 ricinus com
2	1519.5	61.5	448	10 Q8VZ22	Q8VZ22 echium gent
3	1509.5	61.1	448	10 Q8VZ21	Q8VZ21 echium pita
4	1465.5	59.3	448	10 Q9SAUS	Q9SAUS borago offi
5	1461	59.1	446	10 Q8LID7	Q8LID7 aquilegia v
6	1460.5	59.1	448	10 Q8LID7	Q8LID7 borago offi
7	1405.5	56.9	448	10 Q8L177	Q8L177 argania spi
8	1395.5	56.5	449	10 Q9ZRP8	Q9ZRP8 brassica na
9	1391.5	56.3	449	10 Q43469	Q43469 helianthus
10	1372.5	55.6	449	10 Q8LB96	Q8LB96 arabidopsis
11	1372.5	55.6	449	10 Q9ZRP7	Q9ZRP7 arabidopsis
12	1325	53.6	446	10 Q9FR82	Q9FR82 borago offi
13	1293.5	52.4	469	10 Q9ZT08	Q9ZT08 triticum ae
14	663.5	26.9	483	10 Q9LENO	Q9LENO ceratodon p
15	626	25.3	520	10 Q9LEMG	Q9LEMG ceratodon p
16	620	25.1	523	3 Q9HDS8	Q9HDS8 mucor rouxi

17	560.5	22.7	459	10 Q944W4	Q944W4 pythium itr
18	550	22.3	525	10 Q9ZNM2	Q9ZNM2 physcomitre
19	549	22.2	457	3 Q9UVV3	Q9UVV3 mortierella
20	542	21.9	457	3 Q9HEV4	Q9HEV4 mortierella
21	540	21.9	457	3 Q8X173	Q8X173 mortierella
22	539	21.8	457	3 Q9UVY3	Q9UVY3 mortierella
23	528	21.4	457	3 Q9HEV1	Q9HEV1 mortierella
24	528	21.4	457	3 Q8X174	Q8X174 mortierella
25	521.5	21.1	467	3 Q9VCX5	Q9VCX5 mucor circi
26	520.5	21.1	477	10 Q8RXB0	Q8RXB0 phaeodactyl
27	514	20.8	568	3 Q8NKG9	Q8NKG9 saccharomyc
28	502	20.3	573	3 Q8NKG8	Q8NKG8 kluyveromyc
29	461	18.7	443	5 Q23221	Q23221 caenorhabdi
30	460	18.6	443	5 Q6138W	Q6138W caenorhabdi
31	458	18.5	454	13 Q9BSW7	Q9BSW7 oncorhynch
32	455.5	18.4	501	4 Q8NCG0	Q8NCG0 homo sapien
33	454	18.4	444	4 Q9S864	Q9S864 homo sapien
34	453.5	18.4	444	4 Q9NRP8	Q9NRP8 homo sapien
35	453.5	18.4	444	4 Q60427	Q60427 homo sapien
36	450.5	18.2	444	4 Q96139	Q96139 homo sapien
37	449	18.2	444	11 Q9Z122	Q9Z122 rattus norv
38	449	18.2	452	13 Q8UWMS	Q8UWMS oncorhynch
39	448	18.1	444	11 Q9Z0R9	Q9Z0R9 mus musculu
40	447.5	18.1	444	4 Q96T10	Q96T10 homo sapien
41	444.5	18.0	501	4 Q8NCC7	Q8NCC7 homo sapien
42	442.5	17.9	444	4 Q9NXY1	Q9NXY1 homo sapien
43	442	17.9	445	13 Q8AY64	Q8AY64 sparus aurt
44	441	17.9	454	13 Q8QGE2	Q8QGE2 salmo balat
45	439.5	17.8	444	4 Q96SV3	Q96SV3 homo sapien

ALIGNMENTS

RESULT 1
ID Q9ZTY9 PRELIMINARY; PRT; 446 AA.
Q9ZTY9
AC Q9ZTY9;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Desaturase/cytochrome b5 protein.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed endosperm;
RX MEDLINE=97268723; PubMed=9108131;
RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RA "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
RL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC EMBL: AF005096; AAD01240.1; -
DR HSSP: P00171; 115U.
DR InterPro: IPR001199; Cyt B5.
DR InterPro: IPR005804; FA_decat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt B5; 1.
DR ProDom: PD001081; FA_decat_fam; 1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ
SEQUENCE 446 AA; 51418 MW; A1954FDB2DD8600F CRC64;
Query Match 62.5%; Score 1543; DB 10; Length 446;
Best Local Similarity 59.8%; Pred. No. 3.9e-129;
Matches 268; Conservative 77; Mismatches 101; Indels 2; Gaps 2;

QY 1 MEEPKHII SOADLAKH KOPGDLWISIKGYDYSKMTKEHFGELPLLSFAGODVTD AFI 60
 DB 1 MAETKATYTTEDLEKKNHFGDLWISIGKLYNTVDNSKDHFGVSPHLHAGODVTD AFI 60
 QY 61 AYHPTGAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVYCSIFVSV 120
 DB 61 AYHPTGAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVYCSIFVSV 119
 QY 121 VLPALSYGYLYCKSTVAHLCSGLMGMLQSGWVGHDSCHYOVMBNRKLNRLFOIIAG 180
 DB 120 MLALSYGYLYCKSTVAHLCSGLMGMLQSGWVGHDSCHYOVMBNRKLNRLFOIIAG 179
 QY 181 NVLAGSVAMKLDHNTTHFACNSANLDPDLOIPIAISPKEFNLSLTYHNCMTYD AAF 240
 DB 180 NVLAGSVAMKLDHNTTHFACNSANLDPDLOIPIAISPKEFNLSLTYHNCMTYD AAF 239
 QY 241 AAFEPVSFOHMTFYPALLSVRLYLFLSPKVPFSNNKRYKRSOELIGYAAFLTWYSL 300
 DB 240 AAFEPVSFOHMTFYPALLSVRLYLFLSPKVPFSNNKRYKRSOELIGYAAFLTWYSL 298
 QY 301 SRLPNMEPVRVYFTSCIAVAGFOHMOFSLNHFASNVYTGLPSCGDMFHQOTKTLNTAS 360
 DB 299 SRLPNMEPVRVYFTSCIAVAGFOHMOFSLNHFASNVYTGLPSCGDMFHQOTKTLNTAS 358
 QY 361 AAMDMPFGGLHFOIEHNLPRMPKCHFRKISPIYVNLCKOHNLSYETATWMEANKMYST 420
 DB 359 AAMDMPFGGLHFOIEHNLPRMPKCHFRKISPIYVNLCKOHNLSYETATWMEANKMYST 418
 QY 421 LRAVAMEAKDVTKPVPKNNWMEANMTEG 448
 DB 419 LRAVAMEAKDVTKPVPKNNWMEANMTEG 446

RESULT 2

QY 08VZ22 PRELIMINARY; PRT; 448 AA.
 AC 08VZ22;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 GN D6DES.
 OS Echium genitianoideae.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Echium.
 OX NCBI_TaxID=173991;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 Echium: Functional Expression in Yeast and Tobacco."
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY055117; AL23580.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51428 MW; CZA937951B87C183 CRC64;

Query Match 61.5%; Score 1519.5; DB 10; Length 448;
 Best Local Similarity 57.4%; Pred. No. 4.8e-127;
 Matches 255; Conservative 90; Mismatches 98; Indels 1; Gaps 1;

QY 5 KKHISOADLAKH KOPGDLWISIKGYDYSKMTKEHFGELPLLSFAGODVTD AFI 64
 DB 6 KKHISOADLAKH KOPGDLWISIKGYDYSKMTKEHFGELPLLSFAGODVTD AFI 65

QY 65 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVYCSIFVSV 124
 DB 66 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVYCSIFVSV 125
 QY 125 LSVYGYLYCKSTVAHLCSGLMGMLQSGWVGHDSCHYOVMBNRKLNRLFOIIAGVIA 184
 DB 126 LSVYGYLYCKSTVAHLCSGLMGMLQSGWVGHDSCHYOVMBNRKLNRLFOIIAGVIA 185
 QY 185 GVSANWVKLDHNTTHFACNSANLDPDLOIPIAISPKEFNLSLTYHNCMTYD AAF 244
 DB 186 GVSANWVKLDHNTTHFACNSANLDPDLOIPIAISPKEFNLSLTYHNCMTYD AAF 245
 QY 245 FVSFOHMTFYPALLSVRLYLFLSPKVPFSNNKRYKRSOELIGYAAFLTWYSL 304
 DB 246 FVSFOHMTFYPALLSVRLYLFLSPKVPFSNNKRYKRSOELIGYAAFLTWYSL 304
 QY 305 NMEPVRVYFTSCIAVAGFOHMOFSLNHFASNVYTGLPSCGDMFHQOTKTLNTASAMD 364
 DB 305 NMEPVRVYFTSCIAVAGFOHMOFSLNHFASNVYTGLPSCGDMFHQOTKTLNTASAMD 364
 QY 365 WFGGLHFOIEHNLPRMPKCHFRKISPIYVNLCKOHNLSYETATWMEANKMYST 424
 DB 365 WFGGLHFOIEHNLPRMPKCHFRKISPIYVNLCKOHNLSYETATWMEANKMYST 424
 QY 425 AAMEAKDVTKPVPKNNWMEANMTEG 448
 DB 425 AAMEAKDVTKPVPKNNWMEANMTEG 448

RESULT 3

QY 08VZ21 PRELIMINARY; PRT; 448 AA.
 AC 08VZ21;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 GN D6DES.
 OS Echium pitardii var. pitardii.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Echium.
 OX NCBI_TaxID=174255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 Echium: Functional Expression in Yeast and Tobacco."
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY055118; AL23581.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51394 MW; 4B6DEA4905DE263 CRC64;

Query Match 61.1%; Score 1509.5; DB 10; Length 448;
 Best Local Similarity 57.4%; Pred. No. 3.8e-126;
 Matches 255; Conservative 88; Mismatches 100; Indels 1; Gaps 1;

QY 5 KKHISOADLAKH KOPGDLWISIKGYDYSKMTKEHFGELPLLSFAGODVTD AFI 64
 DB 6 KKHISOADLAKH KOPGDLWISIKGYDYSKMTKEHFGELPLLSFAGODVTD AFI 65
 QY 65 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVYCSIFVSV 124
 DB 66 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEKTPGKGVYCSIFVSV 125

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QY 125 LSVYGVLYCKSTWAHLCSGLLMGLMLQSGWGHDSCHYOVMPNRKLNRLFOIIAGNVIA 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 MSYGVLYFCGCVLVLHLAGLMGFWMIQSGWIGHDGHYIVMPNPKLMLGIVASNCIS 185
QY 185 GSVAVAMKLDHNTHTHFACNSANLDPDIQHLPIAISPKFNSLTSYHNCKMTYDRAAF 244
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 GISIGMKMKNNAHNAHIAACNSLDEYDPLQYIPLLVSSKRFSGSLTSHFEKRLTFDSLRSF 245
QY 245 FVSPQHMTFYPALLSVRLYFLISFKVYFNNKRYRKSQELIGYAAFLTWSSLLSLRLP 304
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 246 FVSHQHMTFYPVCSAVNMFVQSL-IMLLTKRNVPFRSQELGLVFWIMYPLVSCLP 304
QY 305 NMBERMYTSCSLAVALPGHMOFSLNHFASNNYTGLPSCNDMFHOOTKGTINTASAMWD 364
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 NMGERIMFVYASLSTVGMOQVQFSLNHFASVYVGKPIDWFKQTCGLTIDISCPMWD 364
QY 365 WPHGGLHFOIEHHLFPRMPKCFPRKISPIVNLCKQKNTSYETATWMEANKMYSTLRAY 424
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 365 WPHGGLHFOIEHHLFPRMPKCFPRKISPIVNLCKQKNTSYETATWMEANKMYSTLRAY 424
QY 425 AMEAKDVTKRPVKNNWMEAMNTFG 448
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 425 ALQARDITKPLPKNLVWEALNTHG 448

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RESULT 4

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ID 09SAUS PRELIMINARY; PRT; 448 AA.
AC 09SAUS;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Delta 6-desaturase.
OS Borago officinalis (Borraghe) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Boraginaceae; Borago.
OX NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RA Nunberg A.N., Beremand P.D., Thomas T.L.;
RT "Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
   (GLA).";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF007561; AAD01410.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 448 AA; 51626 MW; EACJF0BE22E0DE00 CRC64;

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Query Match 59.3%; Score 1465.5; DB 10; Length 448;
 Best Local Similarity 55.4%; Pred. No. 3.2e-122;
 Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

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QY 5 KKHISQADLAKHQPDLWISIKGYVDISKTKENHGGELPLSPFGQDVTATPAFYHP 64
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 KKHITSELDKNHKKPGDLWISIQKADVSDWYKDHPGSGFPPLKSLAGDEVTDAFVAFHP 65
QY 65 GTAMQVLYDRFPTGYVVDYVSSEMSKDYRLVSEFSKMGLEFKTPGKGVNYSIFVSVLPA 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 ASYMKULDKRFETGYLYKDYSEVSQDYRLVSEFSKMGLEFKTPGKGVNYSIFVSVLPA 125
QY 125 LSVYGVLYCKSTWAHLCSGLLMGLMLQSGWGHDSCHYOVMPNRKLNRLFOIIAGNVIA 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 MSYGVLYFCGCVLVLHLAGLMGFWMIQSGWIGHDGHYIVMPNPKLMLGIVASNCIS 185

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QY 185 GSVAVAMKLDHNTHTHFACNSANLDPDIQHLPIAISPKFNSLTSYHNCKMTYDRAAF 244
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 GISIGMKMKNNAHNAHIAACNSLDEYDPLQYIPLLVSSKRFSGSLTSHFEKRLTFDSLRSF 245
QY 245 FVSPQHMTFYPALLSVRLYFLISFKVYFNNKRYRKSQELIGYAAFLTWSSLLSLRLP 304
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 246 FVSHQHMTFYPVCSAVNMFVQSL-IMLLTKRNVPFRSQELGLVFWIMYPLVSCLP 304
QY 305 NMBERMYTSCSLAVALPGHMOFSLNHFASNNYTGLPSCNDMFHOOTKGTINTASAMWD 364
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 NMGERIMFVYASLSTVGMOQVQFSLNHFASVYVGKPIDWFKQTCGLTIDISCPMWD 364
QY 365 WPHGGLHFOIEHHLFPRMPKCFPRKISPIVNLCKQKNTSYETATWMEANKMYSTLRAY 424
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 365 WPHGGLHFOIEHHLFPRMPKCFPRKISPIVNLCKQKNTSYETATWMEANKMYSTLRAY 424
QY 425 AMEAKDVTKRPVKNNWMEAMNTFG 448
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 425 ALQARDITKPLPKNLVWEALNTHG 448

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RESULT 5

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ID 08LBD7 PRELIMINARY; PRT; 446 AA.
AC 08LBD7;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Sphingolipid long chain base delta 8 desaturase.
OS Aquilegia vulgaris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Ranunculaceae; Aquilegia.
OX NCBI_TaxID=3451;
RN [1]
RP SEQUENCE FROM N.A.
RA Longman A.J., Michaelson L.V., Napier J.A.;
RT "Isolation and characterization of a cDNA encoding a delta 8
   sphingolipid desaturase from Aquilegia vulgaris.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF406816; AAN03619.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;

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Query Match 59.1%; Score 1461; DB 10; Length 446;
 Best Local Similarity 56.0%; Pred. No. 7.9e-122;
 Matches 251; Conservative 82; Mismatches 113; Indels 2; Gaps 2;

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QY 1 MEEKKHISQADLAKHQPDLWISIKGYVDISKTKENHGGELPLSPFGQDVTATPAFYHP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTEKREITSELDKNHKKPGDLWISIQKADVSDWYKDHPGSGFPPLKSLAGDEVTDAFVAFHP 60
QY 61 AHNPTAMQVLYDRFPTGYVVDYVSSEMSKDYRLVSEFSKMGLEFKTPGKGVNYSIFVSVLPA 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AHPGSAWYLYDKRFETGYLYKDYSEVSQDYRLVSEFSKMGLEFKTPGKGVNYSIFVSVLPA 119
QY 121 VFALSVGVLYCKSTWAHLCSGLLMGLMLQSGWGHDSCHYOVMPNRKLNRLFOIIAGNVIA 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 ILMALSVGVLYCKSTWAHLCSGLLMGLMLQSGWGHDSCHYOVMPNRKLNRLFOIIAGNVIA 179
QY 181 NVIAGVAVAMKLDHNTHTHFACNSANLDPDIQHLPIAISPKFNSLTSYHNCKMTYDRAAF 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 NCITGISIGMKMKNNAHNAHIAACNSLDEYDPLQYIPLLVSSKRFSGSLTSHFEKRLTFDSLRSF 239

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QY 241 AAFVFSQHTFYPALLSVRLYLFIISFKVFSNNKRVYKRSQELIGYAFLTWYSLRL 300
DB 240 IAFRLISFOHTFYPVMAIRINIFAQSF-ILLISKRPVDRALLEGWFMWYSLLL 298
QY 301 SRLPNBERVYFTSCLAVAGFQHMOPSLNHPASNVTGLPSGNDWFHQOTKTLNTAS 360
DB 299 ACIPNBERAMVYMSFAVSGYQHIOFCLNHFSAHTVGGPPPCNDWEKOTKGPFDISCS 358
QY 361 AMMDWFHGLHFOEHLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYST 420
DB 359 TMDWFHGLHFOEHLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYST 418
QY 421 LRAVAMEAKDVTKVPKPMWMEANTFG 448
DB 419 LRNALQARDLTNPRLVMEANTHG 446

RESULT 6
ID 004353 PRELIMINARY; PRT; 448 AA.
AC 004353;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Delta 6 desaturase.
OS Borage officinalis (Bourrache) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Boraginaceae; Borage.
OX NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97268723; PubMed=9108131.
RA Savyanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; U79010; AAC49700.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase_1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA desat. fam; 1.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 448 AA; 51635 MW; B62EEF701680909F CRC64;

Query Match 59.1%; Score 1460.5; DB 10; Length 448;
Best Local Similarity 55.2%; Pred. No. 8.8e-122;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

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DB 246 FVSQHTFYPIMCAARLNMYVSL-IMLTKNVSYRAHELLGCVFSIMYDLVSLCP 304
QY 305 NMPERVYFTSCLAVAGFQHMOPSLNHPASNVTGLPSGNDWFHQOTKTLNTASAMWD 364
DB 305 NMBERIVFTASLSVTGMQOVPSLNHFSSVYVGRKGNWBEKOTDGLDISCPFMD 364
QY 365 WFGHGLHFOEHLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYSTLRAV 424
DB 365 WFGHGLHFOEHLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYSTLRAV 424
QY 425 AMEAKDVTKVPKPMWMEANTFG 448
DB 425 ALQARDITKPLPKVLWEALHTHG 448

RESULT 7
ID 08L717 PRELIMINARY; PRT; 448 AA.
AC 08L717;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Delta 6-desaturase.
OS Argania spinosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Sapotaceae; Argania.
OX NCBI_TaxID=85884;
RN [1]
RP SEQUENCE FROM N.A.
RA El Filali A., Anderson M., Abbas K.;
RT "Characterization and cloning of delta-6-desaturase in Argania spinosa
RT fruit."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AY13138; AAM94345.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase_1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA desat. fam; 1.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;

Query Match 56.3%; Score 1405.5; DB 10; Length 448;
Best Local Similarity 54.1%; Pred. No. 7.1e-117;
Matches 240; Conservative 86; Mismatches 117; Indels 1; Gaps 1;

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Db		305	NWGEIMFEVSIASLSTGMOQOVFSLNHPSSYYVGKPNNMNFENQTOSTLIDISCPMMWD	365
Qy		365	WFHGLHFOIEHNLEFPPMKCFHKRIKSPYVKLCORHNISETATWEANKRVSTLRAY	424
Db		365	WFHGLOFOIEHNLEPPEKMRCLRTISPVIETCKHNLPHYVASFSKANEMTLTRLNT	424
Qy		425	AMEARDVTKPVPKXNVMEAMNTEG	448
Db		425	ALQARDTTKPLPKNLVMEALHTHG	448
 RESULT 8				
ID	O9ZRP8	PRELIMINARY:	PRT:	449 AA.
AC	O9ZRP8:			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DE	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DN	Delta-8 sphingolipid desaturase.			
GN	SLO1.			
OS	Brassica napus (Rape).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	euroside II; Brassicales; Brassicaceae; Brassica.			
OX	NCBI_TaxID=3708;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Drakkar; TISSUE=Ripening embryos;			
RX	MEDLINE=99003197; PubMed=9786850;			
RA	Sperling P., Zaehring U., Heinz B.;			
RT	"A sphingolipid desaturase from Higher Plants Identification of a New			
RT	Cytochrome b5 Fusion Protein."			
RL	J. Biol. Chem. 273:28590-28596(1998).			
CC	-1 SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.			
DR	EMBL; AJ224160; CAA11857.1; --			
DR	HSSP; p82291; ICXY.			
DR	InterPro; IPR001199; Cyf_B5.			
DR	InterPro; IPR005804; FA_decat_fam.			
DR	Pfam; PF00487; FA_desaturase; 1.			
DR	Pfam; PF00173; heme_1; 1.			
DR	Pfam; PF00612; Cyf_B5; 1.			
DR	Prodrom; PD001081; FA_decat_fam; 1.			
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.			
Kw	Heme.			
SO	SEQUENCE	449 AA; 51490 MW; FEFEE37AFPD390C1 CRC64;		
 Query Match				
	Best Local Similarity	56.5%; Score 1395.5; DB 10; Length 449;		
	Matches 240; Conservative	85; Mismatches 118; Indels 1; Gaps 1		
Qy		5 KGHISQADLANKHOPDLMISIKGVYDISKMTKEHPGEGELPLPSFAGODVTAFTAYHP	64	
Db		7 KRFLTSDDLKKGNQGDLMIISIQGVYDVSHVKGHPGEAAILMLAGODVDAFIAYHP	66	
Qy		65 GTANQYLDRFTGYVVDYSVSEMSKYRRLLVSFFSKNGLFPTPGKVYCISIFPVSVLFA	124	
Db		67 GTAPRHLENLNGHYVKKDHVSDVSRDYRLAAEFSKGLFPKKGHVLTLYTLTCVAAMD A	126	
Qy		125 LSYVGVLYCKSTMAHLCSGLMGMLMLOSQWGHSCHYQVNPKNKLRLPOLINGNYIA	184	
Db		127 AVYGVAVACTSIWAHLISAVALIGLMILOSAYVGHSGHVNVTSTPCNKLVLLEGNCIT	186	
Qy		185 GVSVAWMKLDRNTHHFACNSAULDPDIQHLPIAISPFKFNLSJTYHNCKMYTDRAARF	244	
Db		187 GISIAWMKMTNAHHIISLDHDDLGHIIPLAIVSNKFPEKSMTRFYRKLTTPPLARF	246	
Qy		245 FVSGOHWTFYPALLSVRLYLFLTSFKVVVFSSNNKRVYKKSQEILGYAALFTWYSLLSRLP	304	
Db		247 LISYOHMSFYPIMCGRINLFIOTLLLFSS--RRYVDRLANTAGILVFWTWPLVVSFLP	305	
Qy		305 NMPEVVMVFTSCLAAGAFCQHMFQSLNHNFASNVTYGLPSCNDMFOHOTGTLNITASAWMD	364	
Db		306 NMQEIITVEFJSMAVTAIOHVQFCNLNHPADVDTGPENCNDMPEKQVATAIDLISCRSYMD	365	

Oy		365	WFGHGLHPGLEHHLPFPMKCKGFKFSIPYVKNLCOXNHLSEIATAMWBANKVYSTLRAY	422
Dd		366	WFPGGLOPQLEHHLPFLPLRCHRLAGVSVVQELCKGNLPPRSLSMWEANVTLTILRAK	425
Oy		425	AMEAKDVTKPVPKMWMEANTFG	448
Dd		426	AVQARDVTNPVLNLWEALNTHG	449
 RESULT 9				
ID	Q43469	PRELIMINARY;	PRT;	458 AA.
AC	Q43469			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)		
DE	Delta-8 sphingolipid desaturase.			
GN	SLD1.			
OC	Helianthus annuus (Common sunflower).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;			
OC	Heliantheae; Helianthus.			
OX	NCBI_TaxID=4232;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Inbred line HA89;			
RC	TISSUE=Cotyledons of developing sunflower fruits;			
RX	MEDLINE=96028121; PubMed=7588718;			
RA	Spearling P., Schmidt H., Heinz E.;			
RT	"A cyclochrome b5-containing fusion protein similar to plant acyl lipid			
RL	desaturases";			
RN	Eur. J. Biochem. 232:798-805(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Inbred line HA89;			
RC	TISSUE=Cotyledons of developing sunflower fruits;			
RX	MEDLINE=21116801; PubMed=1171153;			
RA	Spearling P., Blume A., Zechringer U., Heinz E.;			
RT	"Further characterization of delta 8-sphingolipid desaturases from			
RL	higher plants";			
CC	Biochem. Soc. Trans. 28:638-641(2000).			
-1-	SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.			
DR	HSPB; X87143; CAA60621.1; ..			
DR	HSSP; P001731; IF03			
DR	IncePro; IPK001199; CyC_B5.			
DR	InterPro; IPR005804; FA_desat.fam.			
DR	Pfam; PF00487; FA_desaturase; 1.			
DR	Pfam; PF00173; heme_1; 1.			
DR	Prodrom; PD000612; CyC_B5; 1.			
DR	Prodrom; PD001081; FA_desat.fam; 1.			
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.			
Kw	Heme.			
SO	SEQUENCE	458 AA;	52231 MW;	D182287AB0E99245 CRC64;
 Query Match				
Best Local Similarity 52.3%; Score 1391.5; DB 10; Length 458;				
Matches 234; Conservative 90; Mismatches 119; Indels 1; Gaps 1				
Oy		5	KKHISQADLAKHKOPGDLMWSIKGVYDISKWTKEHPGSELPLSPAGODVTDAPIAVHP	64
Dd		16	KKYITSKELKKNNPNPDMLSIILSKVYNVTMAKENHPGDAPIVLINAGODVTDATIAHP	75
Oy		65	GTAHQVYIDRFPTGYVDYSISEMSKDYRLRVSEPSKMGLEKTPEKGYYCSIFPVSVLPA	124
Dd		76	GTAWKHLDKLPLETGHLDXYSDISRDIKLASFAPAKGMKKGGHYIVSYLSCFVSLLS	135
Oy		125	LSTVGTVLYCKSTVAHLLCSGLMGMLTLOSQGWGHSCHGYQVMPRKULRFLQIIANGVYA	184
Dd		136	ACTYGTVLYSGSFVTHMLTSGAILGLANMQVIATLGHDAGHYQMAMTRGMKKFAGIFPGNCIT	195
Oy		185	GVSAVAMKDLHNTHFAFCANSANIPLDIOHLPIAISPKFPNSLTSYYHNCKMTYDRAAP	244

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Db 196 GISTAMKMTNNAHIAICNSLDYDPLQHLPMILAVS SKLFFNSITSVFYGRQLTFDPLARF 255
Qy 245 FVSFOHMTFFPALLSVLVLFLFSFKVVFSSNNKRVRSOEIIICYAFLLTWYSLLSRLP 304
Db 256 FVSFOHMTFFPALLSVLVLFLFSFKVVFSSNNKRVRSOEIIICYAFLLTWYSLLSRLP 314
Qy 305 NMPERVVYFTFSCLAIVAGFOHMFSLNHFASNVYTGSLPSGNDWPHQOTKGTINTITASAMWD 364
Db 315 NMPERVAVFLVSEFVTCIOHIOFTLNHFSFGDVGVPKGDWPFKOTRGTIDICSSMMD 374
Qy 365 WFFGGLHFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTLRV 424
Db 375 WFFGGLHFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTLRV 434
Qy 425 AMEAKDVTXKPVKMWMEANMTFG 448
Db 435 ALQARDLTNPAPQNLWAEAFVTHG 458

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RESULT 10

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O8LB96 PRELIMINARY; PRT; 449 AA.
ID O8LB96;
AC O8LB96;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Delta-8 sphingolipid desaturase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RA Haas B.J., Volicovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 0:0-0(2002).
[2]
RN SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR 1 EMBL; AY087345; AAM64895.1; -
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat fam.
DR Pfam; PF00487; FA desaturase_1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA desat fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 449 AA; 51744 MW; A1EB55788CB03E18 CRC64;
Query Match 55.6%; Score 1372.5; DB 10; Length 449;
Best Local Similarity 51.7%; Pred. No. 6,2e-114;
Matches 231; Conservative 95; Mismatches 120; Indels 1; Gaps 1;
Qy 2 EEPKXHSQADLAKGKQPDLMISIKRVYDISKTEHSGEGLPLSPAGQDVTDAFIA 61
Db 4 ETEKXVITNEDLKGKNSGDMIAIQGKYNVSDMITHPGDVTIILNVGQDVTDAFIA 63
Qy 62 YHPGTAQYLDKFTGYVDDYSVSEMSKDYRLVSEFSKMGFLPTGKGVYCSIFVSV 121
Db 64 FHPGTAAHHDHDLTGTHIRDFQVSEVRDRRAAEFRKGLFENKGHVTLITLAFVAA 123
Qy 122 LFLASVGVLYCKSTWHLCSGLLMGLMLOSQGVNGHDSCHYQVMPKRLNRLFOIAGN 181
Db 124 MFLRLVGLVLAICTSVFANQIAALLGLIMIGSAVIGHDSGHYVIMSNKSYVRPAQLLSGN 183

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Qy 182 VIAGSVAAWKLDHNTTHFACNSANLDPDIOHLPIAISPKEFNSLTSYHNCMTYDRA 241
Db 184 CLGISIAWKKMTNNAHIAICNSLDYDPLQHLPVAVSTKPFSSLSLTFYDKLTFDPV 243
Qy 242 ARFVSFOHMTFFPALLSVLVLFLFSFKVVFSSNNKRVRSOEIIICYAFLLTWYSLLS 301
Db 244 ARFVSFOHMTFFPALLSVLVLFLFSFKVVFSSNNKRVRSOEIIICYAFLLTWYSLLS 302
Qy 302 RLNMPERVVYFTFSCLAIVAGFOHMFSLNHFASNVYTGSLPSGNDWPHQOTKGTINTITAS 361
Db 303 CLNMPERVVYFTFSCLAIVAGFOHMFSLNHFASNVYTGSLPSGNDWPHQOTKGTINTITAS 362
Qy 362 WMDWFGGLHFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTL 421
Db 363 YMDWFGGLHFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTL 422
Qy 422 RAVAMEAKDVTXKPVKMWMEANMTFG 448
Db 423 KTAAYQARDVANPVKNLWAEALNTHG 449

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RESULT 11

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Q9ZRP7 PRELIMINARY; PRT; 449 AA.
ID Q9ZRP7;
AC Q9ZRP7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Delta-8 sphingolipid desaturase (AT3G61580/P2A19_180).
GN SLD1 OR P2A19.180 OR AT3G61580.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RA STRAIN=CV. Columbia; TISSUE=flower, MAINLY GREEN PARTS, and Root;
RC MEDLINE=99003197; PubMed=9766850;
RA Speirling P., Zaehring U., Heinz B.;
RT cytochrome b5 fusion protein."
RL J. Biol. Chem. 273:28590-28596(1998).
[2]
RN SEQUENCE FROM N.A.
RA De Haan M., Maarse A.C., Griveil L.A., Mewes H.W., Lemcke K.,
RA Meyer K.F.X., Queller F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neuman G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Mu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Heuan V.M., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinozaki K., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,

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RA Theologis A., Davis R.W.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AJ224161; CAAL158.1; -
 DR EMBL: AL132962; CAB71088.1; -
 DR EMBL: AF428420; AAL16189.1; -
 DR EMBL: BT000442; AAN17419.1; -
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD00612; Cyt_B5; 1.
 DR ProDom: PD01081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51675 MW; 1450489FPIDJ35964 CRC64;
 Query Match 55.6%; Score 1372.5; DB 10; Length 449;
 Best Local Similarity 51.7%; Pred. No. 6.2e-114;
 Matches 231; Conservative 95; Mismatches 120; Indels 1; Gaps 1;
 QY 2 EEPKKHISQADLAKHOPGDMISIKGVYDISKTKHPGSELPLISFAGQDVTDAFLA 61
 DB 4 ETEKKYITMEDLKKHNSGDLMTAIOGVYVSDWIKTHPGGDTVLINLGVQDVTDAFLA 63
 QY 62 YHFGTAMOVLYDRPFTGVYVODYSVSEMSKDYRLVSEPSKMGLEPKTPGKGVYCSIFPVSV 121
 DB 64 FHEGTIMHMDLFTGTHINDPQVSESRDYRMALEPRKLGLEPKKHVTLTYTLAFVAA 123
 QY 122 LFLASYGVLYCKSTVAHLCSGLMGLMLOSQVGHDSCHYQVMPNKLRLPQIIAG 181
 DB 124 MFLGVLYGVLAGCSVFAHQIAAALLGLIMTQSAVIGHDSGHYIMNSKSNRAQLSGN 183
 QY 182 VIAGSVVAMWKLDMNTHHFAFNSANLDPDIOHLPIAISPFNSLTSYHNCKMTYDRA 241
 DB 184 CLTGISIAMWKTNAHNLACNSLDYDPLQHIPVAVSTKFPSSLTSRPFYDRKLTEDPV 243
 QY 242 ARPFVPOHMTFYPALLSVRLYLFLSPKVFESNNKRYKRSOEILGYAFLTWYSLLS 301
 DB 244 ARLVYQHFTTYVPCFGRINLFIQTFLLFS-KKEVPRALNFAIGLFWTWPFLLVS 302
 QY 302 RLPMNERVWYFTSCLAVAGFQHMQFSLNFAFNSVYTGLPBGNDWFHOQTGTLNITAS 361
 DB 303 CLPWNERRFFVYTSFTVTLQHOITLNFADVYVGPRTGSDWEKQAAGTIDISCS 362
 QY 362 WMDWFGGLHFOLEHNLPRMPKCHFRKISPIYNKLCKOKNLSETATWMEANKVYSTL 421
 DB 363 YMDWFGGLHFOLEHNLPRLPCHLRKYSRVYQELCKGNLPLRSMSPFANVLTINTL 422
 QY 422 RAVAMEAKDVTKRPVKMVMWEANTFG 448
 DB 423 KTAAYQARDVANPVKNLWEALNTHG 449
 RESULT 12
 O9FR82 PRELIMINARY; PRT; 446 AA.
 AC O9FR82;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 8-sphingolipid desaturase.
 GN SLD1.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Borago.
 OC NCBI_TaxID=13353;
 OX 11)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21092516; PubMed=111622428;
 RA Libisch B., Michaelson L.V., Lewis M.J., Shewry P.R., Napier J.A.;

RT "Chimeras of Delta6-fatty acid and Delta8-sphingolipid desaturases";
 RL Biochem. Biophys. Res. Commun. 279:779-785(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21260464; PubMed=11368168;
 RA Sperling P., Libisch B., Zaehring U., Napier J.A., Heinz E.;
 RT "Functional identification of a delta 8-sphingolipid desaturase from
 RT Borago officinalis";
 RL Arch. Biochem. Biophys. 388:293-298(2001).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF133728; AAG43277.1; -
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD00612; Cyt_B5; 1.
 DR ProDom: PD01081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 446 AA; 50926 MW; EBD579F03A3AF0C CRC64;
 Query Match 53.6%; Score 1325; DB 10; Length 446;
 Best Local Similarity 50.7%; Pred. No. 1.1e-109;
 Matches 227; Conservative 95; Mismatches 124; Indels 2; Gaps 2;
 QY 1 MEPPKHISQADLAKHOPGDMISIKGVYDISKTKHPGSELPLISFAGQDVTDAFLA 60
 DB 1 MEGTKKYSVGLGEGKNGDGVWISIOGVYVVTWIKHPPGQDVPINMLAODATDAFLA 60
 QY 61 AYHPGTAMOVLYDRPFTGVYVODYSVSEMSKDYRLVSEPSKMGLEPKTPGKGVYCSIFPVSV 120
 DB 61 AYHPGTAMOVLYDRPFTGVYVODYSVSEMSKDYRLVSEPSKMGLEPKTPGKGVYCSIFPVSV 120
 QY 121 VIAGSVVAMWKLDMNTHHFAFNSANLDPDIOHLPIAISPFNSLTSYHNCKMTYDRA 180
 DB 121 LLLCGGVGLCSNLSLWMTNLSGMLGMCFFIOAVALIGHDSGHYTMWSKGVNKKFAVLNG 180
 QY 181 NVIAGSVVAMWKLDMNTHHFAFNSANLDPDIOHLPIAISPFNSLTSYHNCKMTYDRA 240
 DB 181 NCLTGISIAMWKTNAHNLACNSLDYDPLQHIPVAVSTKFPSSLTSRPFYDRKLTEDPV 240
 QY 241 AARPFVPOHMTFYPALLSVRLYLFLSPKVFESNNKRYKRSOEILGYAFLTWYSLLS 300
 DB 241 LSRFLVYQHFTTYVPCFGRINLFIQTFLLFS-KKEVPRALNFAIGLFWTWPFLLVS 299
 QY 301 RLPMNERVWYFTSCLAVAGFQHMQFSLNFAFNSVYTGLPBGNDWFHOQTGTLNITAS 360
 DB 300 CLPWNERRFFVYTSFTVTLQHOITLNFADVYVGPRTGSDWEKQAAGTIDISCS 359
 QY 361 AAWDFHGGGLHFOLEHNLPRMPKCHFRKISPIYNKLCKOKNLSETATWMEANKVYSTL 420
 DB 360 SWMDWFGGLHFOLEHNLPRMPKCHFRKISPIYNKLCKOKNLSETATWMEANKVYSTL 419
 QY 421 RAVAMEAKDVTKRPVKMVMWEANTFG 448
 DB 420 LRTALQARDLT-VVPQNLWEALNTHG 446
 RESULT 13
 O9ZTU8 PRELIMINARY; PRT; 469 AA.
 AC O9ZTU8;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE 5276.
 GN 5276.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OC NCBI_TaxID=4565;

[1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. E73;
 RA Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;
 RT "Aluminum tolerance in yeast conferred by over-expression of wheat
 RT gene."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF031194; AAD10250.1; -.
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR InterPro: IPR001092; HbH_basic.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROMEBS.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR PROSITE: PS00038; HbH_1; 1.
 KW Heme.
 SQ SEQUENCE 469 AA; 52617 MW; 16F223CCLF79740D CRC64;
 Query Match 52.4%; Score 1293.5; DB 10; Length 469;
 Best Local Similarity 52.0%; Pred. No. 7.3e-107;
 Matches 230; Conservative 75; Mismatches 134; Indels 3; Gaps 3;
 QY 8 ISQADLAKHKOPGDLWISIKGVYDISKWKKEHFGELPLISFAGQVTDAPFIYHGTGTA 67
 DB 30 ISTKELOAHAAADLWISIGDYYDVPPMLRHHGEGVPLITLTAQDAPAFMAVHPSPV 89
 QY 68 WOYLDREFTGYVYDVSVSEMSKDYRLVSEFSKGLFKTPGKGVCSIFPVSVLPALSV 127
 DB 90 RPLLRFFVG-RLTDTYVPASADFRLLQLSAGLPERVGHTRPKLLVAMSVLFCIAL 148
 QY 128 YGVLYCKSTMAHLCSGLLMGLMOSGVGHDSCHYVMPNKKLNRLFOIAGVNIAGVS 187
 DB 149 YCVLACSTGAHMPAGGLIGFVITQSGMIGHDSGHQITRHPALNRLLOYVSGNCLGLG 208
 QY 188 VAWMKLDHNTHTFPCNSANADPDQHPITAIISPFPNSLTSTYHNCKMTYDRAAPFVS 247
 DB 209 IAWMKFHNTHHTSCNSLDHPDQHPPLFAVSTKLNNMLSVCEYRTLLFADLSKEPVS 268
 QY 248 FOHWTFFPALLSVRLYLFIISFKVVFSGNNKRVYKSOEILGYAFLTWYSLLSRLNWP 307
 DB 269 YOHNTFFPWGPFARINLLVOSI-VFLITQKKVROMELIAGVAFWVWYPLVLSCLPMMW 327
 QY 308 ERVWYFTSCLAVAGFOHMQFSLNHFASNVYTGLPSSGNDWPHOQTKTLNTITASAMDMFH 367
 DB 328 ERVAFVLASPVITGIQHVQCLNHFSSAVYVGPKNDFERQTAGTLDIKCSPMDMFH 387
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 DB 388 GGLQFOVEHHLFPLPRCHYRMAPIVRDLCKKHGLSYGAATFEAAVMTWKTLRAAALQ 447
 QY 428 AKDYTK-PVPRKNWMEAMNTFG 448
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RP SEQUENCE FROM N.A.
 RC STRAIN=wc3; TISSUE=Protonemata;
 RX MEDLINE=20307617; PubMed=10848999;
 RA Sperling P., Lee M., Gierke T., Zaehring U., Stryme S., Heinz E.;
 RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
 RT moss Ceratodon purpureus. A new member of the cytochrome b5
 RT superfamily."
 RL Eur. J. Biochem. 267:3801-3811 (2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: A1250734; CAB9492.1; -.
 DR HSSP: P04166; 1BSM.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 2.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 483 AA; 54857 MW; C451D042169ABIC2 CRC64;
 Query Match 26.9%; Score 663.5; DB 10; Length 483;
 Best Local Similarity 35.7%; Pred. No. 1.1e-50;
 Matches 154; Conservative 71; Mismatches 177; Indels 29; Gaps 12;
 QY 9 SQADLAKHKOPGDLWISIKGVYDISKWKKEHFGELPLISFAGQVTDAPFIYHGTGTA 68
 DB 64 SLADVASHDRPGCMVIVKEKYDIDRPAADHGGIV-ISTYGRGCTDVFAFHPPAAW 122
 QY 69 QYLDREFTGYVYDVSVSEMSKDYRLVSEFSKGLFKTPGKGVCSIFPVSVLPALSV 128
 DB 123 KQNDYYIGDLAREEPDLDELKQYRDMRAEFVEGFLFKSSKAWFLQTLINALFAASTA 182
 QY 129 GVIYCKSTMAHLCSGLLMGLMOSGVGHDSCHYVMPNKKLNRLFOIAGVNIAGVS 188
 DB 183 TICYDYSYVAIVLASLMLGLFVQCGMLHDFLHQGFENRRANSFGLVFGCVLGFVS 242
 QY 189 AMWKLHNTHTFPCNSAN-----LDPDQHPITAIISPFPNSLTSTYHNCKMTYDRAAP 243
 DB 243 SWRTKHNTHHTFPCNDEQYTPLEDIDITPLIANSKEILAVES-----KRLR 253
 QY 244 FVSPQHWTFYFALLSVRL-YLF--ILSPKVVSNNKRVYKRSQELIGYAEFLTWYSL 299
 DB 294 -VQYGHVIMLPLFLMARYSWTFGSLLPFNPDLSSTTKGIEKGVAFHYAMP-SNAAPH 351
 QY 300 LSLPLMPPEKVMYFTSCLAVAG-FQHMQFSLNHFASNVYTGLPSSGNDWPHOQTKTLNT 358
 DB 352 I-LPGVAKPLAMVATELVAGLLGFVFTLSINGREYVN--ESKDPVRAQVITTRN-T 405
 QY 359 ASAMW-DMPFGHLPQIEHHLFPRMPKCHPRKISPIYVKLCQKNLSYETATWMEANKMY 417
 DB 406 KRWMPNDWTFGSLDTQIEHHLFPTPRHNYPKIAPVEALCKKHGLEIDVNSVYGSVAV 465
 QY 418 YSTLRVAMEA 428
 DB 466 VKALKELADEA 476

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 ID Q9LENO PRELIMINARY; PRT; 483 AA.
 AC Q9LENO;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 6-fatty acetylase.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Dicranidae; Dicranales; Dicitrichaceae; Ceratodon.
 OX NCBI_TaxId=3225;
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RESULT 15
 ID Q9LEM9 PRELIMINARY; PRT; 520 AA.
 AC Q9LEM9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 6-fatty acid desaturase.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Dicranidae; Dicranales; Dicitrichaceae; Ceratodon.
 OX NCBI_TaxId=3225;
 RP SEQUENCE FROM N.A.
 RC STRAIN=wc3; TISSUE=Protonemata;

RX MEDLINE=20307617; PubMed=10848999;
 RA Sperling P., Lee M., Giske T., Zaehrer U., Stymne S., Heinz E.;
 RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
 RT moss *Ceratodon purpureus*. A new member of the cytochrome b5
 RT superfamily.";
 RL Eur. J. Biochem. 267:3801-3811(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AJ250735; CAB94993.1; -.
 DR HSSP; P00171; IEHB.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme 1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 520 AA; 59160 MW; 5A9332BEC153439 CRC64;

Query Match 25.3%; Score 626; DB 10; Length 520;
 Best local Similarity 35.2%; Pred. No 2,7e-47;
 Matches 156; Conservative 65; Mismatches 176; Indels 46; Gaps 12;

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 DB 93 QPKKPVYSLKDVASHDMPQDCWIIIEKQYDVSTFAEGHGGTV-INTYFGRDATDVFS 151
 QY 61 AHFGTANQYLDREFTGYVQDYSEMSKDYRLVSEPSKMGLEKTPGKGVCSIFPVS 120
 DB 152 TFHASTSMKILQNFYIGNLVREPTLELKEYRELALFLREQLPKS-SKSYVLPKTLIN 210
 QY 121 V-LFALSYGVLYCKSTWMAHLSGLMGMLGSGWVGHDSCHYOVMPPNKKLRLPQIIA 179
 DB 211 VSLVATSIATISLYKSYRAVLISASLMGLFIQCGMWSHDFLHQVFEETRLNDVGYIV 270
 QY 180 GNVIAGVSAVMWKLDNTHHFACNAN-----LDPDIOHLPIAISPKEFNSLTS----- 229
 DB 271 GNVVLGFSVSWMTKINLHLHAAPNECDQKYPIDEDIDTLPIAWSKDLATVESKTMRLR 330
 QY 230 ---YHN---NCKMTYDRAARFFVFSQHWTFYPALLSVRLYLFTLSFKVVFSSNNKRYKRS 283
 DB 331 VLQYQHLFFVLVLTLPARAS-----WLFWSAAFTLRPELTL-----GEKLLERG 373
 QY 284 QELIGYAAFLTWY-SLLLSRLPWPBRVYFTSCLAAGQHWQFSLNHPASNYTGIPS 342
 DB 374 TWALMT-----INNSVAFYLLPGMKPVVMNVVSELMSGFLIGYFVLSHNGMEVYN--T 426
 QY 343 GNDWFHQTKGTINLTASAMWDMFHGSLHFOIEHHLFPRMPKCHFRKISPIYVKLCOKIN 402
 DB 427 SKDPVNAQIASTRDIKAGVFNDFWTGILNRQIEHHLFPTMPRHNLNKISPHVETLCKKIG 486
 QY 403 LSYETATMWEANKMYSTLRVA 425
 DB 487 LYEEDVSMASGTFRVLTKLKDV 509

Search completed: January 1, 2004, 06:33:52
 Job time : 43.4085 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 15.5646 Seconds
(without alignments)
1217.848 Million cell updates/sec

Title: US-09-857-524B-2

Perfect score: 2470
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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6: /cgn2_6/prodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1459.5	59.1	448	1 US-08-366-779-5	Sequence 5, Appl1
2	1459.5	59.1	448	1 US-08-789-936-5	Sequence 5, Appl1
3	1459.5	59.1	448	4 US-08-934-254-5	Sequence 5, Appl1
4	1451.5	58.8	446	2 US-08-833-610-5	Sequence 5, Appl1
5	1451.5	58.8	446	3 US-08-834-033A-15	Sequence 15, Appl1
6	1314.5	53.2	452	4 US-08-934-234-27	Sequence 27, Appl1
7	733.5	29.7	252	2 US-08-834-655-7	Sequence 7, Appl1
8	733.5	29.7	252	3 US-08-834-033A-8	Sequence 8, Appl1
9	733.5	29.7	252	3 US-09-363-574-7	Sequence 7, Appl1
10	733.5	29.7	252	4 US-09-363-526-7	Sequence 2, Appl1
11	549	22.2	457	2 US-08-834-655-2	Sequence 2, Appl1
12	549	22.2	457	3 US-08-834-033A-2	Sequence 2, Appl1
13	549	22.2	457	3 US-09-363-574-2	Sequence 2, Appl1
14	549	22.2	457	4 US-09-363-526-2	Sequence 2, Appl1
15	549	22.2	457	4 US-09-330-235-18	Sequence 18, Appl1
16	549	22.2	458	4 US-09-439-261-10	Sequence 10, Appl1
17	549	22.2	458	4 US-09-439-261-44	Sequence 44, Appl1
18	549	22.2	458	4 US-09-227-613-11	Sequence 11, Appl1
19	549	22.2	458	4 US-09-227-613-41	Sequence 41, Appl1
20	546	22.1	457	2 US-08-833-610-4	Sequence 4, Appl1
21	546	22.1	457	3 US-08-834-033A-14	Sequence 14, Appl1
22	451.5	18.3	444	4 US-09-439-261-11	Sequence 11, Appl1
23	442.5	17.9	444	4 US-09-439-261-12	Sequence 12, Appl1
24	442.5	17.9	444	4 US-09-439-261-39	Sequence 39, Appl1
25	442.5	17.9	445	4 US-09-439-261-45	Sequence 45, Appl1
26	440	17.8	444	4 US-09-439-261-43	Sequence 43, Appl1

28	440	17.8	444	4 US-09-227-613-42	Sequence 42, Appl1
29	436	17.7	355	2 US-08-834-655-5	Sequence 5, Appl1
30	436	17.7	355	3 US-08-834-033A-6	Sequence 6, Appl1
31	436	17.7	355	3 US-09-363-574-5	Sequence 5, Appl1
32	436	17.7	355	4 US-09-363-526-5	Sequence 5, Appl1
33	431.5	17.5	445	4 US-09-048-888-1	Sequence 1, Appl1
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36	429	17.4	465	4 US-09-439-261-40	Sequence 40, Appl1
37	429	17.4	465	4 US-09-227-613-38	Sequence 38, Appl1
38	419	17.0	323	4 US-09-439-261-17	Sequence 17, Appl1
39	419	17.0	323	4 US-09-227-613-17	Sequence 17, Appl1
40	355.5	14.4	125	2 US-08-834-655-8	Sequence 8, Appl1
41	355.5	14.4	125	3 US-08-834-033A-9	Sequence 9, Appl1
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43	355.5	14.4	125	4 US-09-363-526-8	Sequence 8, Appl1
44	320	13.0	446	2 US-08-833-610-2	Sequence 2, Appl1
45	320	13.0	446	3 US-08-834-033A-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
; Sequence 5, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freysinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,779
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-366-779-5
Query Match 59.1%; Score 1459.5; DB 1; Length 448;
Best Local Similarity 55.2%; Pred. No. 3.6e-150;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;
QY 5 KKHISQADLAKHKQGDLLISIKGVYDISKVTKEHGEELPLLSFAGQDVTDATVYHP 64

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; US-08-789-936-5

Query Match      59.1%; Score 1459.5; DB 1; Length 448;
Best Local Similarity 55.2%; Pred. No. 3 6e-150;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

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Qy      125 LSVYGVLYCKSTVAHLCSGLLMGMLMLOSQGVGHDSCHYQVMPNRLNRLFOIAGNVIA 184
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Db      186 GISIGWKKNNHNAHHIACNSLEYDPLQYIPLVSSKFFGSLTSHFYEKRLTFDSLRF 245
Qy      245 FVSFQWMTYIPALLSVRLYLFILSFYVSNKRYVSKSOEILGYAFLTWISLLSLRP 304
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Db      365 WFGGSGQFOIEHLFPRMPCRNLRKISPIYIELCKGHNLPLYNVAASFSSKANEMTLRLTRNT 424
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RESULT 2

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; Sequence 5, Application US/08789936
; Patent No. 5789220
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freysinet, Georges L.
; APPLICANT: Numborg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,936
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/366,779
; FILING DATE: 30-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXW
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; US-08-789-936-5

Query Match      59.1%; Score 1459.5; DB 1; Length 448;
Best Local Similarity 55.2%; Pred. No. 3 6e-150;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

Db      5 KKHISQADLAKHDKPGDLWISIQKAYDVSDWKDHPGSGFFPLKSLAGQVTDAPFAVAFHP 64
Qy      6 KKYITSDCLKNHDKPGDLWISIQKAYDVSDWKDHPGSGFFPLKSLAGQVTDAPFAVAFHP 65
Db      66 ASTWKMLDKFFFTGYIYKDYVSSEMSKDYRLVSEFSKMGLYDKKGHIMFATLCFIAMLFA 125
Qy      65 GRAMQVLDKFFFTGYIYQDYVSSEMSKDYRLVSEFSKMGLFKTPGKGVYCSIFPVSLFA 124
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RESULT 3

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; Sequence 5, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU

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TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-934-254-5

Query Match 59.1%; Score 1459.5; DB 4; Length 448;
 Best Local Similarity 55.2%; Pred. No. 3.6e-150;
 Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

QY 5 KKHISQADLAKKQKQDLMISIKGVYDISKWTKEHPPGELPLSPAGQVTDAPFAIYHP 64
 DB 6 KKYITSDELKNDKDKGDLWISIQKAYVSDWVKDHPGSPFLKSLAQGEVTDAPFAIYHP 65
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 QY 425 AMEADQVTKPVKNNWMEAMNTFG 448
 DB 425 ALQARDITKPLKPLWMEALHTHG 448

RESULT 4

US-08-833-610-5
 Sequence 5, Application US/08833610
 Patent No. 5972664
 GENERAL INFORMATION:
 APPLICANT: KUTUZON, DEBORAH
 APPLICANT: MUKERJI, PRADIP
 APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/833,610
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.123.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-833-610-5

Query Match 58.8%; Score 1451.5; DB 2; Length 446;
 Best Local Similarity 55.2%; Pred. No. 2.6e-149;
 Matches 244; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

QY 5 KKHISQADLAKKQKQDLMISIKGVYDISKWTKEHPPGELPLSPAGQVTDAPFAIYHP 64
 DB 6 KKYITSDELKNDKDKGDLWISIQKAYVSDWVKDHPGSPFLKSLAQGEVTDAPFAIYHP 65
 QY 65 GTAMQYLDREFYGVYVODYSVSEMSKDYRLVSEFSKMGLEFPTPKGVYCSIFPVSVLPA 124
 DB 66 ASTWKNLDRFFGYLYLKDYSEVSKDYRLVFEFSKMGLEFPTPKGVYCSIFPVSVLPA 125
 QY 125 LSVYGVLYCKSTWALHSCGLMGLMLOSQWGHDSCHYQVMPNRLNRLFOIAGNVIA 184
 DB 126 MSYGVLYLCEGVLYHLFSGCLMGFLMIOGWHGDAHYMVVSDRLNKFMCIFPANCIS 185
 QY 185 GVSVAWMLDHTHTHFAACNSANLDPDIQHLPIAISPKFNSLTSYHNCKMTYDRAAF 244
 DB 186 GISIGMWMKNHNAHIIACNSLEYDPLQYIPLVVSSKFFGSLTSHFEKRLTFPSLSRF 245
 QY 245 FVSFQHTFEPYRLLSVRLYFLFSFKVVSNNKRYKSOELGYAAFLTWYSLLSRLP 304
 DB 246 FVSYQHTFEPYRLMCAARLMYVQSL-IMLTGRNVSYRAQELGCLVSIWPLVSCLP 304
 QY 305 NMPERVMYFTSCLAVAGFQHMQFSLNHPASNYTGLPSGNDWFHOOTKGLNITASAMWD 364
 DB 305 NMGERIMFVIALSLVTGMQVQFSLNHPSSVYVGKPKGNMFEKQTDGTLDISCPMWD 364
 QY 365 WFGGLHFOIEHHLFPPRMKCHFRKISPIVNLCKQNLSTETATMEANKVYSLRAV 424
 DB 365 WFGGSQFOIEHHLFPPKPRCNLRKISPIVIELCKQNLPLYVAFSSKANEMTLTLRLNT 424
 QY 425 AMEADQVTKPVKNNWMEAMNT 446
 DB 425 ALQARDITKPLKPLWMEALHT 446

RESULT 5

US-08-834-033A-15
 Sequence 15, Application US/08834033A
 Patent No. 6075183
 GENERAL INFORMATION:
 APPLICANT: KUTUZON, DEBORAH
 APPLICANT: MUKERJI, PRADIP
 APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:

ADDRESS: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834.033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CQAB-300. USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-15


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/ Patent No. 6136574
/ GENERAL INFORMATION:
/ APPLICANT: KNUTZON, DEBORAH
/ APPLICANT: MURKERJI, PRADIP
/ APPLICANT: HUANG, YUNG-SHENG
/ APPLICANT: THURMOND, JENNIFER
/ APPLICANT: CHAUDHARY, SUNITA
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
/ TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
/ STREET: 2001 FERRY BUILDING
/ CITY: SAN FRANCISCO
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/363,574
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WARD, MICHAEL R.
/ REGISTRATION NUMBER: 38,651
/ REFERENCE/DOCKET NUMBER: CGAB-202 USA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 433-4150
/ TELEFAX: (415) 433-8716
/ TELEX: N/A
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 252 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-363-574-7

Query Match      29.7%; Score 733.5; DB 3; Length 252;
Best Local Similarity 49.4%; Pred. No. 1.7e-71;
Matches 144; Conservative 52; Mismatches 74; Indels 1; Gaps 1;

QY 127 VGVLYCKSTMAHLCSGLIMGLMGLMGVGHDSCHYQVMPNKLRLFOIIAGNVIAGV 186
DB 3 LVGVLACTSVFAHQIAAALLGLMIGSAYIGHDSGHVYIMSNKSYNRFQALLSGNCLTGI 62
QY 187 SVAMWKLDNHTTHFAACNSANLDPDIOHLPIAISPKFNSLTSYHNCKTYDRAARFV 246
DB 63 SIAMWKTNAHNAHLACNSLDYDPDLOHIFPAVSTKFFSLTSRFDKLTFFPVARFLV 122
QY 247 SFQHTFYPALLSVRLYLFLSKVVPNSNKKRYKSOEILGYAAELTWYSLSLPLPW 306
DB 123 SYGHFTYVNCGRINLFIQTFLFLFS-KREVDPDALNFAGLVFWTWPLLVSCLPW 181
QY 307 PERVMFTSCLAVAGQHQMSLNHPASNVYTGIPSGNDWFHOOTGTNTITASAWMDWF 366
DB 182 PERFFVFTSFYVTAIOHIOFLNHPADVYVGPPTGSDWFQKQAGTIDISCRSYMDWF 241
QY 367 HGGHAFQIEHH 377
DB 242 FGGLOFOLBHH 252
```

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RESULT 10
US-09-363-526-7
/ Sequence 7, Application US/09363526
/ Patent No. 6410288
/ GENERAL INFORMATION:
/ APPLICANT: KNUTZON, DEBORAH
/ APPLICANT: MURKERJI, PRADIP
```

```
/ APPLICANT: KNUTZON, DEBORAH
/ APPLICANT: MURKERJI, PRADIP
/ APPLICANT: HUANG, YUNG-SHENG
/ APPLICANT: THURMOND, JENNIFER
/ APPLICANT: CHAUDHARY, SUNITA
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
/ TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
/ STREET: 2001 FERRY BUILDING
/ CITY: SAN FRANCISCO
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/363,526
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WARD, MICHAEL R.
/ REGISTRATION NUMBER: 38,651
/ REFERENCE/DOCKET NUMBER: CGAB-201 USA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 433-4150
/ TELEFAX: (415) 433-8716
/ TELEX: N/A
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 252 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-363-526-7

Query Match      29.7%; Score 733.5; DB 4; Length 252;
Best Local Similarity 49.4%; Pred. No. 1.7e-71;
Matches 124; Conservative 52; Mismatches 74; Indels 1; Gaps 1;

QY 127 VGVLYCKSTMAHLCSGLIMGLMGLMGVGHDSCHYQVMPNKLRLFOIIAGNVIAGV 186
DB 3 LVGVLACTSVFAHQIAAALLGLMIGSAYIGHDSGHVYIMSNKSYNRFQALLSGNCLTGI 62
QY 187 SVAMWKLDNHTTHFAACNSANLDPDIOHLPIAISPKFNSLTSYHNCKTYDRAARFV 246
DB 63 SIAMWKTNAHNAHLACNSLDYDPDLOHIFPAVSTKFFSLTSRFDKLTFFPVARFLV 122
QY 247 SFQHTFYPALLSVRLYLFLSKVVPNSNKKRYKSOEILGYAAELTWYSLSLPLPW 306
DB 123 SYGHFTYVNCGRINLFIQTFLFLFS-KREVDPDALNFAGLVFWTWPLLVSCLPW 181
QY 307 PERVMFTSCLAVAGQHQMSLNHPASNVYTGIPSGNDWFHOOTGTNTITASAWMDWF 366
DB 182 PERFFVFTSFYVTAIOHIOFLNHPADVYVGPPTGSDWFQKQAGTIDISCRSYMDWF 241
QY 367 HGGHAFQIEHH 377
DB 242 FGGLOFOLBHH 252
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```
RESULT 11
US-08-834-655-2
/ Sequence 2, Application US/08834655
/ Patent No. 5968809
/ GENERAL INFORMATION:
/ APPLICANT: KNUTZON, DEBORAH
/ APPLICANT: MURKERJI, PRADIP
```

APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,655
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.124.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-2

Query Match 22.2%; Score 549; DB 2; Length 457;
 Best Local Similarity 33.3%; Pred. No. 5.1e-51;
 Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;
 QY 26 IKGKVDISKMTKEHNGGELPLISFAGDVTDAFIAYHPTAQYDRPFTGYVYD---D 82
 DB 36 IONKTYDAEFPDHPGGSV-ILTHVKGDTGVFTDFHPEAAETLANFYVGDIIDSDRD 94
 QY 83 YSVSEMSKYRRLVSEFSKMGLEKTPGKGYVCSIFVSVLFALSVYG---VLVCK---S 135
 DB 95 IKNDDEPAAEVRKRLTLFQSLGYYS-SKAYYA---FKVSFNLCTMGSLTVIAKMGQTS 149
 QY 136 TWAHLCSGLMGMLWQSGVGHDSCHYOVNPKRLNRLFQIIAGNVIAVGVAAWKLDH 195
 DB 150 TLANTVLSAALLGLFMQCCGLAHDFLHQVFODRFWGDLFGAFLGVCQGFSSSWKDKH 209
 QY 196 NTHHFACSANLDPDIOHLPIAISPKFNSLTSYHNCKMTYD-----RAARFVS 247
 DB 210 NTHHAAPNVHGEDPDIDTHPL-----LTWSEHALEMFSDVDEELTRMMSRFVVL 259
 QY 248 FOHMTFYPALLSVRLYLFIISFKVVFNSNK-----RYKRSQELIGVAAFLTWYSLLL 300
 DB 260 NQWMEFFPLISFARLSWCOSILFVLPNGQAHKPGSARVPSILVEQLSLAMHTWYLATM 319
 QY 301 SRLPNP-ERVMYFTISCLAVAG-FOHMQSFLNHFASNVYGLP-----SGNDWFHQOT 351
 DB 320 FLFIKDPVVMVLVYFLVSOAVCGNLAIIVESLNH-----NGMVISKEEAVDMDFPTXOI 373
 QY 352 KGTLLNTASAMWDFEGSLHFOIEHNLPRMPKCHRKISPIYNTKCOGNLSYEFATWM 411
 DB 374 IIGRDVHFGGLFAWMEFGGLNYQLEHNLPSMPRHNSKIQPAVELCKKYNNVYHTTGM 433
 QY 412 EANKVYVSTLRAVAMEAKDVTK 433

DB 434 EGTAEVSRLENEVSXAASKMGK 455
 RESULT 12
 US-08-834-033A-2
 Sequence 2, Application US/08834033A
 Patent No. 6075183
 GENERAL INFORMATION:
 APPLICANT: KUTZON, DEBORAH
 APPLICANT: MUKERJI, PRADIP
 APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
 STREET: 2001 FERRY BUILDING
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,033A
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: WARD, MICHAEL R.
 REGISTRATION NUMBER: 38,651
 REFERENCE/DOCKET NUMBER: CGAB-300. USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-033A-2

Query Match 22.2%; Score 549; DB 3; Length 457;
 Best Local Similarity 33.3%; Pred. No. 5.1e-51;
 Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;
 QY 26 IKGKVDISKMTKEHNGGELPLISFAGDVTDAFIAYHPTAQYDRPFTGYVYD---D 82
 DB 36 IONKTYDAEFPDHPGGSV-ILTHVKGDTGVFTDFHPEAAETLANFYVGDIIDSDRD 94
 QY 83 YSVSEMSKYRRLVSEFSKMGLEKTPGKGYVCSIFVSVLFALSVYG---VLVCK---S 135
 DB 95 IKNDDEPAAEVRKRLTLFQSLGYYS-SKAYYA---FKVSFNLCTMGSLTVIAKMGQTS 149
 QY 136 TWAHLCSGLMGMLWQSGVGHDSCHYOVNPKRLNRLFQIIAGNVIAVGVAAWKLDH 195
 DB 150 TLANTVLSAALLGLFMQCCGLAHDFLHQVFODRFWGDLFGAFLGVCQGFSSSWKDKH 209
 QY 196 NTHHFACSANLDPDIOHLPIAISPKFNSLTSYHNCKMTYD-----RAARFVS 247
 DB 210 NTHHAAPNVHGEDPDIDTHPL-----LTWSEHALEMFSDVDEELTRMMSRFVVL 259
 QY 248 FOHMTFYPALLSVRLYLFIISFKVVFNSNK-----RYKRSQELIGVAAFLTWYSLLL 300
 DB 260 NQWMEFFPLISFARLSWCOSILFVLPNGQAHKPGSARVPSILVEQLSLAMHTWYLATM 319
 QY 260 NQWMEFFPLISFARLSWCOSILFVLPNGQAHKPGSARVPSILVEQLSLAMHTWYLATM 319

QY 301 SRLPNP-ERWYFTSCLAVAG-FQHWQSLNHFASNYTGLP-----SGNDWPHQQT 351
 DB 320 FLFIKDPVMMLVYFVLSQAVCGNLIAIVFSLNH-----NGMVISKEBAVDMDFTTKQ1 373
 QY 352 KGTLNITASAMMDWPHGGLHFOIEHHLFPRMPKCHFRKISPIYNKLCQKNLSYETATW 411
 DB 374 ITRGDVHPLGFPAWFFGGLNYQIEHHLFPRMPKCHFRKISPIYNKLCQKNLSYETATW 433
 QY 412 EANKWYSTLRVAVAMEAKDVTX 433
 DB 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 13

US-09-363-574-2
 ; Sequence 2, Application US/09363574
 ; Patent No. 6136574
 ; GENERAL INFORMATION:
 ; APPLICANT: KNOTZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
 ; STREET: 2001 PERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/363,574
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-202 USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEFAX: (415) 433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-363-574-2

Query Match 22.2%; Score 549; DB 3; Length 457;
 Best Local Similarity 33.3%; Pred. No. 5, 1e-51;
 Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

QY 26 IAGKYVDISKMTKEHFGGLPLISFAGQVTDAPFIAYHGTAMQYLDREFTGYVQ--D 82
 DB 36 IINXKYVDVEHFVVDHFGGSV-ILTHVKGQDGVDFDFHPEAAMELTANFYVDIDSSRD 94
 QY 83 YSVSEMSKQYRRLVSEFSKWLKTPKGVYCSIFPVSVFALSYVG---VLXCK----S 135
 DB 95 IKNDDPFAAEFRKRLTFLQSLGYVDS--SKAYYA---FKVSFNLCIWSLSTVIAKKGQTS 149
 QY 136 TWAHLCSGLLMGLMQLQSGWVGHDSCHYQVMPNRKLNRLFOIAGNVIAQSVAMWKLDR 195

DB 150 TLANVLASALLGLFWQCCMLAHPFHQVFDPRFMDLFGAFLGVCQGFSSWMKDKH 209
 QY 196 NTHFPAQNSANLDPDIOHLPITAIISPKNLSYHNCMTVD-----RAAPFVS 247
 DB 210 NTHAAPNWHGEBDDIDTHPL-----LWSEHLEMSDVEDDEELTRMWSFVTL 259
 QY 248 FQHWTEYPLLVSRYLFLFISFQVFSNNK-----RYVKRQELIGVAAFLTWYSLLL 300
 DB 260 NQTFWFFPLISFARLWSGLQSLIFVLPNGQAHKPSGARVPISLVEQLSLAMHTWYLATM 319
 QY 301 SRLPNP-ERWYFTSCLAVAG-FQHWQSLNHFASNYTGLP-----SGNDWPHQQT 351
 DB 320 FLFIKDPVMMLVYFVLSQAVCGNLIAIVFSLNH-----NGMVISKEBAVDMDFTTKQ1 373
 QY 352 KGTLNITASAMMDWPHGGLHFOIEHHLFPRMPKCHFRKISPIYNKLCQKNLSYETATW 411
 DB 374 ITRGDVHPLGFPAWFFGGLNYQIEHHLFPRMPKCHFRKISPIYNKLCQKNLSYETATW 433
 QY 412 EANKWYSTLRVAVAMEAKDVTX 433
 DB 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 14

US-09-363-526-2
 ; Sequence 2, Application US/09363526
 ; Patent No. 6410288
 ; GENERAL INFORMATION:
 ; APPLICANT: KNOTZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
 ; STREET: 2001 PERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/363,526
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-201 USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEFAX: (415) 433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-363-526-2

Query Match 22.2%; Score 549; DB 4; Length 457;
 Best Local Similarity 33.3%; Pred. No. 5, 1e-51;
 Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

[illegible]

Db 66 ASTMKULDFEFTGYLLKDYSESVSKDYRLVFEFSKMGJYDKKGHIMFATLCFIAMLFA 125
Qy 125 LSYGYVLYCKSTMAHLCGSLMGMLMGVGHDSCHYQVMPNRKLNRLFOIIAGNVIA 184
Db 126 MSYGYVLFCEGYLVHLSGCLMGFLWIGQWIGHDGHVWVSDSRINKMKGIFAANCIS 185
Qy 185 GVSVAWKKLDHNTTHFACNSANLDPDIOHPLIAISPFKFNLSLTSYHNCMTYDRAARF 244
Db 186 GISIGWKKNNHNAHIAACNSLEYDPLQYIPLVSSKFFGSLTSHYEKRLTFDSLRSF 245
Qy 245 FVSFOHMTFYPALLSVRLYLFIISFKVVSNNKRVYKRSOEIIQYAAFLTWYSILSRP 304
Db 246 FVSFOHMTFYPICARLNNYVOSL-IMLLTKRNVSYRAHELLGCLVFSIWPPLVSCLP 304
Qy 305 NMPERVMTFSCLAIVAGFOHMOFSLNHPASNYVTGLPSGNDWFHOQTKTTLNTASAMWD 364
Db 305 NMGERIMFVIASLSVTGMQOVQFSLNHPSSVYVGRKNNWFEKQTDGTLDISCPMWD 364
Qy 365 WFFGGLHFOIEHLLFPRMPCFKFRKISPIVNLCKQKHLSEYATYTWAEANKMYSTLRAY 424
Db 365 WFFGGLHFOIEHLLFPRMPCFKFRKISPIVNLCKQKHLSEYATYTWAEANKMYSTLRAY 424
Qy 425 AMEAKDVTKPVKNNVMEAMNTFG 448
Db 425 ALQARDITKPLPKNLVWEALHTHG 448

RESULT 2

US-10-029-756-5
Sequence 5, Application US/10029756
Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029, 756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 448 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 59.1%; Score 1459.5; DB 14; Length 448;

Best Local Similarity 55.2%; Pred. No. 4,3e-135;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

Qy 5 KKHISQADLAKKQKQPDMLWISIKGYDYSKMTKEHPGELPLPSAGQDYDAFAIYHP 64
Db 6 KKYITSDELKNDKPDMLWISIQKAYDVSQVWKPCHPGSFLPKSLAGQGVDAFAIYHP 65
Qy 65 GTAWQYLDKDFFTGYVQDYVSESEMSKDYRLVSEFSKMGJYDKKGHIMFATLCFIAMLFA 124
Db 66 ASTMKULDFEFTGYLLKDYSESVSKDYRLVFEFSKMGJYDKKGHIMFATLCFIAMLFA 125
Qy 125 LSYGYVLYCKSTMAHLCGSLMGMLMGVGHDSCHYQVMPNRKLNRLFOIIAGNVIA 184
Db 126 MSYGYVLFCEGYLVHLSGCLMGFLWIGQWIGHDGHVWVSDSRINKMKGIFAANCIS 185
Qy 185 GVSVAWKKLDHNTTHFACNSANLDPDIOHPLIAISPFKFNLSLTSYHNCMTYDRAARF 244
Db 186 GISIGWKKNNHNAHIAACNSLEYDPLQYIPLVSSKFFGSLTSHYEKRLTFDSLRSF 245
Qy 245 FVSFOHMTFYPALLSVRLYLFIISFKVVSNNKRVYKRSOEIIQYAAFLTWYSILSRP 304
Db 246 FVSFOHMTFYPICARLNNYVOSL-IMLLTKRNVSYRAHELLGCLVFSIWPPLVSCLP 304
Qy 305 NMPERVMTFSCLAIVAGFOHMOFSLNHPASNYVTGLPSGNDWFHOQTKTTLNTASAMWD 364
Db 305 NMGERIMFVIASLSVTGMQOVQFSLNHPSSVYVGRKNNWFEKQTDGTLDISCPMWD 364
Qy 365 WFFGGLHFOIEHLLFPRMPCFKFRKISPIVNLCKQKHLSEYATYTWAEANKMYSTLRAY 424
Db 365 WFFGGLHFOIEHLLFPRMPCFKFRKISPIVNLCKQKHLSEYATYTWAEANKMYSTLRAY 424
Qy 425 AMEAKDVTKPVKNNVMEAMNTFG 448
Db 425 ALQARDITKPLPKNLVWEALHTHG 448

RESULT 3

US-10-340-779A-11

Sequence 11, Application US/10340779A

Publication No. US20030152983A1

GENERAL INFORMATION:

APPLICANT: Napier, Johnathan A.

APPLICANT: Michaelson, Louise

APPLICANT: Stobart, Keith

TITLE OF INVENTION: Desaturase

FILE REFERENCE: 005407.00004

CURRENT APPLICATION NUMBER: US/10/340,779A

CURRENT FILING DATE: 2003-03-24

PRIOR APPLICATION NUMBER: US 09/582,034

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: PCT/GB98/03895

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: UK 9814034.6

PRIOR FILING DATE: 1998-06-29

PRIOR APPLICATION NUMBER: UK 9727256.1

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PaetSeq for Windows Version 4.0

SEQ ID NO 11

TYPE: PRT

ORGANISM: Helianthus annuus

US-10-340-779A-11

Query Match 56.3%; Score 1391.5; DB 12; Length 458;
Best Local Similarity 52.7%; Pred. No. 2.2e-128;

Matches 234; Conservative 90; Mismatches 119; Indels 1; Gaps 1;

Qy 5 KKHISQADLAKKQKQPDMLWISIKGYDYSKMTKEHPGELPLPSAGQDYDAFAIYHP 64
Db 16 KKYITSDELKNDKPDMLWISIQKAYDVSQVWKPCHPGSFLPKSLAGQGVDAFAIYHP 75
Qy 65 GTAWQYLDKDFFTGYVQDYVSESEMSKDYRLVSEFSKMGJYDKKGHIMFATLCFIAMLFA 124


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DB 76 GTAMHLDLFTGYHLDKQVDSIDRDYKLSSEFAKAGMFEKKGHVYSLCFYSLLS 135
QY 125 LSVGYLVYCKSTWMAHLCGSLMGMLTLOSQWGHDSCHYQVMPNKLRLFOIIGANYA 184
DB 136 ACVYGLVSGSFWIMHLSGAILGLAMMOQYAVLGHDAIGHYQMMATRGWNFAGIPIGNCT 195
QY 185 GVSVMWKLNDHTTHFACNSANLDDPDLOHLPFAISPKFENSLTYSYHCKMCTYRAAF 244
DB 196 GSIAMWKTNAHNLHACNSLDYDPLQHLFPLAVSSKLFNSITSVFYGRQUTPDLARF 255
QY 245 FVSFOHMTFYPALLSVRLYLFIISFKVVSNNKRVYKSOEILGYAFLTWYSLLSRLP 304
DB 256 FVSYQHYLYYPMICVARVNLVLOTILLISKRR-IPDRGLNITGLIFMTWPEPLVSRP 314
QY 305 NMPERVMYTSCLAVAGFQHMOPSLNHPASNYTGLPSGNDWPHOOTKGTNLITASAMD 364
DB 315 NMPERVAFLVSCVGLIOHIOFTLNHFGSDYVGPCKDNWFEKOTGTIDTIDACSSMD 374
QY 365 WFGHGLHFOIEHNLPRMCKCHFKRISPIVNLCKOHNLSYETATWMEANKVYSLRAV 424
DB 375 WFFGGLOFQLEHNLPRMCKCHFKRISPICRELCKXNLPYSLFYDANVTTLKTLRJA 434
QY 425 AMEAKDVTKVPKMWMEAMNTEG 448
DB 435 ALQARDLTNPAPONLAMEAFNTHG 458

```

RESULT 4

US-10-029-756-27
Sequence 27, Application US/10029756
Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SAMS UR

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-029-756-27

Query Match 53.2%; Score 1314.5; DB 14; Length 452;
Best Local Similarity 51.8%; Pred. No. 8.6e-12;
Matches 233; Conservative 86; Mismatches 126; Indels 5; Gaps 5;

```

QY 3 EPKHSIQADLAKKQPPDLMISIKGYDDISKMTKEHPGGLPLPSAGODVDTAFAY 62
DB 4 BAKYITMEDLRNHNKSDMLISIQKVDYCSMAHEHPGVEPLSLAGODVDTAFAY 63
QY 63 HPGTAMQYLDPEFTG-YVVDYVSSEMSKDYRLVSEFSKMGLEFPTPKGVYCSIFVSV 121
DB 64 HPGTAMRHLDPFTGYLYLKDFEVEISKDYRLNENSRSGIFPKKHHLMTFVGVAV 123
QY 122 LPLSVGYLVYCKSTWMAHLCGSLMGMLTLOSQWGHDSCHYQVMPNKLRLFOIIGAN 181
DB 124 MDAIVYGLVASESGVAMLCGALLGLMTIQAAVYGHDSGHYQVMPNKLRLFOIIGAN 183
QY 182 VIAGSVAMWKLNDHTTHFACNSANLDDPDLOHLPFAVSTRLENISVIFYGRVLKFEV 241
DB 184 ILTGISIAMWKTNAHNLHACNSLDYDPLQHLFPLAVSSKLFNSITSVFYGRVLKFEV 243
QY 242 ARFVSFOHMTFYPALLSVRLYLFIISFKVVSNNKRVYKSOEILGYAFLTWYSLLS 301
DB 244 ARFVSYQHYLYYPMICVARVNLVLOTILLISKRR-RDVPDRALNMGIAVFTWPEPLV 302
QY 302 RLPNPERVMYTSCLAVAGFQHMOPSLNHPASNYTGLPSGNDWPHOOTKGTNLITAS 361
DB 303 CLPNPERGFLVLSFAVYALQHVQFTLNHFGSDTYVGPCKDNWFEKOTGTIDTICP 362
QY 362 WWDWFGHGLHFOIEHNLPRMCKCHFKRISPIVNLCKOHNLSYETATWMEANKVYSL 420
DB 363 WWDWFFGGLOFQLEHNLPRMCKCHFKRISPIREGLRKIAPLARDLCKGHMPSFGWDDANVT 422
QY 421 LRAVAMEAKDV-TKVPKMWV-EAMNTEG 448
DB 423 LRDAVQARDLNSAPCKLGYGEAYNTHG 452

```

RESULT 5

US-09-967-477B-8
Sequence 8, Application US/09967477B
Patent No. US20020156254A1

GENERAL INFORMATION:

APPLICANT: Xiao Qiu
TITLE OF INVENTION: FAD4, FAD5, FAD6, AND FAD6, NOVEL
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: BNZ-001
CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 459
TYPE: PRT
ORGANISM: *Thraustochytrium* sp.

Query Match 22.7%; Score 560.5; DB 10; Length 459;
Best Local Similarity 31.0%; Pred. No. 1.8e-46;
Matches 149; Conservative 70; Mismatches 182; Indels 79; Gaps 17;

```

QY 5 KHAISQADLAKKQPPDLMISIKGYDDISKMTKEHPGGLPLPSAGODVDTAFAY 64
DB 9 KRLVSWKEIREHATPATAMIVIHKKYDISKW-DSHPGSAV-MLTQAGEDATDAFAVFP 66
QY 65 GTAMQYLDPEFTGYVVDYVSSEMSK-----DYRLVSEFS 100
DB 67 SSALKLLEQFYV-----DVTETSALEIGEPASDEERARRRINEFLASVRLAVYK 120

```

QY 101 KMGLEKPGKGVCSIFPVSVLFAISVYGLVC---KSTWALCSGLMLGMLQSGWVG 157
 Db 121 GNGLY--DASALYAMKLVST-FGIAVLMAICFFPNSFAMYMAGVLMGLFYQSGMLA 177
 QY 158 HDSCHYQVMPKRLNRLFOIAGNVAGSVAMKLDHNTHFACNSANT-----DPD 210
 Db 178 HDPFHNOVCENRTLGNLIGCLVGNAMQGSVQVMWKNKLNHVAVNLHSADEGFIQDPD 237
 QY 211 IQHPIAISPFNSLTSYHNCKMTYDRAARFFVSQHTFFPALLSVLYLFIISFK 270
 Db 238 IDTMPLAMSKEMARKAPESAH-----GPFIRNOAFLYPLLLNLMLAOSFF 288
 QY 271 VVFSNNK-----RYKRSQELIYAALFTWYSLLSRLPNMP--ERYVYF---TSC--- 316
 Db 289 YVFTESFGIPDKYEPFGPEKAGLIYHYI--QLAIPYFCNMSLEGVAYFLMGQASGCLL 347
 QY 317 LAVAGFQHWQPSLNHFASNVYTGILPSGNDWFHQCTGLNTTASAMWDFHGLHFOIEH 376
 Db 348 LALV-----FSIGHNGMSVYE--RETKPDEFWOLQVTTNRIRASVFMDFGTGLNYQIDH 400
 QY 377 HLFPRMKCHPRKISPIVNLCKCKNLSYFATWMEANKWYSLRAVAMEAKDVTCPVP 436
 Db 401 HLPFLVPRHLPKXNVLIKSLCKEFPDLPFHTGFWEG--IYEVVDHLADISKEFTTEFP 457

RESULT 6
 US-10-278-391-4
 ; Sequence 4, Application US/10278391
 ; Publication No. US20030159164A1

GENERAL INFORMATION:

APPLICANT: KOPCHIK, JOHN J.

KELDER, BRUCE

HUANG, YUNG-SHENG

KIRCHNER, STEPHEN J.

MUKERJI, PRADIP

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM

PRODUCTS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,391

FILING DATE: 23-Oct-2002

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/087,578

FILING DATE: 29-MAY-1998

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: OHU-03348

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20030159164A1 Relevant

TOPOLOGY: No. US20030159164A1 Relevant

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-278-391-4

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Query Match

Best Local Similarity

Matches 147; Conservative

58; Mismatches 181; Indels 56; Gaps 13;

Score 549; DB 12; Length 457;

Pred. No. 2,4e-45;

Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

Qy 26 IKGVYDISKTKHEHGGELPLISFAGQVDTDAFIAYHPCGTAMQVYDRFETGYVVO---D 82
 Db 36 IDNKYDVAREFVDPDHGGSV-ILTHVGKGTDTVDFHBEAAMELTIANFYVDIDESDD 94

Qy 83 YSVSEMSKDYRLVSEFSGMLFKTPGKGVCSIFVSVLFALSVYG---VLXCK---S 135
 Db 95 IKNDPFAAEVRKRLTFLQSLGYDS- SKAYYA---FKVSFNLCTIGSLSTVIAAKMGOTS 149

Qy 136 TPAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIAGNVIAGVAVAMKLDH 195
 Db 150 TLANYLSAALLGLFMQCCGMLAHDFLHQVFDREMGDLFGAFLGVCVCGFSSSWMKDGH 209

Qy 196 NTHHACNSANDPDIQHLPIAISPFPNSLSTYHNCCKMTYD-----RAARFVS 247
 Db 210 NTHHAAPVHGEPDIDTHPL-----LTWSEHLEMFSDVPDEBLTMMWSFVVL 259

Qy 248 FOHMTFYPALLSVRLYLFLISFKVFSNNK-----RYKKRSOELLGYAAFLTWYSLTL 300
 Db 260 NOTWTFYFPLSFARLSWCLQSLFLVLPNGQAHKPSGARVPISLVQSLAMHMTWYLATM 319

Qy 301 SRLPMP-ERVVYFISCLAVAG-FOHWPQSLNHFASNVYGLP-----SGNDWFHOQT 351
 Db 320 FLFIKDPVNMVLYFLVQAVCGNLLAIVPSLNH-----NGMPVSKERAVMDPFTKQI 373

Qy 352 KGTLNITASAMWDFHGLHFOIEHLLFPRMPKCHPRKISPIVNLCOCHNLSEYATM 411
 Db 374 ITGRDVHGLFANWFTGGLNYQIEHLLFPSMPRHNSKIQPAVELTCKKYVRYHTTGM 433

Qy 412 EANKVYSTLRVAMEADVTK 433
 Db 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 8
 US-10-191-513A-41
 ; Sequence 41, Application US/10191513A
 ; Publication No. US20030104596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradiip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.US.D3
 ; CURRENT APPLICATION NUMBER: US/10/191,513A
 ; PRIOR FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 41
 ; LENGTH: 458
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (458)...(458)
 ; OTHER INFORMATION: Xaa = Unknown or other at position 458
 US-10-191-513A-41

Query Match 22.2%; Score 549; DB 15; Length 458;
 Best Local Similarity 33.3%; Pred. No. 2.4e-45;
 Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

Qy 26 IKGVYDISKTKHEHGGELPLISFAGQVDTDAFIAYHPCGTAMQVYDRFETGYVVO---D 82
 Db 36 IDNKYDVAREFVDPDHGGSV-ILTHVGKGTDTVDFHBEAAMELTIANFYVDIDESDD 94

Db 36 IDNKYDVAREFVDPDHGGSV-ILTHVGKGTDTVDFHBEAAMELTIANFYVDIDESDD 94

Qy 83 YSVSEMSKDYRLVSEFSGMLFKTPGKGVCSIFVSVLFALSVYG---VLXCK---S 135
 Db 95 IKNDPFAAEVRKRLTFLQSLGYDS- SKAYYA---FKVSFNLCTIGSLSTVIAAKMGOTS 149

Qy 136 TPAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIAGNVIAGVAVAMKLDH 195
 Db 150 TLANYLSAALLGLFMQCCGMLAHDFLHQVFDREMGDLFGAFLGVCVCGFSSSWMKDGH 209

Qy 196 NTHHACNSANDPDIQHLPIAISPFPNSLSTYHNCCKMTYD-----RAARFVS 247
 Db 210 NTHHAAPVHGEPDIDTHPL-----LTWSEHLEMFSDVPDEBLTMMWSFVVL 259

Qy 248 FOHMTFYPALLSVRLYLFLISFKVFSNNK-----RYKKRSOELLGYAAFLTWYSLTL 300
 Db 260 NOTWTFYFPLSFARLSWCLQSLFLVLPNGQAHKPSGARVPISLVQSLAMHMTWYLATM 319

Qy 301 SRLPMP-ERVVYFISCLAVAG-FOHWPQSLNHFASNVYGLP-----SGNDWFHOQT 351
 Db 320 FLFIKDPVNMVLYFLVQAVCGNLLAIVPSLNH-----NGMPVSKERAVMDPFTKQI 373

Qy 352 KGTLNITASAMWDFHGLHFOIEHLLFPRMPKCHPRKISPIVNLCOCHNLSEYATM 411
 Db 374 ITGRDVHGLFANWFTGGLNYQIEHLLFPSMPRHNSKIQPAVELTCKKYVRYHTTGM 433

Qy 412 EANKVYSTLRVAMEADVTK 433
 Db 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 9
 US-09-769-863-14
 ; Sequence 14, Application US/09769863
 ; Publication No. US20030157144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradiip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763.US.O1
 ; CURRENT APPLICATION NUMBER: US/09/769,863
 ; CURRENT FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRN
 ; ORGANISM: Saprolegnia diclina
 US-09-769-863-14

Query Match 21.0%; Score 519; DB 12; Length 453;
 Best Local Similarity 30.2%; Pred. No. 2.1e-42;
 Matches 132; Conservative 78; Mismatches 165; Indels 62; Gaps 13;

Qy 8 ISQADLAKHQPGLMISIKGVYDISKTKHEHGGELPLISFAGQVDTDAFIAYHPCGT 67
 Db 10 ISMATIREHNRQDNAMVIYHKKVYDISAF-EDHPGG-VVMFTQAGBDATDAFAVHPSSA 67

Qy 68 WOYLDREFFTGYVVO-----DYSVSEMSK-----DYRLVSEFSGMLFKTPGKGVY- 113
 Db 68 LKLEQYVGVGDVOSTAVIDTISDEVKKSODFIASRYKRLLEVRLGLYDS-SKLYL 126

Qy 114 --CSIFPVSVPALSVYGLVCKSTMAHLCGLMGMLVQSGVGHDSCHYQVMPNRKL 171
 Db 127 YKCASTLIALVSAI--CLHFDSTAMTMAVAIVILGLYQCCGMLAHDFLHQVFNHLF 184

Qy 172 NRLFQIAGNVIAGVAVAMKLDHNTTHFACN-----SANDPDIQHLPIAISPFP 224
 Db 185 GDLVGVMGNLQGSVQVMWKKKNTHTHALPVLHATPELAHPGDDIDTMTPLANSKKA 244

```

QY 225 NSLTSTYHNCKMTYDBAARFVSFOHWTYPALLSVRLYLFIISFKVFN--NKRUYK 281
DB 245 QHADV-----SPVGLFPMRYQAVLYPILFARISVVISASAMAFNVNPGGFEDK 295
QY 282 RSOEILGYAFLTWYSLLSRLPNWPERVNY-----FTSCLAVAGPQHMOPS 328
DB 296 VOYPLERAGLLLY-----GMNLGLVYAANMSLLQAAFLFVSQASCGFLAMVFS 347
QY 329 LNHFAENVYTGSLPSGNDWFHQOTKGLTINTASAMWDMFHGGLHFOIENHLFPRMPKCHFR 388
DB 348 VGNHNGEVEF-DKDSKDPFWKLQVLSLRTNVTSSLMIDFMWGLNYQIDHHLFPMVPRHNL 406
QY 389 KISPIVVKLCQKHNLSY 405
DB 407 ALNVLVKSJCKOYDIPY 423

RESULT 10
US-10-054-534B-14
; Sequence 14, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763-US-P1
; CURRENT APPLICATION NUMBER: US/10/054,534B
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PR
; ORGANISM: Saprolegnia diclina
US-10-054-534B-14

Query Match 21.0%; Score 519; DB 12; Length 453;
Best Local Similarity 30.2%; Pred. No. 2,1e-42;
Matches 132; Conservative 78; Mismatches 165; Indels 62; Gaps 13;

QY 8 ISQADIAKHQOPDMLWISIKGVYDISKWTKEHPGGLPLSPAGODVTDATAYHPTA 67
DB 10 ISWATIREHNRQDNAMIVIHKKYDISAF-EDHPGG-VVMFTQAGEDATDAFAVHPHSSA 67
QY 68 WQYLDKRFPTGYVQ-----DYVSEMSK-----DYRLVSEPSKMLFKTPGKGV- 113
DB 68 LKLEQYVGDVDQSTAAVDTISIDEVKKSQSDFIASRYKRLLEVYKRLGLYDS-SKLYYL 126
QY 114 --CSIFVSVLFAISYGVLYCKSTWHLCSGLMGLMLQSGVGHGDSCHYOVMPNRKL 171
DB 127 YKCASTLSTALVSAI--CLHFDSTAMVVAAYIIGLFYQCGGLAHDLPHHOVENHLF 184
QY 172 NRLFQIIAGNVIAGVSAWMLKLDHNTHPACN-----SANDPDIQHLPIIASPKFF 224
DB 185 GDLVGVVGNLWQGFVSQWKKKKNHTHAIPLHATPEIAFHDGDPDIDTPIAMSLKMA 244
QY 225 NSLTSTYHNCKMTYDBAARFVSFOHWTYPALLSVRLYLFIISFKVFN--NKRUYK 281
DB 245 QHADV-----SPVGLFPMRYQAVLYPILFARISVVISASAMAFNVNPGGFEDK 295
QY 282 RSOEILGYAFLTWYSLLSRLPNWPERVNY-----FTSCLAVAGPQHMOPS 328
DB 296 VOYPLERAGLLLY-----GMNLGLVYAANMSLLQAAFLFVSQASCGFLAMVFS 347
QY 329 LNHFAENVYTGSLPSGNDWFHQOTKGLTINTASAMWDMFHGGLHFOIENHLFPRMPKCHFR 388

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DB 348 VGNHNGEVEF-DKDSKDPFWKLQVLSLRTNVTSSLMIDFMWGLNYQIDHHLFPMVPRHNL 406
QY 389 KISPIVVKLCQKHNLSY 405
DB 407 ALNVLVKSJCKOYDIPY 423

RESULT 11
US-10-431-952-14
; Sequence 14, Application US/10431952
; Publication No. US20030190733A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763-US-O1
; CURRENT APPLICATION NUMBER: US/10/431,952
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/769,863
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PR
; ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match 21.0%; Score 519; DB 12; Length 453;
Best Local Similarity 30.2%; Pred. No. 2,1e-42;
Matches 132; Conservative 78; Mismatches 165; Indels 62; Gaps 13;

QY 8 ISQADIAKHQOPDMLWISIKGVYDISKWTKEHPGGLPLSPAGODVTDATAYHPTA 67
DB 10 ISWATIREHNRQDNAMIVIHKKYDISAF-EDHPGG-VVMFTQAGEDATDAFAVHPHSSA 67
QY 68 WQYLDKRFPTGYVQ-----DYVSEMSK-----DYRLVSEPSKMLFKTPGKGV- 113
DB 68 LKLEQYVGDVDQSTAAVDTISIDEVKKSQSDFIASRYKRLLEVYKRLGLYDS-SKLYYL 126
QY 114 --CSIFVSVLFAISYGVLYCKSTWHLCSGLMGLMLQSGVGHGDSCHYOVMPNRKL 171
DB 127 YKCASTLSTALVSAI--CLHFDSTAMVVAAYIIGLFYQCGGLAHDLPHHOVENHLF 184
QY 172 NRLFQIIAGNVIAGVSAWMLKLDHNTHPACN-----SANDPDIQHLPIIASPKFF 224
DB 185 GDLVGVVGNLWQGFVSQWKKKKNHTHAIPLHATPEIAFHDGDPDIDTPIAMSLKMA 244
QY 225 NSLTSTYHNCKMTYDBAARFVSFOHWTYPALLSVRLYLFIISFKVFN--NKRUYK 281
DB 245 QHADV-----SPVGLFPMRYQAVLYPILFARISVVISASAMAFNVNPGGFEDK 295
QY 282 RSOEILGYAFLTWYSLLSRLPNWPERVNY-----FTSCLAVAGPQHMOPS 328
DB 296 VOYPLERAGLLLY-----GMNLGLVYAANMSLLQAAFLFVSQASCGFLAMVFS 347
QY 329 LNHFAENVYTGSLPSGNDWFHQOTKGLTINTASAMWDMFHGGLHFOIENHLFPRMPKCHFR 388
DB 348 VGNHNGEVEF-DKDSKDPFWKLQVLSLRTNVTSSLMIDFMWGLNYQIDHHLFPMVPRHNL 406
QY 389 KISPIVVKLCQKHNLSY 405
DB 407 ALNVLVKSJCKOYDIPY 423

RESULT 12
US-10-369-493-4137
; Sequence 4137, Application US/10369493
; Publication No. US2003023675A1

```

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; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4137
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4137

Query Match      19.3%; Score 477; DB 12; Length 366;
Best Local Similarity 31.6%; Pred. No. 2,2e-38;
Matches 113; Conservative 63; Mismatches 156; Indels 26; Gaps 9;

QY 90 KDRRLVSEFSKMGLEKTPGKGVYCSIFFVSVLFALSVGLYC-----KSTMAHLSG 143
DB 5 RYKRELNERIKAEGLVD-----CN--YVAVAIEGFRITLFCGLLPLKMGV-YVPSA 54

QY 144 LLMGLMLQSGVGHDSCHYQVMPNRLKRLFOIAGNVIAGVAVAMKLDHNTTHFACN 203
DB 55 FCLGSFMHQLVFAYADAGHMGITHHFHVDTVIGIILADFGISLGMWKNHNVHIIITN 114

QY 204 SANLDDIQLHPLIAISPKRFNSLTSYHNCKTTPRAARFFSPQHWTFYPLLSVRLY 263
DB 115 SPEDHDIHLPLFAISHPFTMLRSTYYDRVMEYDIFAKFFVSLQHYLYIIMFARLN 174

QY 264 LFLISEKVF-----SNKRKYVSQELGYAFLTW--YSLLSRLP--NMPEPVYFTS 315
DB 175 LVRLSWEYLLKGAPRGHGRAMWHRHLELVQVFWFCMGYIMYKALDGNM-NRPFFPMI 233

QY 316 CLAVAGFQHWQFSLNFPASNVTYGLPSGNDWFHQQTGLNTITASAMWDFHGLHFOIE 375
DB 234 SHAVTSPRLHVQITLSHFAMST--SDLGPHSEFPQRMRLRTTMDVDCPEMLDPFHGLQFOAI 292

QY 376 HHLFPMPCHPKIKIPYVVKLCQKKNLSYETATMEANKMYSTIRAAVAMEKDYTK 433
DB 293 HHLYPRIPRHNLKTKLVQDFCNDVGIPYALYGVFEGNKHVIGRLADVARQALIRK 350

RESULT 13
US-10-340-779A-20
; Sequence 20, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Jonathan A.
; APPLICANT: Michelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407,00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 443

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; TYPE: PRT
; ORGANISM: C. elegans
US-10-340-779A-20

Query Match      18.7%; Score 461; DB 12; Length 443;
Best Local Similarity 29.5%; Pred. No. 1.1e-36;
Matches 116; Conservative 65; Mismatches 188; Indels 72; Gaps 17;

QY 17 KQPGDLMSIKGR-VYDISKTKRHPGGLPLSPAGOVNTAFIAYHGTAMQY----- 70
DB 5 KASGLRMKVDGKMWLYLSEELVYKHPGANV-IEQYKNSDATIIFHAHFEGSSOAYKQLDL 63

QY 71 -----LDREFTGYVYDVSVSEMSKDRRLVSEFSK-----GLF 105
DB 64 LKKHGEHDEFLKQLEKRLDKVDIVNSAVDVAQEK-----MVSEFELRQKLHDDGLM 119

QY 106 KTPGKGVYCSIFVSVLFPALSVYG-VLYCKSTMAHLSGGLMGLMLQSGVGHDSCHYQ 164
DB 120 KANE-----TYFLFPAISTLSIMAFYLYQVIGWYTSACLIALAMQCFGMLTHERCHQO 174

QY 165 VMPNKLRLFOIAGNVIAGVAVAMKLDHNTTHFACNSANLDDIQLHPLIAISPKRF 224
DB 175 PKNRPLNDTISLFGNPLQGSRDWWKDKHNTTHAATNVIDHDGIDILAPLFAFIP--- 231

QY 225 NSLTSYHNCKMTYDRAARFFVSPQHWTFYPALLSVRLYFLISPKVFSNNKRVYKRSQ 284
DB 232 GDLCKY-----KSPFKALIKVYPQHLVFTALPMLRFSWTOGSQVQWVKEKNOMEKYKYO 287

QY 285 E-----ILGYAFLTWYSLLSRLPMPERVMYFTSCLAVAG--FQHWQFSLNHPAS 334
DB 286 RAUFMEQATIVGHMAWV-FYQFL--LPTWPRVAFAFISQGGGLLIH-VYTFHNSV 343

QY 335 NYITGLPSG---NDWFHQQTGLNTITASAMWDFHGLHFOIEHLFPRPKCHKFKRI 390
DB 344 DRY---PANSRLINFPALQILITRNMTSPSPIDMLGGLNYQIEHILFPTMPCNLNAC 400

QY 391 SPIVVKLCQKKNLSYETATMEANKMYSTIRAAV--MEAK 429
DB 401 VYVKECKENLPLVLDYFDGYAMNLQQLKQMAEHIOAK 441

RESULT 14
US-10-262-617-3
; Sequence 3, Application US/10262617
; Publication No. US20030077747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guejter, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/048,888
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030077747A1 2056310CD1
US-10-262-617-3

Query Match      18.3%; Score 451.5; DB 15; Length 444;
Best Local Similarity 27.0%; Pred. No. 9.4e-36;
Matches 121; Conservative 69; Mismatches 193; Indels 65; Gaps 12;

QY 6 KHISQADLAKKHQPGDLWMSIKGYVDISKTKRHPGGLPLSPAGOVNTAFIAYH-- 63

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Db      18 RYFTWDEVAGSGCEERMLVIDRKVNISETTRRHPGSGRVISHYAGQDATDEPVAEHIN 77
Qy      64 PGTAWOYLRBFRTGY-----VQDYSVSEMSKDYRLVSEFQKGLFRTPKGVCSIF 117
Db      78 KGLVKKTKMSLLIGELSPQPSFEPTKKNKELTDFEFLRATVERKGLMK--ANHVFELLY 135
Qy      118 FVSVL-----PALSVYGVLYCKSTWHLCSGLLMGLMLOSQWVGHSCHYQVMPNRK 170
Db      136 LHLIILLDGAAMLTLWVFGT-----SFLPFLLCVLLSAVOAGQWGLDHDGHSVSTSK 191
Qy      171 LNLFLQIAGNVAGSVAMWKLDHNTHPACNSANIDPDIQHLPIAISPKEFNSITSY 230
Db      192 WNLHLHFVIGHKGA PASWMMNHMFQHNKPCFRKDPDINNHPESFALGXILSVELGK 251
Qy      231 YHNCMTYDAARFPVSFOHMTFY-----PALLSVRLYLFLLSPKVSNNK----- 277
Db      252 QKKKYPYHN-----QHKYFFLIGRPALPLPYFQWYFYF--VYQKKWVDLMMIT 301
Qy      278 ---RVYKRSQELIGYAAFLTWSLLSRLPNWPBRVWYFTSCLAVAGFOHMOFSLNHFAS 334
Db      302 FYVRPFLTYVPLGLKAFGLFLFIVRLESNW-----FV-----WYQMMHIMP 345
Qy      335 NVTTGLPBGNDMFHQOTKGLNTITASAMDWPHGGLHFOIEHILFPRMPKCHFRKISPIV 394
Db      346 HI--DHDNRNDWYSTOLOATCNVHKSAFNDWFSGLHNFQIEHILFPTMPRHNYHKVAPLV 403
Qy      395 NKLCOKNLSYETATWMEANKWYSTLR 422
Db      404 QSLCAKHGLEYQSKPLSLAFADIIHSLK 431

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RESULT 15

```

US-10-369-493-6108
; Sequence 6108, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIORITY FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6108
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6108

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```

Query Match      18.2% Score 449; DB 12; Length 473;
Best Local Similarity 28.2%; Pred. No. 1.8e-35;
Matches 138; Conservative 65; Mismatches 187; Indels 100; Gaps 18;

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```

Qy      17 KQPGDLWISIKG-VYDISKTKHEHPPG-----ELPLLS----- 49
Db      5 KNSAGLRMKVDGKMLYSELVKKHPCGAVIEQYSIPLNKIETRGIIITRGSNNLMDI 64
Qy      50 ---FAGQDVTDAFLAHPTAMQY----- 83
Db      65 LVEFYRNSDATHIFHAFHEGSSQAYKQDLCLKHGEHDEPLEKOLEKRLDKVDINVSAYDV 124
Qy      84 SVSEMSKDYRLVSEFQKGLFRTPKGVCSIFPVSVLPALSVYG-VLYCKS 135
Db      125 SVAQERK---WVSEFEKLRQKLDHGDGLMKANE---TYFLPKAISTLSIMAFAYLYQ 175
Qy      136 TWAHLCSGLLMGLMLOSQWVGHSCHYQVMPNRKLNRLFOIAGNVAGSVAMWKLDH 195

```

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Db      176 LGWYITSACLALLAWOQFGMLTHEFCHQOPTKRNPLNDTISLFFGNFLOGFSRDMWKDKH 235
Qy      196 NTHHPACNSANIDPDIQHLPIAISPKEFNSLTSYYHNCMTYDRAARFPVSFOHMTFYF 255
Db      236 NTHHAATNVYIDHDGDDIDLAPLFAFIP--GDLCY---KASFEKAILKIVYQHLFTA 288
Qy      256 ALLSVRLYFLISFKVYFSSNNKRVYKRSQ-----ILGYAFLTWYSLLSRLPNMP 307
Db      289 MLPMLRFSMTGQSVQVVFKNQMEYKVYQRNAFWEGATVGHAWV-FYQLFL--LPTWP 345
Qy      308 ERYMTTSCLAVAG--FOHMOFSLNHPASNVTTGLPBG---NDWFHQOTKGLNTITASA 361
Db      346 LRYAAYFIISQMGGLIAH-VTFNNNSVDKY---PANSRIIINFAALOILTTNNMTPSP 401
Qy      362 WMDWPHGGLHFOIEHILFPRMPKCHFRKISPIYVKLCQKNLSYETATWMEANKWYSTLR 421
Db      402 FIDWLMGLNLYQIEHILFPTMPRCNLNACMKYKXCKENNLPLYLVDDYFDGAYMNLQOL 461
Qy      422 RAVA--MEAK 429
Db      462 KNNAAEHIOAK 471

```

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Search completed: January 1, 2004, 06:58:34
Job time: 86.3457 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:39:42 ; Search time 4426.43 Seconds
(without alignments)
16303.117 Million cell updates/sec

Title: US-09-857-524B-3
Perfect score: 1764
Sequence: 1 gcacagctccctcctcctc.....ttaaaaaaaaaaaaaa 1764

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pl:*
9: gb_pl:*
10: gb_pl:*
11: gb_pl:*
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41: gb_pl:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1074.8	60.9	1788	8 AF031194	AF031194 Triticum
2	1000.6	56.7	96312	2 AP005554	AP005554 Oryza sat
3	536.2	30.4	1681	8 AY234124	AY234124 Primula l
4	535.6	30.4	1385	8 AY234126	AY234126 Primula v
5	491.2	27.8	1702	6 AR200409	AR200409 Sequence
6	470	26.6	1410	8 AY234125	AY234125 Primula f
7	453.8	25.7	110149	8 AC005397	AC005397 Arabidops
8	445	25.2	1491	8 BT003379	BT003379 Arabidops
9	445	25.2	1678	6 AX007241	AX007241 Sequence
10	445	25.2	1704	8 AF428420	AF428420 Arabidops
11	445	25.2	1705	8 ATJ4161	ATJ4161 Arabidops
12	445	25.2	1743	8 BT000442	BT000442 Arabidops
13	445	25.2	95993	8 ATP2A19	ATP2A19 Arabidops
14	441.8	25.0	1652	8 AY087345	AY087345 Arabidops
15	439.2	24.9	1350	6 AX505863	AX505863 Sequence
16	437	24.8	1594	6 AX007239	AX007239 Sequence
17	437	24.8	1610	8 BNAJ4160	BNAJ4160 Brassica
18	417.4	23.7	1856	8 AF005096	AF005096 Ricinus c
19	404.4	22.9	1533	8 AF001394	AF001394 Arabidops
20	391	22.2	1478	8 AY055117	AY055117 Echium ge
21	384.2	21.8	1450	8 AY055118	AY055118 Helianthus
22	370.2	21.0	1591	8 HACTB5RN	HACTB5RN Sequence
23	370.2	21.0	1606	6 AX007273	AX007273 Sequence
24	367	20.8	1687	8 B0U79010	B0U79010 Borago offi
25	365.4	20.7	1684	6 AR076814	AR076814 Sequence
26	365.4	20.7	1684	6 AR084177	AR084177 Sequence
27	365.4	20.7	1684	6 BD062571	BD062571 A sunflow
28	365.4	20.7	1684	6 BD070919	BD070919 An oleost
29	365.4	20.7	1685	6 AR020904	AR020904 Sequence
30	365.4	20.7	1685	6 AR200408	AR200408 Sequence
31	365.4	20.7	1685	6 I38430	I38430 Sequence 4
32	365.4	20.7	1685	6 AF007561	AF007561 Borago of
33	359.6	20.4	1347	8 AY131238	AY131238 Argania s
34	354.4	20.1	1341	8 AF406816	AF406816 Aquilegia
35	352.2	20.0	1618	8 AY234127	AY234127 Primula v
36	325.8	18.5	1869	8 AF133728	AF133728 Borago of
37	275.6	15.6	291	6 AR246607	AR246607 Sequence
38	219.4	12.4	535	6 AX058838	AX058838 Sequence
39	215.8	12.2	266	6 AR247897	AR247897 Sequence
40	165.4	9.4	1572	8 AB090360	AB090360 Nucor cit
41	165.4	9.4	1572	8 AF290983	AF290983 Nucor cit
42	165.4	9.4	1572	8 AF296076	AF296076 Nucor cit
43	132.2	7.5	322194	8 CNG0954S	CNG0954S DNA cent
44	120.6	6.8	300550	1 AP005030	AP005030 Streptomy
45	120	6.8	1926	6 AR217867	AR217867 Sequence

ALIGNMENTS

RESULT 1
AF031194
LOCUS AF031194 1788 bp mRNA linear PLN 29-JAN-1999
DEFINITION Triticum aestivum S276 (S276) mRNA, complete cde.
ACCESSION AF031194
VERSION AF031194.1 GI:4104055
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 1788)
Delhaize, E., Hebd, D.M., Gardner, R.C. and Richards, K.D.
Aluminum tolerance in yeast conferred by over-expression of wheat

Pred. No. is the number of results predicted by chance to have a

genes unpublished
JOURNAL 2 (bases 1 to 1788)
REFERENCE Delhaize, E., Hebb, D. M., Gardner, R. C. and Richards, K. D.
AUTHORS Direct Submission
TITLE Submitted (23-OCT-1997) Plant Industry, CSIRO, Canberra, ACT 2601,
JOURNAL Australia

FEATURES	Location/Qualifiers
source	1. .1788

gene	1. .1788
	/gene="S276"
CDS	121. .1530

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/gene="S276"  
/note="similar to Borago officinalis delta 6 desaturase,  
from GenBank Accession Number U79010"
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/codon_start=1
/product="S276"
/protein_id="AADI0250.1"
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[illegible]

BASE COUNT	321 a	588 c	450 g	429 t
ORIGIN				

Query Match	60.9%	Score 1074.8;	DB 8;	Length 1788;
Best Local Similarity	79.0%	Pred. No. 7.6e-145;		
Matches 1335; Conservative	0;	Mismatches 337;	Indels 18;	Gaps 4;

Qy	27	CCTCCCGCCCTCCCCCTACCAATTCAGCACCAACCCAAAGGCATTCAGACCAAGCCGCG	86
Db	86	CCCCTCCTCGCGCTTCAGCTAAATTCACGCGCACCGATGGCCCGACGGGGCTCGCGAG	145
Qy	87	CAATGCCGCCCTCTGTGCATGCATTCGCCGGGCCCCGGGAGAGCCGCGGCCCGGCACG	146
Db	146	CAAGCGCGCCGAAAGCCGACGCAATGCGGCGCGCAGAA-----GGACCGCCGACG	199
Qy	147	TGCGCATGATTCCTCCCAAGAGCTCCGCGCTCAAGCTTCCGCGCAGACCTTGATCT	206
Db	200	TCCGCATGATTCACACAAAGAGCTGACAGCGCACGCCGCGCGAGACGACCTTGATCT	259
Qy	207	CCATCTCCGCGCAGCGTGTACGACGTCAAGCCCTGGCTCCCCACCAACC CGAGCGCAGC	266
Db	260	CCATCTCCGCGGAGCGTCTACACGTCAGCGCCCTGGCTCCGCGCACCCCGGCGCGAG	319
Qy	267	TCCGCGTTCTCACCCTGGCGGGGACGAGCGCACCGAGCGCCTTGGCGGCTTACCAACCGAC	326
Db	320	TCCGCGTTCATACCTCTCGCCGCGCAGAGCGCACCGAGCCTTCAAGGCTTACACACCGC	379
Qy	327	CCTCGGCGGCGCGCTCTCTCGCGGCTTTCGTTGGCGGCTCTCTGACTACGCCGCT	386
Db	380	CCTCGGTCGCGCGCTCTCTCGCGGCTTTCGTTGGCGGCTCTCTGACTACGACTGTC	439
Qy	387	CCCCCGGCTCCGCGGACATACCGCGGCTCTTCGCGGACATCTCTCGCGGGGCTCTTCG	446
Db	440	CCCCCGCTCTCGCGGACTTTCGCGGCTCTTCGCGGACATCTCTCTCTCGCGGCTCTTCG	499
Qy	447	AACCGTCGCGCCACCCCAAGGTCAGCTCGTCTATGAGCGCTCTCTTATCAGCGG	506
Db	500	AGCGGTCGCGCACACCCCAAGTTCGTCGTCGTGCAATGTCGTCCTTCGCAATG	559
Qy	507	CGCTGTACTGTCTCGCATGCGCAGCGCTTGGGCGACCTCTCGCGGGGGTCTCA	566

Db	560	CCCTCTACGTGGGTCTCGCTGCTCCAGCAACCGGGGGCCCAACATGTGTGCGCGGCGGCTCA	619
Qy	567	TTGGCTTCTGTGTGGATTCAGTCTCGGCTGTGATTTGGGCTCACAGACTGGGGCTCACCGCATCA	626
Db	620	TTGGCTTCTATCTTGATCCAGTCCGGGCTGTGATTTGGCCATGTACTCCGGCCACCACTCAATTTCA	679
Qy	627	CCGGCCATTCGGGTCCTTCGACCGCGCGTCTGCAAGGTCCTCCGGGAACTGCTCACCGGCC	686
Db	680	CCAGGCACTCTGCGCTTCAACCGGCTCTTCGACGGTGTCTCCGGGAATCTGCTTCACTCCGGCC	739
Qy	687	TCAGCATTCGCTGTGTGAAAGTGAACCAACAACGACACACATGTGCTTCGAACAGCCTTG	746
Db	740	TGGCATTCGCTGTGTGAAAGTGAACCAACAACAACAACATCTCTTCGAACAGCCTTCG	799
Qy	747	ACCATGACCCGGACCTTCAGACACATGCGCTCTTTGCGCTCTCCCAAGCTGTTCGACA	806
Db	800	ACCATGACCCCTGACCTTCAGACATTTGCGCTCTTCGCGGTTTCCACCAACTCTTTCAACA	859
Qy	807	ACATATGTCCTTACTTTTACCAAGAACCCGCGGCTTCGATGCGCCGCTCGMAATTTCTCA	866
Db	860	ACCTTTGGTACGTCTGCTACAGCGCACCTTGGCGTTTGATGCCATATTCAGATTCTTTCG	919
Qy	867	TCAGCTACAGACATGAGACCTTCTACCCCGGTAATGTGCATCGCCAGATTAATCTTCTCG	926
Db	920	TCAGCTACAGACATGAGACATTTTACCGCGGATGGGATTTTGCAAGGATTAATCTTCTTG	979
Qy	927	CGCAGTCGCCCTGTGTGTTCTCAGGGAAAGAGGGTCCGCGACGCGGTGTGTTGATTCG	986
Db	980	TGCAGTCATGTGTTCCTGTATCAACAAGAAAGAGTGCGGCAGCGTGTGCTGAGATTCG	1039
Qy	987	CGGGGGTCCGCAATTCGGGCTGTGTATCCGTTGCTGTGGGCTTCCCTCGCGAATTGGT	1046
Db	1040	CGGGTGTGCTGCGCTTCGGGTTTGTGAACCTTGTGTGTCTTGCTCGCCGAATTGGT	1099
Qy	1047	GGAGAGGGTTCGCTTTTGTGCTTTTACGCTTCAACATCTCGGGATTCAGACGCTCCAAAT	1106
Db	1100	GGAGAGGGTTCGCTTTTGTGCTTTTCAAGCTTGTGTGATCAGGGGATTCAGATGTGCAAT	1159
Qy	1107	TCTGCTTGAAACCACTTCTCGCGAGTATGTCCGGACCCCAAGGGCAATGACTGGT	1166
Db	1160	TCTGCTTGAAACCACTTCTCAACCGTTATATGTTGGGCCACCAAGGGGAAACAATGCTGT	1219
Qy	1167	TTTGAAAGACAAGGCAAGGCAAGCTGCACATCCTGTGCTCTCTTGATATGATTTGGTTCC	1226
Db	1220	TTTGAAAGCAAAACGCGACGACACTTATATCAAGTCTCCCGTGAATGATTTGGTTCC	1279
Qy	1227	ACGGTGGCTGCTGACCTTCCAGATTGAGACCACTGTTCGCCGCTCACTCGGTCGCACC	1286
Db	1280	ATGTGTGCTGCAATTCAGGTTTAACCACTTTGTTTCTCTGCGCTGCTGCGTCACT	1339
Qy	1287	TTTCGCAAGTTGACCGGCGCTCCGCACTTTTGCAAGAAAGATGGCTCATTTATCTG	1346
Db	1340	ATTAGATGTGTGACCAATTGTGTGTGACTTTTGCAAGAAAGACGGGCTGCTTATGTTG	1399
Qy	1347	CAGCCCACTTTGSGGGTGTCAAAATGTGCTTACATGTGAAGAACACTCAAGGCTGTGCAATTGC	1406
Db	1400	CTGCACTTCTGTGGAAGCAATATTAATGACATGTGAAGACGCTACGGGCTGCACATTTGC	1459
Qy	1407	AGGCAAGACCGCTACACAAGTGTGTGCTCCGAAGATTTTGTAATGTGGAAGGCTGTGAACA	1466
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Qy	1467	CCCATGTGATTAAT-GGGATGAAGATACGGGCTAATGGCAATTTCTGTGTTCAGACTTGT	1525
Db	1520	CTCATGTGATGACTGGGGATTCAGGACTGGAAGATAGACAAATTCGTACGTCAGACCTTGC	1579
Qy	1526	GCCCATGTGATGTGTGTGATGCTCTTTCAGTTATTTAAGATATTGATCATTTCAACTTGC	1585
Db	1580	GTGATGACGATTAATCTGATGTGCTTCTCGATTTGCTGAAGATATTAATTCCTTTTGTGCTGT	1639
Qy	1586	TGAGTCAAGGTTGAATTTGTGTTTGAACAAGTGTGCTGTATCCAGT-----TGGAGGTT	1641
Db	1640	GGAATCGTGTGTGAATTTTGTGTGTGCGAGGTGCAATCTTTGCAAGTTCAATTTGTGATTT	1699

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OY 1695 AACTAATGA 1704
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Df 1760 AACACATCA 1769

RESULT 2
AP005554
LOCUS

DEFINITION
Oryza sativa [japonica cultivar-group] chromosome 9 clone OJ118 A10, *** SEQUENCING IN PROGRESS **.

ACCESSION
AP005554
VERSION
AP005554.1 GI:21952922
KEYWORDS
HTG; HTGS PHASE2.
SOURCE
Oryza sativa [japonica cultivar-group]
Oryza sativa [japonica cultivar-group]
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
Eleutheroides; Oryzaceae; Oryzae.

REFERENCE
AUTHORS
TITLE
Saasaki,T., Matsumoto,T., Hattori,M., Sakaki,Y. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC clone:OJ118 A10
Published Only in Database (2002)
2 (bases 1 to 96312)

JOURNAL
REFERENCE
AUTHORS
TITLE
Saasaki,T., Matsumoto,T., Hattori,M., Sakaki,Y. and Katayose,Y.
Direct Submission
Submitted (23-JUL-2002) Takuji Saasaki, National Institute of Agricultural Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tanikuba, Ibaraki 305-8602, Japan
(E-mail:sasaakienias.affrc.go.jp, URL:http://rsg.dna.affrc.go.jp/, Tel:81-258-38-7441, Fax:81-258-38-7468)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers

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BASE COUNT
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ORIGIN

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Matches 1307; Conservative 0; Mismatches 349; Indels 37; Gaps 6;

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OY 68 CATCGAGCCAGCGCGCGCATGCGCGCTTGTCGATGCCGATCGCATGGCGCGCG 127
Db 88111 CCGACCATGCTCTCGCGGATCCGACGGCGCATATGCTCCCCCAAAGGCGCA 88170

OY 128 GCAGCGGCGCGCGCGCATGCGCGATATTTCTTCCAAGAGCTCCGCGTACGCTTC 187

Db	88171	AGCCGCGCGCGCGCGCGCTCGCAGATGATCTCTCGAGAGACCTCCGCGCGACCGGTG	88230
Qy	188	GCCGAGGACTCTTGATTTCTTCATCTTCGCGCAGGTGTAGAGTCAAGCCCTGCTCC	247
Db	88231	AGGAGAGACTGTGATCTTCATCTTCGCGGAGGTGTAGAGTCAAGCCGCTGCGGTGCC	88230
Qy	248	CACCAACCGGAGCGGACACTCCCGCTTTCACCTCTGACCGGGCAGAGACGACCCAGCGC	307
Db	88291	CACCAACCGGAGCGGACACTCCCGCTCTTGACGCTGACCGGGCAGAGACGACCCAGCGC	88350
Qy	308	TTGCGCGCTTACCAACCGGCTTCGCGCGCGCGCGCTCTTCGCGCGCTTCTCGTTGGCGC	367
Db	88351	TTGCGCGCTTACCAACCGGCTTCGCGCGCGCGCGCGCTCTTCGCGGAGGTCTCGTTGGCGC	88410
Qy	368	CTCTTGACTAGCCGCTCTCCCGCGGTCCGCGACTACCGCGGCTCTCGCGCAGCTA	427
Db	88411	CTTGAGGACTACACGGTCTTCGCGCGCGGTCCGCGACTTCGCGCGCTCTTCGCGAGCTC	88470
Qy	428	TCTCCGCGGAGCTCTTGAGAGCGGTCCGCGCGCGCGCGCGCGCGAGTCCAGTCCGTGATG	487
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Qy	488	GCCGCTCTTCTTACGCGCGGCTGTATCTCTGACTCTGCAAGCGCGCTTGCGCGAC	547
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Qy	548	CTCTCTGCGGGGGGTTCTATTGACTTGGTGTGATTCAGTCCGCTCGATGGGCGACAGAC	607
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Qy	668	GGGAACTGCTCTCACCGGCTTCAGACATCGCTGTGTGAAGTGTAAACACACACGACACAC	727
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Qy	788	TCCCCCAAGCTGTTCGGCAACATATGTGTCTTCTTACCAAGGACCTTGCGCTTGCAT	847
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Qy	908	GCCAGGATTAATTTCTTCGCGCAGTCCGCGCTGTTCCTTCACGAGAGAGAGGTGCG	967
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Qy	968	CACGCGTTGTGATGATCGCGGGGCTCGCACATTCGTGGCTTGGTACCCGTTGCTGTG	1027
Db	89008	CAGAGGGGCTGTGAGATTCGCGGGGCTCGCGGTTCTGTGGTTGTGTACCAATGTGTGTG	89067
Qy	1028	GCTTCCCTGCGAAATGTGTGGAGAGAGGCTGTGTGTGCTTTCAGCTTACCACTATGC	1087
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Qy	1208	CCTTGATGATTTGTTTTCACAGGTGCGCTGTGACATTCGAGTTTGAGACACATCTGTGTTCC	1267
Db	89248	CCATGATGATTTGTTTTCACAGGTGCGCTGTGACATTCGAGTTTGAACACCATCTGTGTTCT	89307

QY	1268	CGCCTACCTCGAGTCCACCTTCGCAAGATTGCACCGCGCGTCCGCGACCTTTGCAGAAG	1327
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QY	1328	CATGGGCTCACTTAATTTGCAGCCCACTTCGAGGATGCAAAATGCTTACATGAAGACA	1387
Db	89368	CATGGGCTGGCTTAATGCGCGCGCTGCTTCGCGAGGCTAATATGTTGACATGGAAGACA	89427
QY	1388	CTAGGGCTGCTGATTTGACAGGCGCAGCAACGCTCAAAAGTGTGTCCTCGAAGATTGG	1447
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QY	1448	GTAAGGAGGCTGTGAACACCCATGATTAATAGGATGGAAGATACGGGCTAAATGGCACT	1507
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QY	1508	TCTGCTTTACAGCTGTGATGCCCATGATGTCTGATAGCTTTACGTTACTATTTAGAGATA	1567
Db	89537	GCTTGT-----GCATGCATCACTCAATGCTTCTTAATGTGTGAGGACA	89584
QY	1568	TTGATCATTTCAACT-----GCTGAGTCAAGTTGGAAATTTTCGTTGACAAAGTGC-	1620
Db	89585	TTGATCTTTTACTCTTACCCGTTGAGTTGATTCGATTTTTCGTTGGCAAGTCT	89644
QY	1621	TGCTCATCCAGTTGGAGA---GTTCACTTCAATAGTCTGCTGTTTCAACGGATGTTTC	1676
Db	89645	TGCTTTTGACAGTCGAAGAGTGGTTATGCTCAATGTCTCAATCTGTTCTTATGATATTA	89704
QY	1677	TGTTCTCCCTAATC	1689
Db	89705	GATTGTCCGATTC	89717

RESULT 3				
LOCUS	AY234124			
DEFINITION	AY234124	1681 bp	mRNA	linear
	Pr1mula farinosa sp1ngol1pid delta-8 desaturase mRNA, complete			PLN 04-MAY-2003

ACCESSION	AY234124	
VERSION	AY234124.1	GI:30350274
KEYWORDS		
SOURCE	Primula farinosa	
ORGANISM	Primula farinosa	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots; Asteridae; Ericales; Primulaceae; Primula.

REFERENCE
AUTHORS
1 (bases 1 to 1681)
Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and

TITLE	Identification of Primula fatty acid substrate preferences(1)
JOURNAL	FEBS Lett. 542 (1-3), 100-104 (2003)
ADDRESS	FEBS Lett.

PUBMED	12729906
REFERENCE	2 (bases 1 to 1681)
AUTHORS	Savynova, O. V., Beaudoin, F., Michaelson, L. V., Shewry, P. R. and

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JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
Research Station, Long Ashton, Bristol BS41 9AF, UK
FEATURES Location/Qualifiers
SOURCE 1. .1681

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Oy	215	GGCGACGTGTACGACGTACGCGCTTGCTCCCAACAACCCGGGCGCGACCTCCGCTT	274
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Oy	932	TCCGCGCTGTTGTTCTCAACGAGAAGAGGTGCGCAGCGGTTGCTTGAGATCGCGGG	991
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RESULT 4
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 DEFINITION AY234126
 ACCESSION AY234126.1 GI:30350278
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 KEYWORDS
 SOURCE
 ORGANISM
 Primula vialii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Ericales; Primulaceae; Primula.
 REFERENCE
 AUTHORS 1 (bases 1 to 1385)
 Savanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
 Napier,J.A.
 TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3
 substrate preferences(1)
 JOURNAL FEBS Lett. 542 (1-3), 100-104 (2003)
 MEDLINE 22615586
 PUBMED 12729906
 REFERENCE
 AUTHORS 2 (bases 1 to 1385)
 Savanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
 Napier,J.A.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
 Research Station, Long Ashton, Bristol BS41 9AF, UK
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 Best Similarity 63.8%; Pred. No. 1.8e-67;
 Matches 846; Conservative 0; Mismatches 474; Indels 6; Gaps 2;
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DEFINITION AR200409
ACCESSION AR200409
VERSION AR200409.1 GI:20250483
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 1702)
AUTHORS Thomas, T.L.
TITLE Production of gamma linolenic acid by a DELTA-6-desaturase
JOURNAL Patent: US 6355861-A 26 12-MAR-2002;
FEATURES Location/Qualifiers
source 1..1702
BASE COUNT 358 a 471 c 446 g 427 t
ORIGIN

Query Match 27.8%; Score 491.2; DB 6; Length 1702;
Best Local Similarity 62.0%; Pred. No. 4,1e-61;
Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

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 DEFINITION AY234125
 ACCESSION AY234125.1 GI:30350276
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Primula farinosa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Asteridae; Ericales; Primulaceae; Primula.
 1 (bases 1 to 1410)
 Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
 Napier,J.A.
 Identification of Primula fatty acid Delta(6)-desaturases with n-3
 substrate preferences(1)
 JOURNAL
 MEDLINE
 PUBMED
 22615586
 12729906
 2 (bases 1 to 1410)
 Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
 Napier,J.A.
 Direct Submmission
 Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
 Research Station, Long Ashton, Bristol BS41 9AF, UK
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LOCUS Arabidopsis thaliana chromosome 2 clone T3F17 map C1C02B07,
DEFINITION complete sequence.

ACCESSION AC005397

VERSION AC005397.3 GI:20197371

KEYWORDS HTG.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1. (bases 1 to 110149)
Rounseley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M., Shen, M., Rensing, C.M., Frazer, C.M., Somerville, C.R. and Venter, J.C. unpublished

JOURNAL 2. (bases 1 to 110149)
Lin, X.

AUTHORS Direct Submission

REFERENCE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr., Rockville, MD 20850, USA

REFERENCE 3. (bases 1 to 110149)
Town, C.D. and Kaul, S.

AUTHORS Direct Submission

JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
TITL Medical Center Dr., Rockville, MD 20850, USA, cdrom@igr.org
COMMENT On Apr 18, 2002 this sequence version replaced gi:6598465.

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Db	45845	TCATCGCTTACATCCCGGAACCGCATGGACACCTTAGAAAAAGCTTACAAATGGCTATCC	4578
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Db	45785	ACGTGAGAGACCAACACAGTGTCAAGACGTCTCAAGTGACTACCGTCTGTTAGCGCCGAGT	4572
OY	426	TATCTCTCGCGGGCTCTTGCAACGCGTGGGCCCAACCCCAAGTCCAGTCTGCTCTGA	485
Db	45725	TCTCCAAACCGGCGCTCTTGCAAAAAAGGTACAGTACTTTTACACTACGTTCCG	4566
OY	486	TGCGCGTCTCTTCTACGCGCGCGCTGTACCTGTCTCTCGATGCGCCAGCGCTGGAGCG	545
Db	45665	TCGGCGTCAATGCTCGGGCGGTTCTCTAGAGCGTTTGGGCTGTACAGATCTGGGCTC	4560
OY	546	ACCTCTCGCGGGGGGTCTATTTGGCTTCTGTGGATTCAGTCCGAGCTGATGGGCACG	605
Db	45605	ACCTCATCTCCGCGCGTTTACTCGGTCTCTGTGAATCCAAAGGCTTACGTGGGCACG	4554
OY	606	ACTCGGGCCACCAACCGATACCGGCGCATCCGGTCTCTCGACCGCGTGTGAGTGTCT	665
Db	45545	ATTTCGGTCACTACCGGTACGTCACCAACCGGTGTACAACTAATCAGCTTCTCT	4548
OY	666	CCGGGAATCGCTTCAACCGGCTCAGCATTCGCTGTGGAGTGTACCAACACGACCC	725
Db	45485	CCGGTAACTGTCTCACCGGCATCTCATCCGCTGTGTGAATGAGACGACACGCTCAC	4542
OY	726	ACATCGCTTGAACAGCTTGAGACCATGACCCGGACCTTCAGCACATGCGCTTTGGCCG	785
Db	45425	ACATCGCTTGAACAGCTTGAACACAGATCCGAGTCTAACACATCCCATCTTCCGCG	4536
OY	786	TCTTCCCCAAGCTGTTGGCAACATATGTTCTACTTTTACCAACGGAACCTTGCGCTTCG	845
Db	45365	TCTCTAACAAATTTCTTAATTCATGATGACGTACAGTTTCTATGGCAAGAAATTACATTCCG	4530
OY	846	ATGCGCGCTCGAAATTTCTTATGATGATGACGACGACTGACCTTCTACCGCGTATATGCA	905
Db	45305	ATCTCTTAGCTCGAATTTTATCAGCTACCAACACTGAGACATTTTACCAGTATATGTCG	4534
OY	906	TCGCGAGATTAATCTTCTCGCGCAGTCCGCGCTTTCGTTCTTCACGGAGAAGAGGTGC	965
Db	45245	TCGGAAGATCAACCTCTTATCCAAACATTTCTATGTATCTCGAAACGCGACGCTCC	4518
OY	966	CGCAGCGGTGCTTGAGATTCGCGGGGTCGCCACATTTCTGGCTTGGTATCCGTTGCTGG	1025
Db	45185	CAGATCCGGGCTTGAAACATCGCGGAAATTTTAAATTTCTTGACATGGTTCCTCTCTTAA	4512
OY	1026	TGGTTTCCCTGCGAATTTGGTGGGAGAGGGTCGGTGTGCTTTTCACTTCAACCATCT	1085
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OY	1146	CACCCAAAGGCATGACTGTGTTGAGAGACGACGCGACGCTGACATCTGTGCT	1205
Db	45005	CACCAAAACGAAACGATGTGTTGAGAAACAAACCGCGGTACGCTGATATATCGGTGA	4494
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Db	44945	GATCTTTTAAAGATTTGTTCTTTGGTGGATTGCACTTTCAGTTAGACATCATTTGTTTC	4488
OY	1266	CCGCGCTTACCTCGGTGCACTTTCGCAAGGTTGACACCGGCGCTTCGCGACCTTTGCAAGA	1325
Db	44885	CTGGGCTTCCGTGTTGCACTCTCGGACATTAATCCGCGGTGTTTAAAGAACCTTTGTAAGA	4482
OY	1326	AGCATGGGCTCACTTATTTCTGACACCAATTTCTGGGGTGCAAATGTGCTTACATGGAGA	1385

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Db 44765 CTTTGAAGAACGGCGCATTCAGACTG---AGATGCGACTAATCTGTGTGAAGACT 44709

Qy 1446 TGGTATGGAGGCTGTGACACCCCATGATTAATGGG 1482

Db 44708 TGGTATGGAGGCTGTGACACCCCATGATTAATGGG 44702

RESULT 8
BT003379
LOCUS
DEFINITION
BT003379 1491 bp mRNA linear PLN 29-JAN-2003
Arabidopsis thaliana delta-8 sphingolipid desaturase (At3g61580)
mRNA, complete cds.

ACCESSION
BT003379
VERSION
BT003379.1 GI:28059271
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1491)
Southwick, P., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T.,
Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M.,
Deng, J.M., Hayashizaki, Y., Huan, V.W., Lee, J.M., Ishida, J.,
Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shim, P., Tang, C.C.,
Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S.,
Shinozaki, K., Becker, J., Theologis, A. and Davis, R.W.
Direct Submission
Submitted (29-JAN-2003) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
e-mail for correspondence: arabsequence.stanford.edu

COMMENT
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA: "RIKEN
Arabidopsis Full-length cDNA"): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
sequencing and annotation of the RAPL cDNAs: Nguyen, M., Tripp, M.,
Southwick, P., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R.,
Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Huan, V.W., Lee, J.M.,
Kim, C.J., Quach, H.L., Onodera, C.S., Shim, P., Tang, C.C.,
Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Becker, J.,
Theologis, A. and Davis, R.W.

Nguyen, M., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed
equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES
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BASE COUNT
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ORIGIN

Query Match 25.2%; Score 445; DB 8; Length 1491;
Best Local Similarity 59.3%; Pred. No. 1.8e-54;
Matches 795; Conservative 0; Mismatches 540; Indels 6; Gaps 2;

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Qy 249 ACCACCGGGGGCGGACCTCCGCTCTCAACCTGGCGGGGAGAGCGCACCGACGCT 308

Db 122 CTGATCCCGAGGCGACGACGATATCTCAATCTCTGTGTCAAGCTACCGATGCTT 181

Qy 309 TCGCCGCTACACACCC---GCCCTCGGCGCGCCGCTCTCCGCGCTTCTTGTTGGCC 365

Db 182 TCATGCGATTATATCCCGGACCGCTTGGACCATCTCGACCATCTTCCACGGTTACC 241

Qy 366 GCCTCTGTGATGCGCGCTCTCCCGCGTCCGCGCATACGCGCGCTCTTGGCGACG 425

Db 242 ACATCAGAGATTTCCAGTCTCGAAGTCTACGCGCATTAACGCTTATGCGCGGAGT 301

Qy 426 TATCTCCGCGGCGCTCTTGAAGCGGTGGGCGCCACCCCAAGTCCAGCTGTCTGA 485

Db 302 TTGTAATCTCGTCTCTTCTTGAAGAAACAAAGTACCTTACTCTTACCTTACCTTGC 361

Qy 486 TGGCGCTCTCTTCTTCTTACGCGCGCTGTACTCTGCTCTGCATGCGCAGCGCTGGGCG 545

Db 362 TGGCGCGCATGTTCTCGGAGTTCTTCAAGGTGTTTGGCTGTATCTCGCTTTCGCTC 421

Qy 546 ACTCTCTCGGCGGGGCTTCATTTGCTTGTGTGATCCAGTCCGCTGGATGGCGACG 605

Db 422 ACCAAATCGCGCGCGCTCTCGTCTCTCTGATTCAGAGCGCTTCAATATGATGACG 481

Qy 606 ACTCGGGCCACACCGCATACCGGCAATCCGCTCTCGACCGCGCTGATGATGCTCT 665

Db 482 ATCTGATCTTACGTTATCATATGTCGAAACAATCTTATTAACAGATTGCTCAGCTTCT 541

Qy 666 CCGGGAATGCTCTACCGGCTTCAGCATGCGCTGTGTGAAGTGTAAACAACACGACAC 725

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Qy 726 ACATGCTCTGCAACAGCTCTGACATGACCGGACCTCCAGACATGCGGCTTTGGCG 785

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Qy 786 TCTTCCCAACGCTTCTGCGCAATATGATGCTTCTTACCAACGAGCCGCGGCTTG 845

Db 662 TCTTCAACCAATCTTCTCTCTATTAACCTCGAGATTTCTACGATCGGAAATCAGCTTG 721

Qy 846 ATGCGCTCTGAATCTTCTCATGAGTACAGACGACGACTTCTTACCGGTAATGTGA 905

Db 722 ATCTAATGCGGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 781

Qy 906 TCGCAGATTAATCTTCTGCGCAGTCCGCGCTGTTGCTTCTGACGAGAAAGGCTGC 965

Db 782 TTGGAAGATCAATCTTCTCATCAACAGTTCTTCTCTCTCTCAACAGTGAATAC 841

Qy 966 CGCAGCGCTTCTGATGATGCGGCGGCTGCGACATTTCTGGCTTGTATCCGTTGCTG 1025

Db 842 CAGATGCTGTTTAACTTTCGCGGGAATCTTACGCTTCTGAGCTTGTCCACTTTAG 901

Qy 1026 TGGCTTCCCTGCGGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1085

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D	b	962	CGGGGCTTCAACAATTCATTCACGCTTAAACATTTTCGTGTGATGTACAGTTGGTC	1021
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D	b	1022	CACCCACCGGAGCGACTGTGTTCAAGAAAGCAGCGCGGAAACATCATATCTCTGTGA	1081
Q	y	1206	CTCCTTGATGATGATTGTTCCACGCGTGGCTCGACATTCAGATTGACGACCATCTGTTCC	1265
D	b	1082	GATCATACATGATGATTGGTTCTTTGGTGGATTACAGTTTCACTTGGACATCATTTGTTCC	1141
Q	y	1266	CCGCGCTAAGCTCGGTGCCACTTTGGCAAGTTTGCAACGCGCGCTCGCGACCTTTGGCAAG	1325
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Q	y	1326	AGCATGGGCTCACTTATTCGACAGCAATTCGGGGTGCAAAATGTGTTACATGAGAA	1385
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Q	y	1386	CACCTCAGGCGCTGCTGCAATTGCAGGCGCAGGACCGCTACAAATGTGTGTGCTCCGAAGATT	1445
D	b	1262	CTTTGAAGACAGCAGCTTATCAAGCTGAGACGTGGCTAAATCCGCTGGTT---AAGAACT	1318
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AX007241	RESULT 9
LOCUS	AX007241 1678 bp DNA linear PAT 06-SEP-2000
DEFINITION	Sequence 3 from Patent WO0000593.
ACCESSION	AX007241
VERSION	AX007241.1 GI:9995107
KEYWORDS	
SOURCE	
ORGANISM	Arabidopsis thaliana (thale cress)
	Arabidopsis thaliana
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1
AUTHORS	Zehring, U., Heitz, E., Schmidt, H. and Sperling, P.
TITLE	Sphingolipid-desaturase
JOURNAL	Patent: WO 0000593-A 3 06-JAN-2000;
	ZEHRING, ULRICH (DE); HEINZ, ERNST (DE); SCHMIDT, HERMANN (DE);
	SPEHLING, PETERA (DE); GVS GES FUER ERWERB UND VERMER (DE)
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BASE COUNT	416 a 408 c 339 g 515 t

ORIGIN

Query Match	25.2%	Score 445;	DB 6;	Length 1678;
Best Local Similarity	59.3%	Pred. No. 1.7e-54;		
Matches 795; Conservative	0;	Mismatches 540;	Indels 6;	Gaps 2,

QY	189	CCGACGACCTCTGGATCTTCATCTCCGCGCAGTGAACAGTACACGCCCTGGCTCCCC	248
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QY	249	ACCAACCCGGCGGCGACCTCCCGCTTTCACCTTGGCGGGCAGAGCGCACCGAGCTT	308
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QY	309	TTCGCGGCTTACCAACCC---GCCCTCGGCGGCGCCGCTCTCCGCGGCTCTTCTGTGGCC	365
Db	353	TCTATCGATTTCATCCCGGAACCGCTTGGACCACTCTCGACCATCTTTCACCGGTTACC	412
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Db	473	TTCTGTAACCTCGGCTCTTCGAAAACAAAGGTACGTTACTCTGTACACTTTAGCTTCG	532
QY	486	TGGCGGCTCTCTTTCATAGCGCGGCTGTACCGTCTCGATCGCATGGCGCAGCGCTGGGCGC	545
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QY	1146	CATCCMAAGGCATGATCTGTTTGGAGAACGAGACGGAGCAACGCTCGACATCTCTGTCT	1205
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RESULT 11
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 LOCUS Arabidopsis thaliana mRNA for delta-8 sphingolipid desaturase.
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 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 Sperling, P., Zahring, U. and Heinz, E.

TITLE A sphingolipid desaturase from higher plants. Identification of a
 new cytochrome b5 fusion protein
 JOURNAL J. Biol. Chem. 273 (44), 28590-28596 (1998)
 MEDLINE 99003197
 PUBMED 9786850
 REFERENCE 2
 AUTHORS Sperling, P., Zahring, U. and Heinz, E.
 TITLE Identification of cDNAs coding for a sphingolipid desaturase from
 higher plants
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1705)
 AUTHORS Sperling, P.
 TITLE Direct Submission
 JOURNAL Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer
 Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18,
 D-22609 Hamburg, GERMANY
 COMMENT Related sequence: X87143.
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 1 (bases 1 to 1743)
 REFERENCE
 AUTHORS
 Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T.,
 Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M.,
 Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J.,
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 Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinzaki, K.,
 Ecker, J., Theologis, A. and Davis, R.W.
 TITLE
 JOURNAL
 Submitted (24-SEP-2002) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT
 e-mail for correspondence: arab@sequence.stanford.edu
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
 Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.
 The Salk, Stanford, PGEC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Southwick, A.,
 Tripp, M., Nguyen, M., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R.,
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 Wallender, E.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S.,
 Ecker, J., Theologis, A. and Davis, R.W.
 Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed
 equally to this work. Shinzaki, K. (RIKEN GSC) and Davis, R.W.
 (SSP/Stanford) contributed equally to this work as PIs.
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REFERENCE
 1 De Haan, M., Maarse, A.C., Griveall, L.A., Mewes, H.W., Lemcke, K.,
 Mayer, K.F.X., Quefeler, F. and Salanoubat, M.
 Unpublished
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 JOURNAL EU Arabidopsis sequencing, project.
 AUTHORS Direct Submision
 TITLE Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
 Coordinator: Marcel Salanoubat and Francis Quefeler, Grouperment
 d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
 http://www.genoscope.cns.fr
 COMMENT Information on performance of analysis and a more detailed
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 QY 1026 TGGCTTCCCTGCGGAATGCTGAGAGAGGCTGCGGTTTGTCTTTCACTTACCATCT 1085
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QY 1086 GCGGATTCAGCAGCTCCATTTCTGCTGAACCACTTCTGCTCCAGCTGATGTCGCGC 1145
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RESULT 14
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 LOCUS 1652 bp mRNA linear PLN 14-APR-2003
 DEFINITION Arabidopsis thaliana clone 34427 mRNA, complete sequence.
 ACCESSION AY087345
 VERSION AY087345.1 GI:21406069
 KEYWORDS FLI cDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 (bases 1 to 1652)
 Haas, B.J., Volkovskiy, N., Town, C.D., Troupkhan, M., Alexandrov, N.,
 Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
 Full-length messenger RNA sequences greatly improve genome
 annotation
 TITLE Full-length messenger RNA sequences greatly improve genome
 annotation
 JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)
 MEDLINE 22088475
 PUBMED 12093376
 REFERENCES 2 (bases 1 to 1652)
 Brover, V., Troupkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
 Feldmann, K.
 TITLE Full-length cDNA from Arabidopsis thaliana
 JOURNAL Unpublished
 REFERENCES 3 (bases 1 to 1652)
 Brover, V., Troupkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
 Feldmann, K.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
 Malibu, CA 90265, USA
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
 available to TIGR and Genbank. The following quality assessment of
 this set was done by comparison with known proteins: two percent
 of the clones are estimated to be 5'-truncated; less than one percent
 are 3'-truncated; approximately two percent represent alternative
 splice variants, including unspliced introns and spliced exons; one
 percent may contain premature stop codons; five percent may have
 frame shifts in a coding region. A sequence is considered to be
 5'-truncated if it lacks the translation initiation start (ATG). A

sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Luer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genes carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

source

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/mol_type="mRNA"

/db_xref="taxon:3702"

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207.1556

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/protein_id="AA064895.1"

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KREVPDRALNFAGILVFWTFPLVSLPMPERFPFVPTVTLQHOIOTLNHFA
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BASE COUNT 412 a 403 c 342 g 495 t

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Best Local Similarity 59.1%; Pred. No. 5e-54;

Matches 793; Conservative 0; Mismatches 542; Indels 6; Gaps 2;

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QY 366 GCGCTCTGACTAGCGGCTTCCCGCGCTCGCGCGACCTACGCGCGCTCTCGCGGACG 425
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QY 426 TATCTCCGCGGCGCTCTTGAAGCGCTGCGGCGACCCCGCAAGGTCAGCTGCTCTGA 485
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DB 808 ATCTAGCT 867

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DB 1585 TTCTTGGGTTAAATTTGATG 1605

RESULT 15

AX505863

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabisopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Location/Qualifiers

1350 bp DNA linear PAT 27-SEP-2002

Sequence 558 from Patent WO0216655.

AX505863

AX505863.1 GI:23387100

The Scripps Research Institute (US); Syngenta Participations AG (CH)

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/mol_type="genomic DNA"
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Best Local Similarity 59.8%; Pred. No. 1.2e-53;
Matches 773; Conservative 0; Mismatches 513; Indels 6; Gaps 2;

QY 189 CCGACGACCTCTGGATCTCCATCTCCGCGACGTGAACGACGTACAGCCCTGGCTCCCC 248
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QY 249 ACCACCCGGGGCGGACCTCCGCTTCTACCTCGCGGGGAGAGACGCACTCGAGCCCT 308
DB 122 CTCATCCCGAGGCGACGCGTATCTCAATCTCGTGGTCAAGACGTCAACCGATGCTT 181
QY 309 TCGCCGCTACCAACC---GCCCTCGGCGCGCCGCTCCCTCGCGGCTTCTTGTGGCC 365
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QY 366 GCGCTCTGTACTAGCGCGCTTCCCGCGCTCGCGCACTAACCGCGCTCTCTCGCGCAG 425
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Search completed: December 31, 2003, 21:04:25
Job time : 4432.43 secs

XX WPI; 2000-412336/35.
DR P-PSDB; AA071552.
XX
PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries -
XX
XX
PS Claim 2; Page 41-42; 57pp; English.
XX
XX The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone cdeic.p001.08.115 isolated from corn developing
CC embryo cDNA library, cdeic. The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
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SQ Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 other;

Query Match 100.0%; Score 1764; DB 21; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1741 AAGATTTAAAAAATTTAAAAA 1764
Db 1741 AAGATTTAAAAAATTTAAAAA 1764

RESULT 2
 AAD01353
 ID AAD01353 standard; cDNA; 1972 BP.
 XX
 AC AAD01353;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Wheat sphingolipid desaturase cDNA #1.
 XX
 KW Wheat; sphingolipid desaturase; membrane-bound desaturase;
 XX transgenic plant; fatty acid; ss.
 XX
 OS Triticum aestivum.
 XX
 FH Key Location/Qualifiers
 FT CDS /tag= a
 FT /product= "sphingolipid desaturase"
 XX
 PN MO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PR 03-DEC-1998; 98US-0110784.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
 XX
 DR MPI: 2000-412336/35.
 DR P-PSDB; AA71555.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Disclosure; Page 48-49; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone wrel.pK004.c7:fls isolated from wheat etiolated
 CC seedling root cDNA library, wrel.
 CC
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
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Query Match 61.9%; Score 1091.4; DB 21; Length 1972;
 Best Local Similarity 79.0%; Pred. No. 3,8e-211;
 Matches 1355; Conservative 0; Mismatches 341; Indels 19; Gaps 4;

QY 27 CCTCCCGCTCCCTTACCAATCAGCACCAAGGCGATCCGAGCCAGCGCGG 86
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 DB 149 CAACGCGCGCGGAGCGGAGCGGAGCGGAGCGGCGCGCGCGCGCGCGCGCGGAG 202
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 QY 207 CCATCTCCGCGCGGAGCTGATGAGCTCAAGCGCTCCGCGCGCGCGCGCGCGCGGAGC 266
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 QY 447 AAGCGTCCGCGCGCAACCCCAAGTCCAGCTGCTCCGAGGCGGCTTCTTCTTCCGCGG 506
 DB 503 AAGCGTCCGCGCGCAACCCCAAGTCCAGCTGCTCCGAGGCGGCTTCTTCTTCCGCGG 562
 QY 507 CGCTGTAACCTGCTCTGCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCA 566
 DB 563 CCTCTACTGCGCTTCTGCGCTGCTCCAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCTCA 622
 QY 567 TTGGCTTCTGTCGATCCAGTCCGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGATCA 626
 DB 623 TTGGCTTCTGTCGATCCAGTCCGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGATCA 682
 QY 627 CCGGCGGCTCCGCTCCAGCGGCTGCGGAGTGGCTTCCGCGGAACTGCTTCCAGCGGCG 686
 DB 683 CCGGCGGCTCCGCGCTCCAGCGGCTGCGGAGTGGCTTCCGCGGAACTGCTTCCAGCGGCG 742
 QY 687 TCAGCATGCGCTTGGTGAAGTGAACACACACGACACATGCTGCGACACGCTTGG 746
 DB 743 TCGGCACTGCGCTTGGTGAAGTGAACACACACGACACATGCTGCGACACGCTTGG 802
 QY 747 ACCATGACCGGAGCTCCGACGACATGCGGCTTGGCGGCTTCCGCGGAACTGCTTGGCA 806
 DB 803 ACCATGACCGGAGCTCCGACGACATGCGGCTTGGCGGCTTCCGCGGAACTGCTTGGCA 862
 QY 807 ACAATGCTCTACTTCTTCAACAGGAGCTGCGGCTTCCGCGGAACTGCTTGGCA 866
 DB 863 ACCTTTGGTGGCTTCTTCAACAGGAGCTGCGGCTTCCGCGGAACTGCTTGGCA 922
 QY 867 TAGCTACGAGCATGAGACTTCTTACCGGTAATGTCATCGGCAATTAATCTTCTCG 926
 DB 923 TAGCTACGAGCATGAGACTTCTTACCGGTAATGTCATCGGCAATTAATCTTCTCG 982
 QY 927 CCGAGTCCCGCTTCTTCTTCAACGAGAGAGGTCGCGGCTTCTTGGATG 986
 DB 983 TCGAGTCAATCGTGTCTTCAACGAGAGAGGTCGCGGCTTCTTGGATG 1042
 QY 987 CCGGCGGCTCCGATTTCTGCGGCTTGGTACCGGTCGCGGCTTCTTGGATG 1046
 DB 1043 CCGGAGTTCAGCGCTTCTGCGGCTTGGTACCGGTCGCGGCTTCTTGGATG 1102
 QY 1047 GGAAGAGGTCGCTTGTGCTTCACTTCACTTCCGAGATTCAGAGCTTCAAT 1106
 DB 1103 GGAAGAGGTCGCTTGTGCTTCACTTCACTTCCGAGATTCAGAGCTTCAAT 1162
 QY 1107 TCTGCTGAACCACTTCTGCGGCTTGTGAGTGTGCGGCGGCGGCGGCGGCGGCTTGT 1166
 DB 1163 TCTGCTGAACCACTTCTGCGGCTTGTGAGTGTGCGGCGGCGGCGGCGGCGGCTTGT 1222
 QY 1167 TTGAGAGGAGGAGCGGAGGAGCGTCACTGCTGCTCTCTTGGATGATGATGTTGCTTC 1226
 DB 1223 TTGAGAGGAGGAGCGGAGGAGCGTCACTGCTGCTCTCTTGGATGATGATGTTGCTTC 1282
 QY 1227 ACGGTGCGCTGAGTTCAGATTTGAGCAACATCTTCTCCGCTTACCTCGGTGCGAC 1286
 DB 1283 ATGTGTGCTGAGTTCAGATTTGAGCAACATCTTCTCTGCTGCTGCTGCGAC 1342
 QY 1287 TTGCGAAGGTTCACCGGCGGCTTCCGCGGCTTTCGAGAGAGATGGGCTCACTTATTCG 1346
 DB 1343 ATGAGATGTTCGCGCGATTTGCGGTGACCTTTGAGAGAGATGGGCTCTTATGAGTG 1402
 QY 1347 CAGCCACATTTCTGGGAGTGAATGTGCTTACATGAGAGACATCAGGCGTGTGATTCG 1406

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Db      1403  CCGCCACATTTCTGGAGGCAAAATGATATGACATGAAAGCTAAGGGCTGCAGCATTCG 1462
Qy      1407  AGGCCGAGACCGCTACAAAGTGTGCTGCTCCGAAAGATTGGATGAGAGCTGTGAACA 1466
Db      1463  AGGCCGAGGAGGACCACTAGTGAAGCTGCTCCAAAGATCTGCTGGGAAGCTTTGAAAC 1522
Qy      1467  CCCATGATTAATGAGATGAAAGATAGAGGCTTAATGCAACTTCTGGTTCAGCTTGTTG 1526
Db      1523  CTCATGATGATCTGGGATCAGAGCTGAGATGAGACAAATTGAAAGCTGAGACCTTGGC 1582
Qy      1527  CCCATGATGATCTGGGATCAGAGCTGAGATGAGACAAATTGAAAGCTGAGACCTTGGC 1586
Db      1583  TCGATCAGATTAATCTGATTCCTTCGATTCGAGTAGATTAATGATCCTTTAGCTGTTG 1642
Qy      1587  GAGTCAGTGTGAATTTGCTGTGACAAAGTGTCTGTATCCAGT---TGAAGAGTTC 1642
Db      1643  GAATCTGTGTGATTTTGTGCTGTGACAGTGAATCTTGTGCAATCAATCGTGGGTTTC 1702
Qy      1643  ATGCTTCATTAATCTGATTCCTTGTGCTGCTTCACTTCACTTCACTTCACTTCACTT 1695
Db      1703  ATGCTTCATTAATCTGATTCCTTGTGCTGCTTCACTTCACTTCACTTCACTTCACTT 1762
Qy      1696  ACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1730
Db      1763  ACTACATCA--ATAGTACTTATTAATCATCAATAA 1795

```

RESULT 3
ABK49503
ID ABK49503 standard; DNA; 1702 BP.

ABK49503;

15-JUL-2002 (first entry)

DNA encoding Evening primrose delta6-desaturase.

delta6-desaturase; sunflower; soybean; maize; tobacco;
peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
chilling tolerance; gene; db; evening primrose.

Oenothera biennis.

Key Location/Qualifiers

FT CDS 48..1406
FT /tag= a
FT /product= "delta6-desaturase"

US6355861-B1.

12-MAR-2002.

19-SEP-1997; 97US-0934254.

13-OCT-1992; 92US-0959952.

10-OCT-1991; 91US-0774475.

08-JAN-1992; 92US-0817919.

14-SEP-1994; 94US-0307382.

28-JAN-1997; 97US-0789936.

(RHON) RHONE-POULENC AGROCHIMIE.

Thomas TL;

WPI; 2002-380944/41.

P-PSDB; AAU79851.

Novel nucleic acid encoding evening primrose delta6-desaturase which
converts linolenic acid to gamma linolenic acid useful for producing
gamma linolenic acid in transgenic plant or bacteria

Claim 2; Column 41-46; 53pp; English.

XX The invention describes an isolated nucleic acid encoding an evening
CC primrose delta6-desaturase. The nucleic acid and a vector expressing the
CC nucleic acid are useful for producing a plant such as sunflower, soybean,
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC gamma linolenic acid (GLA) content, and also for inducing or increasing
CC production of GLA in a bacteria or plant deficient, lacking in or
CC production of low levels of GLA. The nucleic acid is also useful for inducing
CC chilling tolerance in plants. This sequence encodes the evening primrose
CC delta6 desaturase involved in the production of gamma linolenic acid.

SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;

Query Match 27.8%; Score 491.2; DB 24; Length 1702;

Best Local Similarity 62.0%; Pred. No. 6,9e-90;

Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

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Qy      155  ATCTCTCCAGAGAGCTCCGCGCTCAAGCTTCGCGGAGAGCTTGATCTTCATCTCC 214
Db      72  ATCAGCGCGGAGAGAGCTCCGCGCGCACAAAGTCCGGGATCTTGATCTTCATCTCAG 131
Qy      215  GGGGAGGTGATGAGAGTCAAGCTTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 274
Db      132  GGGGAGGTGATGAGAGTCAAGCTTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 191
Qy      275  CTCACCTGCGCGGCGGAGAGAGCGGAGAGAGCGGCTTCGCGGAGAGAGCGGCTTCGCGG 334
Db      192  CTCAGTCTGCGCGGCGGAGAGAGCGGAGAGAGCGGCTTCGCGGAGAGAGCGGCTTCGCGG 251
Qy      335  CGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 388
Db      252  TGGCGGCGATCTGAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 311
Qy      389  CCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 448
Db      312  GAGATCTCCAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
Qy      449  CGCGTCCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508
Db      372  AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
Qy      509  CTGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 568
Db      432  GTCTACGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491
Qy      569  GCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 628
Db      492  GCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 551
Qy      629  GCGCATCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 688
Db      552  CCAAGCGGAGATACCAAGATACCAAGATACCAAGATACCAAGATACCAAGATACCAAGATAC 611
Qy      689  AGCATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 748
Db      612  AGCATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 671
Qy      749  CATGACCGGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 808
Db      672  TAGACCGGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 731
Qy      809  ATATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 868
Db      732  ATCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 791
Qy      869  AGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
Db      792  AGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
Qy      929  CAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 988
Db      852  CAGACCTTTTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 911

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QY	989	GGGGTGGCAATCTTGGGCTTGGAAACCGGCTTGGGGCTTCCCTCCGAATTGGG	1048
Db	912	GGTATCCGGGTTTCTGSAAGTGGTCCCGCTTTGATCTTGTCTCCGAATGGGCT	971
QY	1049	GAGAGGTCGCGTTTGTCTTTTCACTTCACATCTCGGGATTACAGAGTCCAAATTC	1108
Db	972	GAAAGGTTCCGGTTCGTCTCATCAGTTTGGGGTCAAGGGATCAGACAGTCCAGTTT	1031
QY	1109	TGCTGAACCACTTCTCGTCCGACGTATGTCCGGCCACCCAGGGCAATGCTGTTT	1168
Db	1032	ACGCTCAACCACTTCTCCGGGACACATAACGTGGCCCCCAGGGGAGCAACTGTTT	1091
QY	1169	GAGAAAGCAGAGGAGGACGCTGACATCTCGTGTCTCTCTGGATGGATTGTTCAC	1228
Db	1092	GAGAAAGCAGAGAAAGGACATCATATCAAGTCCACCGTGGATGACTGTGTTT	1151
QY	1229	GGTGGCTCGAGTTCCAGATTGAGACCATCTGTTTCCCGCTTACCTCGGAGCACTT	1288
Db	1152	GGTGGGCTCGAGTTTCCAGTTGGAGACACACTTGTTCCTTAGGCTGCCGTGGGACCTT	1211
QY	1289	CGCAAGGTTGACCGGCGCGCTCGGACCTTTGCAAGAACATGGGCTCACTTATTTGCA	1348
Db	1212	AGGAAGATTGGCGCCCTTGGCTCGGAGCTTGTGTAAAGAACGGGATCCGTAATGAGAC	1271
QY	1349	GCCACATTTCTG---GGTCAATGTGTCTTACATGAAGACCTCAGGGCTGTGCATTTG	1405
Db	1272	TTCCGGGTTTTGGGACGACGCTAATGTACAGCAATTTCCGACGCTGAGGGATTCGGCGGTT	1331
QY	1406	CAGGCCAGGACCGCTACAGATGTGTGTCTCCGAAGATTTGTGT---GGAGGCTGTG	1462
Db	1332	CAGGCGGCTGACTTAAATTCGGGCCCGCTCCCTAAGAAACTTGGGTATGGGGAAGCTTAT	1391
QY	1463	AACACCCATGATTAATGGGAT	1484
Db	1392	AACACCCATGTGATTTGTGT	1413

RESULT 4	
ABX15367	
ID	ABX15367 standard; cDNA; 1702 BP.
XX	
AC	ABX15367;
XX	
DT	16-APR-2003 (first entry)
XX	
DE	Evening primrose delta-6-desaturase #1 cDNA.
XX	
KM	Delta-6-desaturase; gene; ss; delta-13-desaturase; sunflower; soybean;
KW	maltze; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KM	octadecatretraenoic acid; alpha-linolenic acid; delta-15-desaturase;
XX	evening primrose.
OS	Oenothera biennis.
XX	
XX	
PH	Key
FT	Location/Qualifiers
FT	48..1406
FT	/+tag= a
FT	/product= "Evening primrose delta-6-desaturase #1"
XX	
PN	US2002108147-A1.
XX	
PD	08-AUG-2002.
XX	
PF	21-DEC-2001; 2001US-0029756.
XX	
PR	13-OCT-1992; 92US-0959952.
PR	19-SEP-1997; 97US-0934254.
PR	10-OCT-1991; 91US-0774475.
PR	08-JAN-1992; 92US-0817919.
PR	14-SEP-1994; 94US-0307382.
PR	26-JAN-1997; 97US-0789936.
DA	(THOMAS T L.

XX Thomas TL;
PI
DR WP1, 2003-066659/06.
DR P-PSDB; ABG73416.
XX
PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
PT for producing plant with increased gamma linolenic acid content, and
PT for inducing octadecatrienoic acid production in plant
PS
PS Claim 2, Fig 10, 55pp; English.
XX
CC The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GLA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GLA content from the plant
CC cell, for inducing or increasing production of GLA in an organism lacking
CC in or producing low levels of GLA and for inducing production of
CC octadecatrienoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecatrienoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GLA substrate. This sequence represents
CC cDNA encoding an evening primrose delta-6-desaturase polypeptide.
XX
SQ Sequence 1702 BP, 358 A, 471 C, 446 G, 427 T, 0 other;

Query Match	Similarity	Score	DB	Length
Best Local	62.0%	Pred. No. 6.9e-90		
Matches	832	Conservative	0	Mismatches 496
				Indels 12
				Gaps 3

Query	Match	Similarity	Score	DB	Length
Db	155	ATCTCTCCAGAGAGCTCCGGCTTCAGCGCTTCGCGCGAGCACTCTGTGATCTCCATCTCC	214		
Qy	72	ATCAGCGGCGAGGAGCACTCCCGCGCACAAAGTTCGGCGATCTCTGTATCTCATCCAG	131		
Db	215	GGCGACGTGTACGACGTACAGCCCTGTGGCTCCCCACCACTCCGGGCGGAGACTCTCCCGCTT	274		
Qy	132	GGCAAGGCTTACGACTGCTCTCGGTGGCGGCGAGCACCCCGGGGAGAGGTCTCCGCTC	191		
Db	275	CTCAACCTTGGCGGGGAGAGAGCCAGCAGCAGCCCTTCGCGCGCTACACACCGCGCTTCGCG	334		
Qy	192	CTCAGTCTGGCGGGGAGAGAGTACAGACCGCTTTCATGTGGTACACCCGGGACCGGCG	251		
Db	335	CGCCCGCTCTCCGCGCGCTTCTTCTGTGG-----CGCGCTCTGTGACTAGCGCGCTCTCC	388		
Qy	252	TGGGGGATCTGTGATTCGCTCTTTCACCGGCTACTACTACCTTCAAGAGCTTGGAAAGTGTGCG	311		
Db	389	CCCGCGTCCGCGGAGCTACCGCGCGCTCTCGCGGAGCATCTCCGGGGGCGCTTTCGAA	448		
Qy	312	GAGATCTTCCAAAGGACTACCGGAGGCTTTTGAACGAGATGTGCGGCTCCGGGATCTTCGAG	371		
Db	449	CGCGTCCGCGCCCAACCCCAAGGTCAGGCTGCTCCGTGATGCGCGTCTCTTCTACGCGCGG	508		
Qy	372	AAGAAAGGCCACCAACATATATGTGAGACGTGTGCGGCGTGTGGGTCATGATGTGGCGGCATTC	431		
Db	509	CTGTACTCTCGTCTTCGCAATGCGCAGGCGCTTGGGCGCACTTCTCTCGCGGGGAGTCTCATTT	568		
Qy	432	GTCTACGCGCGTGTGGGGTCCGAGTCCGTCGGAATTCACATGCTCTGCGGCGCACTGCTG	491		
Db	569	GGCTTCGTCGTGAGATTCACAGTCCGGCTGTGATGTGGGCGACAGACTCGGGGCGACCAACCGATCC	628		
Qy	492	GCGTTCGTCGTGAGATTCACAGTCCGGCTGTGATGTGGGCGATGCTCTCCGCGCATTTACAGGTATG	551		
Db	629	GGCCATCCGCTCTTCGACCGCGCTGTGAGTGTCTTCGCGGAACTGTGCTTACCGGCGCTC	688		
Qy	552	CCAAACCGTGGATTCACACAGATCACCGCACTCATAGAGGCAACATCTTAACCGGAATC	611		
Db	689	AGCATTCGCGCTGTGAGATGTGATACCAACACGACACCATCTGCGCTGACACAGCTTGAC	748		
Qy	612	AGCATTCGCGCTGTGAGATGTGATACCAACGCGCACACCTTCGCTGACACAGCTTCGAC	671		

QY	749	CATACCCGAGACCTCCAGCACATGCGCTCTTTGGCCGCTCCGCAACCTGTCGGCAAC	808
Db	672	TACAGACCCGACCTCCAGCACATCCCGTATTGCGCGCTCCACCCACTCTTCACTCC	731
QY	809	ATATGTCCTCACTTCTACCAAGGACCCCTGCGCTTCAGTGCGCCCTCGAAATCTTCATC	868
Db	732	ATCACTCTGCTCTTATGCGCCGAGTCTGAAATTCGACGAAGTGGACGGTTCCTACTC	791
QY	869	AGCTAACGACCTGGACCTTTACCCGGTAATGTCATCGCCAGATTAATCTTCTCGCG	928
Db	792	AGCTACCAAGCACTGGACCTTACTACCCGGTCAATCTTCGCGCAGTCAACCTCTTCATC	851
QY	929	CAGTCGCGCCCTGTCGTTCTCAGCGAAGAAAGGGGCGCGACGCGTTCCTTGAATCGCG	988
Db	852	CAGACTCTTTTATTGCTCTCTACCAAGCGCGACGCTCCTGACCGCGCTTAACTTAATG	911
QY	989	GGGGTCGCACTTCTGGGCTTGGTACCCGCTGCTGATGGCTTCCTCGTCCGAAATGGTGG	1048
Db	912	GGTATCGGGGTTTCTTGGACGTGGTCCGCTCTTCGATCTTGTCTCCGAACTGGCGCT	971
QY	1049	GAGAGGGTCGCGTTTGTGCTTTTCACTTCAACCATCTGCGGATTCAGACGCTCCAAATTC	1108
Db	972	GAAACGTTCCGGGTTCTGCTCTCATCAGCTTTCGCTCAAGCGAGATCAGCAGTCCAGTTTC	1031
QY	1109	TGCTGAAACCACTTCTGTCGCGAGTGTATGCGGGCCACCCAGAGGCAATGACTGCTT	1168
Db	1032	ACGCTCAACCACTTCTCTCGCGACACATACGGGGCCCCCCAGAGGCGACACTGGTTTC	1091
QY	1169	GAGAAAGCAAGCGGAGGACCGCTCGACATCTGTGCTCTCTTGGATGATTTGTTCCAC	1228
Db	1092	GAGAAAGCAAGAAAGGAGCATGATGATTCACGTGCCACCGTGATGATGATCGGTTCTTT	1151
QY	1229	GGTGGCTTCAGTTTCAGATTGAGCACCATCTGTTTCCCGCTTACTCTGCTGCCACTT	1288
Db	1152	GGTGGGCTTCAGTTTCAGTTGAGGACCACTGTTTCCCTAGGCTGCGCGTGGCGACGCTT	1211
QY	1289	CGCAAGGTGACCGGCGCGTCCGCGACCTTTGCAAGAAAGCAATGGGCTCACTTAATCTGCA	1348
Db	1212	AGGAAGATTGGCCCTTGGCTGGGACTTGTGTAAAGACAGGGATGCCGTAATGAGAGC	1271
QY	1349	GCCCACTTCTGG---GGTCAAAATGTGCTTACATGAAGACACTCAGGGCTGTGCATTG	1405
Db	1272	TTGGGGTTTTGGAGGACGCTAATATGTACGACAAATTCGAGCGCTAGGGATTCGGCGGTT	1331
QY	1406	CAGGCCAGGACCGCTACAAAGTGTGTGCTCCGAAATTTGTAT---GGAGGCTGTG	1462
Db	1332	CAGCGCGGTGACTTAAATTCGCGCCCGTCCGCTTAAGAAACTTGGGATGGGGAAGCTTAT	1391
QY	1463	AACACCACTGATTAATGGGAT	1484
Db	1392	AACACCCATGGTGAATGTGGT	1413
RESULT 5			
AAD01352			
ID	AAD01352 standard; cDNA; 1934 BP.		
XX	AAD01352;		
XX	AC		
XX	12-OCT-2000 (first entry)		
XX			
DE	Soybean sphingolipid desaturase cDNA #2.		
XX			
KW	Soybean; sphingolipid desaturase; membrane-bound desaturase;		
KW	transgenic plant; fatty acid; ss.		
XX			
OS	Glycine max.		
XX			
XX			
Key	Location/Qualifiers		
PH	CDS		
FT	305..1657		
FT	/*tag= a		
FT	/product= "Sphingolipid desaturase"		
XX			

XX	MW0200032790-A2.
PD	08-JUN-2000.
XX	
PF	02-DEC-1999; 99MW-US28589.
XX	
PR	03-DEC-1998; 98US-0110784.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
PI	Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
XX	
DR	WP1: 2000-412336/35.
DR	P-PSDB; MAFY71554.
PT	
PT	Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT	transgenic plants and for producing antibodies specific to which is
PT	useful for screening cDNA expression libraries -
XX	
PS	Claim 2; Page 46; 57pp; English.
XX	
CC	The present sequence is a cDNA encoding sphingolipid desaturase
CC	from clone sbl.jk0017.b4:ris isolated from soybean seedling cDNA
CC	library, ssl. The present sequence is useful for producing
CC	transgenic plants having altered levels of sphingolipid desaturase which
CC	in turn would alter the fatty acid composition. The enzyme is useful
CC	for producing polyclonal or monoclonal antibodies. The polynucleotide
CC	is also useful as primer or probe for screening cDNA libraries to
CC	isolate desired full-length cDNA clones.
XX	
SQ	Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;
Query Match	27.2%; Score 479.8; DB 21; Length 1934;
Best Local Similarity	60.9%; Pred. No. 1.4e-87;
Matches 816; Conservative	0; Mismatches 517; Indels 6; Gaps 2
Oy	155 ATCTCCTCCAGGAGGCTCCGGGCTCACGCTTCGCCGACGACTGTGATCTCCATTCCC 214
Db	335 ATAACTTAGAGGAGCTGAAGGGTCAACAAGAGGAGATTTATGATCTCAATTCCA 394
Oy	215 GGCGACGTGTACAGCATCGCCCTGTGCCTCCCAACAACCGGGCGGCACTCCGCTT 274
Db	395 GGTAAAGGTATCAATGTCTCAGATTGGGTCAAGAAGCACTCGTGATGATGTTCCATTC 454
Oy	275 CTCAACCTGTGGGGGAGAGACGCAACGACGCTTTCGCCCTTACCACACCCGCTTGCG 334
Db	455 TCAAACCTTGTGGGACAGATGTACATGATGATCATATCAGATACCATCTGGACAGCA 514
Oy	335 CGCCCGCTCTCCGCGCGCTTTTGTGG---CGGCTCTGTGATAGCCGTCTCCCC 391
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Oy	392 GCGTCGCGGACATACCGCGCGCTCTCGCGAGCATCTCCGCGGGGCTCTTTCAGACGC 451
Db	575 GTGTCCAAAGCTACAGAAACTTTCATCTGAATTCTCAAATTTGGGCTTTTGTACACC 634
Oy	452 GTGCGCCCAACCCCAAGTCCAGCTGTCTGTATGCGGCTCTTTTACGCGCGCTG 511
Db	635 AAAGGACATGCATCTTCATGACACCTTGATCTGTGTATGTTATGTTCTCATTTAATCTC 694
Oy	512 TACTCTGTCTTCGATGTGGCCAGCGGCTGGGGCGAACCTCTCGCGGGGGGTCTATTGGC 571
Db	695 TATGATGTCTTGAAGGTGACATAGTGTGTGGGCTCATTTTGGGTACAGGATGCTCTTAAAG 754
Oy	572 TTGCTGTGATCCAGTCGCGGCTGTGATGGGCGACGACGATCGGGCAACCGCATCCGGAC 631
Db	755 TTGCTTTGATGACAAAGTCTTATGTGGGCCATGATTTTGCCACATATGTGTTATGACA 814
Oy	632 CATCCGCTCTTCGACCGCGCTGTGACAGGTGCTCTCCGGAACTGCTCCACGGGCTTCAGC 691
Db	815 ACCAATGGTTTTCAACAGAGTTTGACAGATCTCTCTGTGGAACTGTTGACCGGATTAAGC 874
Oy	692 ATGCGCTGTGTGAAGTGAACCAACAACGACACATCGCTCTGACAAGCTTGACAT 751

PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142883.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
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 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
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 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 21-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
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 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 12-AUG-1999; 99US-0148319.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152353.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.

PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
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 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
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 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
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 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
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 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160981.
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 PR 25-OCT-1999; 99US-0161405.
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 PR 26-OCT-1999; 99US-0161359.
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 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 25.6%; Score 452; DB 21; Length 1465;
 Best Local Similarity 60.4%; Pred. No. 5, 6e-82;
 Matches 781; Conservative 0; Mismatches 505; Indels 6; Gaps 2;
 QY 189 CCGACGACCTTGTGATCTCATCTCGGCGAGGTGACAGCTCAGCCCTGCTCCCC 248
 DB 177 CTGGAGATTATGATTGATTGATTCAAGTAAAGTTTACAGCTTCCGATTGGTTAAAT 236
 QY 249 ACCACCCGGGCGGCGAAGCTCCGCTTCTACCCCTGCGGGGAGAGACGACGACGCT 308
 DB 237 CTGATCCCGAGGCGAGAGAGCATTTCTCAATCTGCGCGGCAAGCGTACCGAGCGT 296
 QY 309 TCGCCGCTTACCAACCGGCGCTCGGCGCGCGCTCTCTCGCGCGCTTCTTGTGAGC--C 365
 DB 297 TCAATCGCTTACATCCCGAAGCGCATGACACCACTTAAGAAAGCTTCAATGCTATC 356
 QY 366 GCGTCTGTACATAGCGCGCTCTCCCGCGCTCCGCGACATACAGCGCGCTCTCGCCACG 425
 DB 357 ACCTGAGAGACCAACCAAGTGTACAGAGTCTACAGTACTACTTTTACAGCGCGAGT 416
 QY 426 TATCTCTCGGCGGCGCTTCTGAAAGCGGTGCGGCCACCCCAAGGTCCAGTCTGTCTGA 485
 DB 417 TCTCAAGCGGCGCTTCTGACAAAAAAGTACAGTACTTTTACACATCAGCTGGG 476
 QY 486 TGGCGCTCTCTTCTTACGCGCGGCTGTACTCTGCTCTGATCGGACGCGCTGGGCGC 545
 DB 477 TGGGCGTCAATGCTCGGGGGGTTTCTTACGGGTTTGGCGGTATACAGCATCTGGGCTC 536
 QY 546 ACTCTCTCGGGGGGCTCATGCTTGTCTGTGATTCAGTCCGAGTGGAGGACAG 605
 DB 537 ACCTCATCTCGCGGCTTACTCGGTCTCTCTGATTCAGAAAGCGCTTACGTCGCGACG 596
 QY 606 ACTGGGGCACACACGCGATCACCGGCGATCCGCGTCTCTGACCGCGCTGTGAGGTCTCT 665

PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
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 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143562.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
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 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
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 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
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 PR 20-AUG-1999; 99US-0149723.
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 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
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 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.

PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
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 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 25.2%; Score 445; DB 21; Length 1650;
 Best Local Similarity 59.3%; Pred. No. 1,5e-80;
 Matches 795; Conservative 0; Mismatches 540; Indels 6; Gaps 2;

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 268 CTGAGATCTATGATCGGATTCGAAGGTCTACAGCTCTCGATTGATTAATA 327
 QY 249 ACCACCCGGGGCGGACCTCCGCTTCTGACCTGCGGGGAGAGAGCCACCGAGCCT 308
 DB 328 CTATCCCGGAGGCGACAGGTATCTCAATCTCGTGGTCAAGACGTACCGATGCTT 387
 QY 309 TCGCCGCCCTACACCC---GCCCTGGCGCGCCCGCTCTCCGCCCTTCTTGCGCC 365
 DB 388 TCATCGCATTTATCCCGGAACCGCTTGGACCATCTGACCATCTTTCACCGGTTACC 447
 QY 366 GCCTCTCTGACTAGCGCGCTCTCCCGCGTCCGCGGACTACCGCCGCTCTCCGCGAGC 425
 DB 448 ACATCAGAGATTTCAGAGTCTCCGAGTCTCAGCGCATTAACGTCATATGAGCCGAGT 507
 QY 426 TATCTCCGGGGGCTCTTGAACGGGTGGGCCCAACCCCAAGTTCAGCTGCTGA 485
 DB 508 TTGTAACCTCGGTCTCTTGAACCAAGGTACGTTACTCTACACTGAGCTTGC 567
 QY 486 TGCCGCTCTCTTTCAGCGCGCGCTTACTGCTCTCTCGATGCGGAGCGCTGAGCGC 545
 DB 568 TCGCCGCGCATGTTCCCGGAGTTCCTACGAGTTCCTGAGTTCCTGCTTGGCTC 627
 QY 546 ACCTCTCGGGGGGTCTCATTTGCTTGTGATTCAGTCCGCGTGGATGGGACAG 605

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Db      628 ACCAAATCCGCGCGGCTTCGTCTCTCTGATCCAGACGGCTTACATAGTCAGC 687
Qy      606 ACTCGGGCCACCAACCGATACCGGCCATCCGGTCTCTGACCGCGCTGTCAGAGTCTCT 665
Db      688 ATCTGTGATTAAGTATCATATCGAACAATCTTATTAACAATTCGCTACCTTCTCT 747
Qy      666 CCGGGAAGTCCCTCACCGGCTCAGCATCGCTGTGTGAAGTGAATTAACCAACCAACGACC 725
Db      748 CCGGTAAGTGTCTCACCGGAATTCATTCGCGTGTGTGAAGTGAATTCATTCATTCATC 807
Qy      726 ACATGCGCTTGCAACAGCTTGACATGACCGGACCTTCAGACATGCGCTCTTGGCCG 785
Db      808 ATCTAGCTTGAACAGCTCGATTAAGATCAGATCTAACAACATCCCTGCTTGGCCG 867
Qy      786 TCTCCCCCAAGCTTTCGGCAATATGATCTCTTCTTCAACGAGACCTTGGCTTG 845
Db      868 TCTCCACCAAAATCTTCTCTCTCATTAAGCTCGAGATCTAAGATCGGAAATCAGCTT 927
Qy      846 ATGCGGCTTGAAATCTTCTCATGAGTACAGGACCTGAGACCTTCTACCGGTAATGCA 905
Db      928 ATCTAGTCCGAGATCTTATGATGATCAACAATTTATTTATCCAGTATGCT 967
Qy      906 TCGCAGAGTAAATCTTCTCGCGAGTCCGCTGTTCTTCTCAAGAGAGAGGATGC 965
Db      988 TTGGAAGATCAATCTTCTCATTAACAAGTTCCTTCTGCTCTTCCAAACGTAAGTAC 1047
Qy      966 CGAGAGGCTTCTTGAGATGCGGGGGTCCCAACATTTGGGCTTGGTACCGCTGCTG 1025
Db      1048 CAGATGCTGTTAACTTCTCGCGGAATCTTATGCTTGGAGCTTGGCTTCCACTT 1107
Qy      1026 TGGCTTCCCTGCGGAATTTGGTGGAGAGGGTGGGTTTGGCTTTCAGCTTACCATCT 1085
Db      1108 TCTCATGCTTACCAACTGCTGAGAGATTTCTTCTGCTTCAACAAGCTTACCGTCA 1167
Qy      1086 GCGGGAATGAGCATGCTCAATTTGCTGTAACCACTTCTGTCGAGCTGATGTCGGC 1145
Db      1168 CGGCGTTAAACATTTCAATTCACGCTTAAACATTTCCGCTGATGATGATGCTG 1227
Qy      1146 CACCCAAGGCAATGATGCTGTTGAAGAGAGAGGAGGACGCTGAGATCTTGTCT 1205
Db      1228 CACCCACCGGTAGCGATGCTGTTGAAGAGAGAGGAGGAGCAATGATCTTGTGA 1287
Qy      1206 CTCTGATGATGATGCTGTTGAGGCTGAGTGGCTGAGTTCAGATTTGAGGACATCTG 1265
Db      1288 GATCATACATGATGATGCTGTTGAGGATTTCAAGTTTCAAGTTCATTTGCTCC 1347
Qy      1266 CCGGCTTACCTCGATGCACTTTCGCAAGGTTGACCGGCGCTCCGCACTTTGCAAG 1325
Db      1348 CTGCTTACCTGCTTCCATCTCCGGAAGTTCTCCGCTGTTCAAGAGCTTTCGAAG 1407
Qy      1326 AGCATGAGCTCAATTAATTCGAGCAATTTCTGGGCTGCAAAATGCTTCAATGAGA 1385
Db      1408 AGCATATATCTTCGATGAGGATGATGCTGTTGAAGCAAAATGCTTCAATTAACA 1467
Qy      1386 CACTCAGGCTGCTGATTCGAGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1445
Db      1468 CTTTGAAGACAGAGCTTATCAAGCTAAGAGAGGAGGAGGAGGAGGAGGAGGAG 1524
Qy      1446 TGGTATGAGAGGCTGAGACACCATGATTAATGAGGATGAGGAGGAGGAGGAGGAG 1505
Db      1525 TGGTTTGGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1584
Qy      1506 CTTCGCTGCTGAGCTTGGT 1526
Db      1585 TTGTTTGGGTTAATTTGATG 1605

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RESULT 8
AAZ44833 standard; DNA; 1678 BP.
XX
AC AAZ44833;

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XX      27-APR-2000 (first entry)
DT      A. thaliana sld1 DNA.
XX      Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;
XX      transgenic plant; crop plant; delta-8-unsaturated long-chain base;
XX      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
XX      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
XX      pharmaceutical; food; chemical raw material; ds.
XX      Arabidopsis thaliana.
OS      Key Location/Qualifiers
FH      CDS 172..1521
FT      /tag=a
FT      /product="sphingolipid desaturase"
XX      .DE19828850-A1.
PN      30-DEC-1999.
PD      27-JUN-1998; 98DE-1028850.
XX      27-JUN-1998; 98DE-1028850.
XX      (GVSE-) GVS GES ERWERB & VERM LANDWIRTSCHAFTLICH.
XX      Heinz E, Zaehring U, Schmidt H, Sperling P;
XX      MPI; 2000-127549/12.
XX      P-PSDB; AAY51334.
XX      New sphingolipid desaturase that selectively introduces double bond
XX      into sphingolipids and capnoids -
XX      Claim 11; Fig 3; 62pp; German.
XX      This invention describes a novel sphingolipid desaturase that selectively
XX      introduces a double bond into the sphingobase of the ceramide residue of
XX      sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
XX      desaturase, or a vector containing the DNA sequence, can be used to
XX      produce transgenic plants, especially crop plants, with an increased or
XX      decreased delta-8-unsaturated long-chain base content or an altered
XX      delta-8-unsaturated long-chain base cis/trans ratio, especially to
XX      compensate for a delta-8-unsaturated long-chain base deficiency, to
XX      exclude production of delta-8-unsaturated bases, to increase tolerance
XX      or resistance to soil salinity, ion stress or toxicity, drought, wet
XX      conditions, cold or frost and/or phytopathogenic microorganisms, or to
XX      alter size growth and flowering time. Cells, transgenic organisms or
XX      plants containing the DNA sequence can be used to produce sphingolipids
XX      and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
XX      can be used in cosmetics, pharmaceuticals and foods and as chemical raw
XX      materials. This sequence encodes the Arabidopsis thaliana sphingolipid
XX      desaturase sld1 protein described in the method of the invention.
XX      Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 other;
SQ

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Query Match 25.2%; Score 445; DB 21; Length 1678;
Best local similarity 59.3%; Pred. No. 1.5e-80;
Matches 795; Conservative 0; Mismatches 540; Indels 6; Gaps 2;

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Qy      189 CCGAGCACTTGTGATCTTCATCTCCGGGAGCGTGTACGACGTACGCCCTGGCTCCCC 248
Db      233 CTGAGATCTATGATTCGCGATTCGAAGGCAAGGTCTAACAAGCTTCGATGGATTA 292
Qy      249 ACCACCGGCGGCGGACCTCCGCTTCAACCTGCGGGGAGAGAGCGCACCGAGCT 308
Db      293 CTCATCCGAGGAGGAGCAAGTGTATCTAATCTGTTGTGAAGCGTACCGAGATCT 352
Qy      309 TCGCGGCTTACCAACC--GCCCTGCGCGCGGCTCTCGCGGCTTCTTGTGAGCC 365
Db      353 TCATGCAATTTATCCCGGAACCGCTTGGCACATCTGACCATCTCTTCCACCGGTTACC 412

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QY 366 GCCTCTGACTAGCCGCTCTCCCGCGTACCGCGACTACCGCGGCTCTCGCGAGC 425
DB 413 ACATCAGAGATTCCAGTCTCCGAGTCTACCGGATTACCGTGTATGGCTGCCAGT 472
QY 426 TATCTCCGGGGGCTCTTGAAGCGTGGCCCGACCCCAAGTCCAGCTCGTCTGA 485
DB 473 TTGTAATACTGGGCTCTTGGAAAAAAGGTACGTTACTCTTACACTAGACCTTCG 532
QY 486 TGGCGGCTCTCTTACAGCCGCGCTGTACTCGTCTCGATGCGCGAGGCTTGGGCGC 545
DB 533 TCGCGCGCACTGCTCTGAGGTTCTTACGAGTCTTGGCTTGTACCTCGCTTCGCTC 592
QY 546 ACCTCTCGGGGGGGGCTCTTATGAGTCTTCTGATCCAGTCCGCGTGTAGGGGCGACG 605
DB 593 ACCMAATGCGCGCGCGCTCTCGGTCTCTCTGATCCAGCGCTTACATAGGTACG 652
QY 606 ACTCGGGCCACCAACCGCATACCGCGCTCGTCTGACCGGCTGTGACAGTCTCT 665
DB 653 ATTCTGGTCAATACGTTATCATGTCGAACAAATCTTATAAGATTGCTCAGCTTCTT 712
QY 666 CCGGGAATGCTCTACCGGCTCAGCATCGCTGTGTGAAGTGAACCAACACGAC 725
DB 713 CCGTAATCTGTCAACCGAATCTCAATCGGTGTGAATGGAATGCAATGCTCATC 772
QY 726 ACATCGCTGCAACGCGCTGACCATGACCGGACCTCCAGCACATGCGGCTCTTCCG 785
DB 773 ATCTAGCTTAAACGCTGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 832
QY 786 TCTCTCCCAAGCTGTGTGAGCAATATGTTCTTCTTCAACGAGACCGCTGCTTCG 845
DB 833 TCTTCCACCAATCTTCTCTCATGTACCTCGAGATTCAGATTCAGATTCAGATTCAG 892
QY 846 ATGCGGCTTGAATTTTTCATCAGTACCAACGATGACCTTACCGGTATGTGCA 905
DB 893 ATCAGTGGGAGATTTCTTGTACGCTATCAACCTTACTTATATCCAGTATGTGCT 952
QY 906 TCGCAGGATTAATCTTCTGCGGAGTCCGCGCTGTGTTTTCAGCGAAGAGGGTGC 965
DB 953 TTGGAGAAATCAATCTTCTTCAACGTTTCTCTTCTTCTTCCAAACGTGAAGTAC 1012
QY 966 CGCAGCGGTTGCTTGAATCGCGGGGCTGCCACATTTGCGGCTGTGTACCGCTGCG 1025
DB 1013 CAGATGCTGTTTAACTTCCGCGGAATCTTAACTTCTTCTGAGTGTGTTCCACTCTAG 1072
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DB 1073 TCTCATGTCTAACCAACTGCGCTGAGATTTCTTCTGCTTCAACAGCTTCACTCTCA 1132
QY 1086 GCGGATTTAGCAAGTCAATTTGCTGAGCACTTCTGCTGCGAGGTGATGCGGGC 1145
DB 1133 CGGCGCTTCAACATTTCAATTTCACTTAACTTTCGCTGCTGATGTCTTACGTTGCTC 1192
QY 1146 CACCAAGGCAATGACTGTGTTGAGAAGCAAGCAGGACGCTGACATCTGTGCT 1205
DB 1193 CACCAACGGTAGGACTGTGTGAGAAGCAGGAGGAGGAGCAATGATATCTTGTGA 1252
QY 1206 CTCCTTGAATGATTTGTTTCAAGGCTGCTGAGTTCCAGATTTAGACCACTGTGTTTC 1265
DB 1253 GATCATGATGATGATTTGTTTCTTGTGATTAACAGTTTCAAGCTTGAACATATTTGTTCC 1312
QY 1266 CCGGCTTACCTCGGTGCTGACCTTGGCAAGGTGACCGGCGCTGCGGACCTTTGCAAGA 1325
DB 1313 CTGCTTACCTCGGTGCTGACCTTGGCAAGGTGTTTTCGCGGTGTTCAAGCTTTGCAAGA 1372
QY 1326 AGCATGGGCTCACTTATTTGACGCAATTTGCGGTGCAAAATGTCTTACATGAAGA 1385
DB 1373 AGCATATCTTCCGTATAGAGATGTCTGTGTTTGAAGCAAAATGTCTTACATGAAGA 1432
QY 1386 CACTCAGGCTGTGCTGATTCAGGCGCAGACCGCTACAGTGTGTCTCCAGAAAT 1445
DB 1433 CTTTGAAGACAGCTTATCAAGCTAGAGCGTGGCTAATCCGCTGTT---AAGAACT 1489

QY 1446 TGGTATGGAGGCTGTGAACCCATGATTAATGGATGAAGATACGGGCTAATGCA 1505
DB 1490 TGGTTTGGAGAGCTTTGAATACATCATGCTAATGATTTTAAACAAATAATGCTT 1549
QY 1506 CTTCTGTGTTCAGCTTGTG 1526
DB 1550 TTGTTTGGGTTAATTTGATG 1570
RESULT 9
AAC3846
ID AAC3846 standard; DNA; 1650 BP.
XX
AC AAC3846;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 4526.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-AZ.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
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PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 21-MAY-1999; 99US-0135629.
PR 24-MAY-1999; 99US-0136021.
PR 25-MAY-1999; 99US-0136392.
PR 27-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142290.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145813.
PR 27-JUL-1999; 99US-0145818.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148865.
PR 13-AUG-1999; 99US-0148884.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155479.
PR 23-SEP-1999; 99US-0155439.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 25.0%; Score 441.8; DB 21; Length 1650;

Best Local Similarity 59.1%; Pred. No. 6, 6e-80; Mismatches 542; Indels 6; Gaps 2;

Matches 793; Conservative 0; DB 266 CCGAGACTGTATGATTCGCGGATTCACAGGCAAGCTCTACCAAGCTCTCCGATTGGATTAAAA 325

QY 249 ACCACCGGCGGAGACTCCCGTTCTACCCCTGGCGGGGAGAGACCCAGCAGCCT 308
 Db 326 CTATACCCGAGGCGAGACAGGTATCTCATCTCGTTGGTCAAGAGCTACCGATGCTT 385
 QY 309 TCGCCGCTACCAACC--GCCCTGGCGCGCCGCTCTCTCCGCGCTTCTTGTGGCC 365
 Db 386 TCATCGCATTTCAATCCCGGAACCGCTTGGACCATCTGACCAATCTTTCACCGGTACC 445
 QY 366 GCGTCTCTGACTACCGCTCTCCCGCGCTCCCGGCTACACCGCGCTCTCTGGCGAGC 425
 Db 446 ACATCAGAGATTTCCAAAGTCTCCGAAGTTCACCGCATACCGGTATGAGCTGCGAGT 505
 QY 426 TATCTCCGCGGCGCTTTCGAAGCGCTCGAGCCCAACCCCAAGGTACAGTCTGCTGA 485
 Db 506 TTGCTAAACTCGGCTCTTGGAAAACAAGGTACAGTTACTCTCTACACTCTAGCCTTCG 565
 QY 486 TGCCTGCTCTTCTTACGCGCGCTGACTCTGCTCTGAGATGCGCAGCGCTGGGCGC 545
 Db 566 TCGCCGCGCATGTTCTCTAGAGTTCTTACGAGTGTGTTGGCTTGACTCTCGTCTTGCTC 625
 QY 546 ACTCTCTCGGGGGGGTCTATGGCTTGTGCTGATTCAGTCCGCTGGATGGGCGACG 605
 Db 626 ACCAAATCGCGCGCGCTTCTGCTCTCTGATCCAGAGCGCTTACATAGGTACG 685
 QY 606 ACTCGGCGCACACCGCATACCGCGCATCCGCTCTGACCGCGCTGCTGAGGTGCTCT 665
 Db 686 ATTCTGTCTATTACGTTATATGTCGAACAATCTTAAACAGATTGCTCAAGCTTCTT 745
 QY 666 CCGGGAATGCTCTACCGCGCTTACAGATGCTGTGGAAAGTATACACACACGCGACC 725
 Db 746 CCGTAACTGCTACACCGGAATCTCAATCGTGTGGAATGGAATCAACAATGCTCATC 805
 QY 726 ACATGCTGTGCAACAGCTTGACCATGACCCGAGCTTCCAGACATGCGCTCTTGCCG 785
 Db 806 ATCTAGCTGTAAACAGCTGTGATTAAGATCAAGATCAACAACATCTGCTTCCCGC 865
 QY 786 TCTCCCGCAAGCTGTGTGGCAACATATGTCCTACTCTACCAACGAGACCTGGCGCTTG 845
 Db 866 TCTCCACCAAAATCTTCTCTCTCATGACCTGAGATTTCTAGATCGAATACTCAAGTTG 925
 QY 846 ATGCGCGCTGGAATTTCTTATGATGATGATGATGATGATGATGATGATGATGATG 905
 Db 926 ATCCAGTCCGAGATTTCTTATGATGATGATGATGATGATGATGATGATGATGATG 985
 QY 906 TCGCCAGGATTAATCTTCTGCGCAGTCCGCGCTGCTGCTTCTCAAGGAAAGGCTGC 965
 Db 986 TTGGAAGAAATCAATCTTCTTCAATCAACGTTTCTTCTCTCAACGTTGAAGTAC 1045
 QY 966 CCGAGCGGTTGTTGAGATGCGGCGGGTGGCACATTTCTGGGCTTGGTACCCGTTGG 1025
 Db 1046 CAATGTGTGTTTAACTTGGCGGAATCTTATGCTTCTGAGACTTGGTTCCTACTTAG 1105
 QY 1026 TGGCTTCCCTGCGGAATGTTGGAGAGAGGTGCGGTTTGTCTTTCAGCTTCAACATCT 1085
 Db 1106 TCTCATGTATACCAAACTGCGCTGAGAGATTTCTTCTGCTTCAACAGGCTTCAACG 1165
 QY 1086 GCGGAGATTGAGAGCTTCAATTTGCTGAAACCACTTCTGCTGAGAGTATGTCGGGC 1145
 Db 1166 CCGCGCTTCAACATTTCAATTCACGCTTAAACATTTGCTGTGATGCTTACGTTGCTC 1225
 QY 1146 CACCAAGGCAATGACTGTTTGAAGAGAGAGCGGAGGACGCTGAGATCTGTGCT 1205
 Db 1226 CACCCACCGTACGACTGTTGAGAGAGAGAGCGGAGGAGCAATGATATCTTGTGA 1285
 QY 1206 CTCTTGATGATGATGTTTCAAGGTGCTGAGATTCAGATTCAGATTCAGATTCAGAT 1265
 Db 1286 GATCATATCATGATGATGTTTCTTGTGATTAAGATTCAGATTCAGATTCAGATTCAGAT 1345
 QY 1266 CCGGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1325
 Db 1346 CTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1405

QY 1326 AGCATGGGCTCACTTATTCGACGCCAATTCCTGGGTCGAATGCTTACATGAGAGA 1385
 Db 1406 AGCATATATCTTCGATATAGAGATATGCTGTTGTAAGCAAAATGTTGACATTAA 1465
 QY 1386 CACTCAGGCTGTGCTGATTCAGAGCCGCTTCAAGTGTGCTCTCCGAAGAATT 1445
 Db 1466 CTTTGAAGACAGAGCTTATCAAGCTAGAGAGCGTGTATCCGGTGT--AAAGACT 1522
 QY 1446 TGGTATGGAGGCTGTGAACACCATGATTAATGGATGAAGATACGGGCTTAATG 1505
 Db 1523 TGGTTGGAGAGCTTTGAATTAATCAATGCTAATGATTTTAAATCAAAAATATGCTT 1582
 QY 1506 CTCTGTGATTCAGCTTGGTG 1526
 Db 1583 TTGTTGGGTTAATTGATG 1603

RESULT 10
 AB212753
 ID AB212753 standard; DNA; 1350 BP.
 XX
 AC AB212753;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN MO20021655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001MO-US26685.
 XX
 PR 24-AUG-2000; 2000US-227866P.
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 XX
 PS Claim 6; SEQ ID NO 558; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 SQ Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 other;
 Query Match 24.9%; Score 439.2; DB 24; Length 1350;
 Best Local Similarity 59.8%; Pred. No. 2.1e-79;

CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence encodes the *Brassica napus* sphingolipid
CC desaturase sld1 protein described in the method of the invention.

XX Sequence 1594 BP; 382 A; 369 C; 375 G; 468 T; 0 other;

Query Match 24.8%; Score 437; DB 21; Length 1594;
Best Local Similarity 59.7%; Pred. No. 6.1e-79;
Matches 772; Conservative 0; Mismatches 515; Indels 6; Gaps 2;

189 CCGACGACCTCTGATCTCCATCTCCGCGACGTGACGACGCTCAGCCCTGCTCCCC 248
112 CCGGAGTTATGATTTCAATCCAGGAAAGTCTAGAGCTCTCCCATGCGGTCAAT 171
249 ACCACCGGCGGCGACCTCCGCTTCTACCTCGCGGCGAGAGCCACCGACGCT 308
172 CCGATCCGCGGCGGCGAGGACGACGCTTAAACCTCGCGGCTCAAGAGCTACCGACGCT 231
309 TCGCGCGCTACGACCC--GCGCTCGCGGCGCGCTCCCGCGCTTCTGCTGCGC 365
232 TCACTGCTTACCAATCCCGGACGATGCGGACCTCGAAAACCTTCACACGCGCTACC 291
366 GCGCTCTGACGACGCTCCCGCGCTCCCGGACGACGCTCCCGCGCTCTGCGGACG 425
292 AGCTGAAGAGCAACAGCTGCTCGAGCTGCGGCTAGCTACGCTTGAAGCGCGGAGT 351
426 TATCTCCGCGGCGCTCTTGAAGCGCTCGGCGGCGGCGGCGGCGGCGGCGGCTCTGA 485
352 TTTCCAAACGCGGACTCTTGTGATTAATAAAGTCAAGTCTTTACACGCTACGCGG 411
486 TGGCGGCTCTCTTCTACGCGCGCGCTGACCTGCTCCGCGGACGCGCGCTGCGGCG 545
412 TCGCTCCGACGCTCGCGGCGGCTGTAAGCTGTTGATGATGACAGATATGCGGCC 471
546 ACCTCTCTCGCGGCGGCTCTGATGCTTCTGATGATGATGATGATGATGATGATGATG 605
472 ACTTATATTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 531
606 ACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 665
532 ACTCTGCTATTAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCTGT 591
666 CCGGGAAGCTGCTCCAGCGGCTGACGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
592 CTGCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 651
726 ACATGCGCTGCAACAGCTGCAACAGCTGCAACAGCTGCAACAGCTGCAACAGCTGCTG 785
652 ATATCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711
786 TCTCCCGCAAGCTGTTGCGGACATATGCTCTACTTCTTCAACAAGGAGCGCTGCTG 845
712 TCTCAACAAGTCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCTG 771
846 ATGCGCGCTGCAACAGCTGCAACAGCTGCAACAGCTGCAACAGCTGCAACAGCTGCTG 905
772 ATCACTAGTCAATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 831
906 TCGCGGAGATTAATCTTCTGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 965
832 TGGGAGAGATCAATCTTCTTATCCAAAGTACTTCTTCTGATCTTCTGAGAGCTTAGCT 891
966 CCGAGCGGTTGCTGATGATGCGGCGGCTGCGCAATCTGCGGCTTGTGCTGCTGCTG 1025
892 CTGATGAGGCTTGAACATAGCTGCGGATCTTGTCTTCTGAGAGCTGCTTCTTCTT 951
1026 TGGCTTCTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1085
952 TATCTCTCTTCAACAACTGCGCAAGAGAGATCACTTCTTCTTCTTCTTCTTCTTCT 1011
1086 GCGGAGTTCAGACGTCATCTGCTGTAACAACATCTTCTGCTGCGAGCTGATGCTGCG 1145

DB 1012 CCGGAGTTCAGACGCTTCAAGTCTGTTAAACCATTTTGGCGAGATGTTTACACCGCTC 1071
QY 1146 CACCAAGGCGATGATGCTGTTGAGAACAGACGCGGACGCTGCAATCTGCTGCT 1205
DB 1072 CCGCTAATGGAACGATGCTGTTGAGAACGACCTGCTGATGATATGCTGTA 1131
QY 1206 CTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1265
DB 1132 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1191
QY 1266 CCGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1325
DB 1192 CTAGGCTACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1251
QY 1326 AGATGAGCTCACTTATTTCTGACGACCAATCTTGGGCTGCAATGCTTACATGAAGA 1385
DB 1252 AGCATATCTACCGTATGAGAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
QY 1386 CACTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445
DB 1312 CTCTGAGGAAGGCGGCTTCAAGCTAG--AGATGACTAATCTCTGCTTGAAGATT 1368
QY 1446 TGGTATGAGAGCTGTAACACCATGATTA 1478
DB 1369 TGGTATGAGAGCTGTAATCTGATGCTGTA 1401

RESULT 12
AAZ44851
ID AAZ44851 standard; DNA; 1606 BP.
XX
AC AAZ44851;
XX
DT 27-APR-2000 (first entry)
XX
DE Sphingolipid desaturase DNA.
XX
KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 88..1464
FT /tag= a
FT /product= "sphingolipid desaturase"
XX
FN DE19828850-A1.
XX
XX 30-DEC-1999.
XX
PF 27-JUN-1998; 98DE-1028850.
XX
PR 27-JUN-1998; 98DE-1028850.
XX
PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
PI Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
XX MPI; 2000-127549/12.
XX
XX P-PSDB; AAY51348.
XX
XX New sphingolipid desaturase that selectively introduces double bond
XX into sphingolipid and capnoids -
XX
XX disclosure; Fig 15; 62pp; German.
XX
XX This invention describes a novel sphingolipid desaturase that selectively
XX introduces a double bond into the sphingobase of the ceramide residue of

CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base c18/18:1 ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size, growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence encodes a sphingolipid desaturase protein
 CC described in the method of the invention.

XX Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 other;

Query Match 21.0%; Score 370.2; DB 21; Length 1606;

Best Local Similarity 56.0%; Pred. No. 1.9e-65;

Matches 743; Conservative 0; Mismatches 578; Indels 6; Gaps 2;

155 ATCTCTCCAGAGAGCTCCGCGCTCAAGCTTCGCGCAGACCTGTGATCTTCATCTCC 214
 142 ATAAACATCAAAAGAGTTAAAGACATTAACAACCTTAAGACCTTGGATCTCAATTTTG 201
 215 GGGAGAGTGTAGACGTCAAGCCTCGCTCCCGACACCCGGGGCGGACCTCCCGCTT 274
 202 GGGAAAGTTTACACCTTACAGATGGGCTAAAGACATTCGGGTGGCGATGCCCGTTG 261
 275 CTCACCTCGGCGGGGAGAGCGCCACGACGCTTCGCGCCTTACACCGCGCTCGGCG 334
 262 ATTAACTCGCGGGCGAGAGTGTATGACGATTTATGCAATTCATCCGCTACTGGG 321
 335 CGCGCGCTCTCT--CGCGCGCTTCTTGTGGCGCGCTCTGTACTAGCGCGCTCTCC 391
 322 TGGAGACATCTAGACAACTATTCACGGGTATCACTTAAAGATTACAGAGTTCTGAC 381
 392 GGGTCCCGGACATACCGCGCGCTCTCGCGGACATCTCTCGCGGGCGCTTTGCAAGC 451
 382 ATTTCTAGAGACTACCGGAAATCTCGCTTACAGATTGTGCAAAAGCGGTATGTTGAG 441
 452 GTGCGCCCAACCCCAAGGCTCCAGCTCGTCTGATGGCGCTCTTCTACGCGCGCTG 511
 442 AAAGGTCAAGGTGTATTTACTCATCTTGTTCGTCTGCTACTGCTTCGCGCTGTG 501
 512 TACCTTCGCTCGCATGCGCCAGCGCGCTCGGCGCACCTCTCGCGGGGCTCTCATGGC 571
 502 TATGGGTGTATATTCGGAAGCTTCTGATTCATATGCTTTTGGGGCGCATATTGGGA 561
 572 TTGCTGTGATCCAGTCCGGCTGATGGGCGCACGATCGGGCCACACCGCATACCGGC 631
 562 TTAGCATGTGATCAAAATTCCTATTTGGGTCAAGAGCGGTCTATTCAAATGATGGG 621
 632 CATCCGCTCTCGGACCGCGCTGCGAGTCTCTCGGGAACTGCTCAACCGCGCTCAGC 691
 622 ACCCGGGGTGGAACAAGTTTGGCGGAATTTATGGGAATTTATTAACCGGAATTAAGC 681
 692 ATGCGCTGTGTGAAAGTGTAAACAACAACGACACCATGCGCTGCAACAGCTGTGACAT 751
 682 ATGCGGTGTGTGAAATGTAGAGCATTAACGACATCATGCTGTGTAAAGTCTGTATAT 741
 752 GACCGGACCTCGAGACATGCGCTCTTGGCGCTCTCCCGCAAGTGTTCGGCAATTA 811
 742 GATCCGATCTTCAGCATTTACGATTTAGCGGTCTTTCCAAGCTTTTAACTCAATA 801
 812 TGGTCTACTTCTTACCAACGAGACCTGGGCTGTGATGGCGCGCTCGAAATCTTCAATCAGC 871
 802 ACTTCTGTTTCTTATGAGAGACAGTTGAACCTTGAACCGGTGACCGGTCTTCTGAGAC 861
 872 TACGACACTGTGACCTTCTACCGGTATGTGATCGCGAGATAATCTTCTCGCGCAG 931
 862 TACGACACTTACTTATTAATTAACCGGATCATGTGTGTGGCGGGTCAACCTCTATTAACA 921

932 TCCGCTCTGTTGTTCTACAGAGAGAGGNGCCGACGGTGTGATTCGCGGG 991
 922 ACATCTCTGTTGTTCTTCAAAAGAAAGATTCGCGACAGAGTTTAACTACTCGGA 981
 992 GTCCGACATCTTGGGCTTGGTACCGGTGCTGTGAGCTTCCTCGGAATGTGGAG 1051
 982 ACCTAATCTCTGACCGGTGTTCCGTACTGTTTCTCGCTTACCGAATGGCCCGGA 1041
 1052 AGGTCGGTGTGTTGCTTTCAGCTTACACATTCGCGGATTCAGACGTCCAAATTCGC 1111
 1042 CGCGGGGTGTTGTTGTTAGCTTCTGTGTACGGGTATACACATTCAGTTTACA 1101
 1112 CTGACACCTCTGTCGACGATGTATGCGGGCCACCCCAAGGGAATGATGTTGAG 1171
 1102 CTGAACCATTTTCTTGGGAGTGTATGATGCGGCCCGCCAAAGAGACATTTGTCAG 1161
 1172 AAGCAGACGGAGGACGCTGACATCTGTGCTCTCTTGTGATGATTTGTCACGGT 1231
 1162 AAACAAACGGGTGGGACCATGATATCGGTGTTCTTGTGATGATTTGTTTCGGA 1221
 1232 GGCCTGCACTTCCAGATTGAGACCATCTGTTTCCCGCTACCTCGGTCCACTTCCG 1291
 1222 GGTTCAGATTTCACCTTGAGCACCATTGTTTCTTACGTTGCGCAGGTGTCACTTGA 1281
 1292 AAGTTGACCGGCGCGCTCGGACCTTTGCAAGAGCANGGCTCACTTATTCGACGC 1351
 1282 TCGATTTCTCTATATGTAGAGAACTGTGCAAGAAATTAATTAATTAATGATTTG 1341
 1352 ACATCTGCGGGGTCAAAATGTGCTTACATGAGAAGACATCAGGGCTGTGATTCAGGCG 1411
 1342 TCGTTTATGATGGAATGTAAACGACCTTGAAGAGCTTGAAGACAGCGGCTTACAGGA 1401
 1412 AGGACCGTACAAAGTGTGTGCTTCCGAAGATTTGTATGAGGAGCTGTGAACCCAT 1471
 1402 CGTGAACCTTACGA--ACCGCGCCCAAGAAATTTAGCTTGGAAAGCTTTCAACACCAT 1458
 1472 GGATTA 1478
 1459 GGTGAA 1465

RESULT 13

AAV34398
 ID AAV34398 standard; DNA; 1684 BP.

AAV34398;

02-MAR-1999 (first entry)

Borage delta-6 desaturase gene.

Upstream region; regulatory region; sunflower; albumin; seed; expression;

lipid metabolism; delta-6 desaturase; transgenic plant; ds.

Borage officialis.

OS
 FH Key Location/Qualifiers
 FT CDS 43..1389
 FT /*tag= a
 FT /product= "delta-6 desaturase"
 FT primer_bind complement (616..632)
 FT /*tag= b
 FT primer_bind 1165..1181
 FT /*tag= c

MO9845460-A1.

15-OCT-1998.

09-APR-1998; 98MO-US07178.

09-APR-1997; 97US-0831570.

XX (RHON) RHONE-POULENC AGROCHIMIE.
 XX Beremand PD, Nunberg AN, Thomas TL;
 XX WPI; 1998-583201/49.
 XX P-PSDB; AAM67471.
 XX
 PT New sunflower albumin 5' regulatory region - useful for directing
 altered lipid metabolism in plant seeds
 PS Example 2; Fig 1; 38p; English.
 XX This sequence is the gene encoding the borage (Borago officinalis)
 CC delta-6 desaturase enzyme. The lipid metabolism gene is an example
 CC of a heterologous gene which can be expressed at high levels in a
 CC seed-specific manner in transgenic plants, when placed under control
 CC of the sunflower albumin gene 5' regulatory region (AAV34397).
 XX
 SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;
 Query Match 20.7%; Score 365.4; DB 19; Length 1684;
 Best Local Similarity 55.8%; Pred. No. 1.8e-64;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCCGCGCTCAAGCTTCGCGCGAGACCTCTGATCTCATCTCC 214
 DB 67 ATTACCTCAGATGATGATCTCAAGAACACGATTAACCCGAGATCTATGATCTGATTCAA 126
 QY 215 GGGAGCGTGTAGACGCTGAGCGCTGCTCCCAACCCGCGCGGAGACTCCGCTT 274
 DB 127 GGGAAAGCTATGATGTTTGGATTTGGATGAAAGACCATCAGATGAGCTTCCCTTG 186
 QY 275 CTACCTCTGGCGGGGAGAGAGCGACCGAGCTTGGCGGCTTACCAACCGGCTTGGCG 334
 DB 187 AAGAGCTTGTCTGTCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
 QY 335 CGCGCGCTCTCGCGCGCTCTCTGTTG---CGGCTCTGATGAGCGCTCTCGCGC 391
 DB 247 TGGAAAGATTTGATGATGATTTTCTACGAGGATTTATTTAAAGTTTACTGTTTCTGAG 306
 QY 392 GCGTCCGCGAGTACCGCGCGCTCTCTGCGAGCTATCTCTCGCGGCTCTTTCGAGCGC 451
 DB 307 GTTCTTAAGATTAATGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 366
 QY 452 GTGCGCGCGCGCGCGCGCGCTCTCTGATGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 511
 DB 367 AAGAGCTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
 QY 512 TACCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 571
 DB 427 TATGGGCTTTGTTTGTGTGAGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 486
 QY 572 TTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 631
 DB 487 TTTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
 QY 632 CATCCGCTCTGAGAGCGCTGTGAGAGCTCTCTCGGGAATGCTCTACCGGCTCTGAGC 691
 DB 547 GATTCAAGGCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
 QY 692 ATGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
 DB 607 ATTGTTGTTGAGAAATGAGAACTATGATGATGATGATGATGATGATGATGATGATGATGAT 666
 QY 752 GACCCGAGCTCTGAGAGCTGCTTGTGCGCTCTCTCCCAAGCTGTTCGCAACATA 811
 DB 667 GACCTGATTTACATATATATACATCTCTGTGTGTGTCTTCAAGTTTGTGTGTGTGTGTGT 726
 QY 812 TGGTCTACTTGTACCAAGAGAGCTTGGCTGTGATGAGCGCTCGGAATTTCTTCTATGAGC 871
 DB 727 ACCTCTCATTTTATGAGAAAGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 786

QY 872 TACGACACTGAGACCTTCTACCCGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 931
 DB 787 TATCAACATTTGAGACATTTTACCTTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 846
 QY 932 TCCGCGCTGT 991
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 QY 992 GTGCGCAATTCCTGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
 DB 907 TGCCTAGT 966
 QY 1052 AGGTCGCTGT 1111
 DB 967 AGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
 QY 1112 CTGACCACTTCTGT 1171
 DB 1027 TTGAAACACTTCTGT 1086
 QY 1172 AAGCAACGAG 1231
 DB 1087 AAGCAACGAG 1146
 QY 1232 GGCCTGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291
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 QY 1352 ACAATCTGGGAG 1411
 DB 1267 TCTTTCTCAAGGAG 1326
 QY 1412 AGGACCGCTACAG 1471
 DB 1327 AGG---GATTTATCAAG 1383
 QY 1472 GGATTA 1478
 DB 1384 GGTTAA 1390

RESULT 14
 AAX24917
 ID AAX24917 standard; cDNA; 1684 BP.
 XX
 AC AAX24917;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Borage delta-6 desaturase cDNA.
 XX
 KW Delta-6 desaturase; borage; oleosin; Afs21; promoter;
 KW transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 KW gamma-linolenic acid; octadecatrienoic acid; ds.
 XX
 OS Borago officinalis.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..1389
 FT /tag= a
 XX
 PN W0845461-A1.
 XX
 PD 15-OCT-1998.
 XX
 XX 09-APR-1998; 98MO-US07179.
 PF
 PR 09-APR-1997; 97US-0831575.
 XX

XX MO9621022-A2.
 XX 11-JUL-1996.
 XX 28-DEC-1995; 95WO-1B01167.
 XX 30-DEC-1994; 94US-0366779.
 XX (RHON) RHONE POULENC AGROCHIMIE.
 XX Freysinet Gl., Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 XX WPI; 1996-333997/33.
 XX P-PSDB; AAR98455.
 XX Transgenic plants comprising the borage delta-6-desaturase gene -
 XX show increased production of gamma linolenic acid and having
 XX increased resistance to chilling
 XX Claim 2; Page 51-52; 75pp; English.
 XX A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455),
 XX which catalyzes the conversion of linoleic acid to gamma-linolenic
 XX acid (GLA). It was isolated from a borage membrane-bound polysomal
 XX library using probes based on abundantly expressed seed storage
 XX protein cDNAs and with an isolated partial cDNA clone. The gene
 XX can be incorporated into a vector, pref. incorporating a
 XX tissue-specific promoter, for the expression of delta-6-desaturase
 XX in transgenic plants, esp. sunflower, soybean, maize, tobacco,
 XX peanut, carrot or oilseed rape, resulting in increased GLA prodn.
 XX Alteration of plant lipids may also lead to improved chilling
 XX resistance.

SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

Query Match 20.7%; Score 365.4; DB 17; Length 1685;

Best Local Similarity 55.8%; Pred. No. 1.8e-64; Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCCGCTGACGCTTCGCGCGAGACCTTGATCTGCATCTCC 214
 DB 68 ATTACCTCAGATGAACCTCAAGAACACAGATTAACCCGAGATCATGATCTGCATCAA 127
 QY 215 GGGGAGCTGACACGACGACGCTGCTCCCGACACCGCGCGGCGACCTCCGCTT 274
 DB 128 GGGAAAGCTATGATGTTTGGATGGGTGAAGAACCATCCAGGTGCACTTTCCTTG 187
 QY 275 CTCACCTGAGCGGGGAGAGCGCACCGACCTTCGCGCTACACCGCGCTCGGGG 334
 DB 188 AAGAGCTTCTGTGTCAAGAGTACGATGATCTTGTGATCTTCCATCTGCTCTACA 247
 QY 335 CGCGCGCTCTCGCGCGCTTCTTGTTGG---CGGCTCTGATCAAGCGCTTCCCG 391
 DB 248 TGAAGAATCTTGATTAAGTTTTCACGTGGGATTAATCTTAAGATTAAGTCTTGAG 307
 QY 392 GCGTCCGCGACATACCGCGCGCTCTCGCGACGATATCTCCGCGCGCTCTGAAAGC 451
 DB 308 GTTCTTAAAGATTATAGAAAGCTTGTGTGAAGTTTCTTAAATAGGATTTGATGACAA 367
 QY 452 GTGCGCGCGCGCGCGCGCGCTGATGCTGATGCGCGCTCTCTTACGCGCGCTG 511
 DB 368 AAGAGCTATATATATGTTTGAACCTTGTGCTTATAGCAATGCTGTTGCTATGAGTGT 427
 QY 512 TACCTGCTCTCGATGCGCGCGCGCTGAGCGACCTCTCGCGGGGCTCATTTGGC 571
 DB 428 TATGGGCTTTTGTGTTGAGGGGTTTGGTACATTTGTTCTGCGGTGTTGATGGGG 487
 QY 572 TTGCTGATCCAGTCCGCGTGGATGGCGACGATCGGGCGCACCGGATCACCGGC 631
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 QY 632 CATCCGGTCTCTGACCGCGCTGTCAGAGTCTCTCGGGAAGTCCCTCACCGGCTCAGC 691

DB 548 GATTCAAGGCTTATATAGTTTATGGTATTTTGTGCAAAATGTCTTCAGAAATAGT 607
 QY 692 ATGCGCTGTGTGAAGTGAACCAACACAGACCAATGCGCTGCAAGCGCTGAGCAT 751
 DB 608 ATTGTTGGTGGAAAGAAAGCAATTAATGACATCAATGCTGTATATGCTGTATAT 667
 QY 752 GACCGGACCTCCAGACATGCGCGCTTGTCCGCTCCCGCAAGCTGTTCGCAACATA 811
 DB 668 GACCTGATTTACAAATATATACCATCTTGTGTGTCTTCCAAAGTTTTTGGTTCACTC 727
 QY 812 TGGTCTACTTTCACCAAGGACCTGCGGTGATGCGCGCTGCAATTTCTTCATGAC 871
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 QY 872 TACCAAGCTGACCTTTCACCGGTATATGATGATGCCAGATTAATCTTCGCGGAG 931
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 QY 1112 CTGAACCACTTCGTGCGAGCGTATGTCGGGCGCACCGCAAGGCAATGACTGTTGAG 1171
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 QY 1172 AAGCAGACGAGAGGACGCTGACATCTGTGCTCTCTTGAATGATTTGTTCAAGGT 1231
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 QY 1412 AGCAGCGTACAAAGTGTGTGCTCCGAAAGATTTGATGAGAGCTGTGAACACCCAT 1471
 DB 1328 AGG---GATATTAACCAAGCGCTCCGAAAGATTTGTATGGAAAGCTCTTCACTCAT 1384
 QY 1472 GATATAA 1478
 DB 1385 GGTATAA 1391

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Searched: 22781392 seqs, 12152238056 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	509.4	28.9	785	14	CB381262
8	495.4	28.1	497	29	BZ730988
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10	486	27.6	497	14	CD484487
11	462.8	26.2	489	28	BH785221
12	462.6	25.2	691	28	BH465389
13	456.8	25.9	562	13	CD230348
14	455.8	25.8	679	13	BQ788546
15	441	25.0	575	9	AL691910
16	433.4	24.6	665	14	CA502522
17	432	24.5	488	12	BM323877
18	429.2	24.3	528	18	BI075599
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20	417	23.6	465	28	BH230086
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22	410.6	23.3	465	28	BH229656
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29	382.2	21.7	640	12	BU230767
30	381.8	21.6	554	14	CA501548
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35	374.8	21.2	573	6	AL810658
36	372.6	21.1	576	29	CC344270
37	370.2	21.0	429	28	BH229798
38	370.2	21.0	718	14	CD453035
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43	347.8	19.7	521	12	BQ464683
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ALIGNMENTS

RESULT 1
LOCUS AY103762 1764 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0087385 mRNA sequence.
ACCESSION AY103762
VERSION AY103762.1 GI:21206840
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Hukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
1 (bases 1 to 1764)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitte, M.S., Arthur, L.W., Hanfey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
2 (bases 1 to 1764)
Coe, E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones these are publicly available from ZmDB and may be found by BL searching at MSU, maizemap.org/; ZmDB, www.zmdb.iastate.edu/; www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

Source

Location/Qualifiers

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ORIGIN

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PostgreSQL	100.0%	Score 1764;	DB 11;	Length 1764;

Bebe Local similarly 100.0%; Pred. No. 2.2E-291;

Matches 1/64; conservative 0; mismatches 0; indels 0; gaps 0;

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QY	301	CGAGCGCTTCGCGCGCTACCAACCGGCTTGGCGGCGCGCTCTCTCGCGCTTCTTGCT	360
Db	301	CGAGCGCTTCGCGCGCTACCAACCGGCTTGGCGGCGCGCTCTCTCGCGCTTCTTGCT	360
QY	361	TGGCGGCGCTCTGACTAGGCGGTATGCCCGGCGGTCCGCGCATACCGCGCGCTCTGCG	420
Db	361	TGGCGGCGCTCTGACTAGGCGGTATGCCCGGCGGTCCGCGCATACCGCGCGCTCTGCG	420
QY	421	GCACTATCTCTCGCGGGGCTTCTTGAAAGCGGTGGGCCCAACCCCAAGATCAGCTGCT	480
Db	421	GCACTATCTCTCGCGGGGCTTCTTGAAAGCGGTGGGCCCAACCCCAAGATCAGCTGCT	480
QY	481	CTGATGGCGGTCTCTTCTTACGCGCGGCTGTACTCTGCTCTGCATGCGCCAGGCGCTG	540
Db	481	CTGATGGCGGTCTCTCTTCTTACGCGCGGCTGTACTCTGCTCTGCATGCGCCAGGCGCTG	540
QY	541	GGCGCACTCTCGCGGGGGGTCTTATGGCTTGTCTTGATTCAGTCCGGCTGATGGGG	600
Db	541	GGCGCACTCTCTCGCGGGGGGTCTTATGGCTTGTCTTGATTCAGTCCGGCTGATGGGG	600
QY	601	CCAGAGCTCGGGGACCAACCGCATACCGGCGATCGGTCCTCGACCGCGTGTGCAGGT	660
Db	601	CCAGAGCTCGGGGACCAACCGCATACCGGCGCATCGGTCCTCGACCGCGTGTGCAGGT	660
QY	661	GCTTTCGGGAAATGCTCTCACCGGCGCTCAGATCGCTGTGTGAAGTGAACCAACAAC	720
Db	661	GCTTTCGGGAAATGCTCTCACCGGCGCTCAGATCGCTGTGTGAAGTGAACCAACAAC	720
QY	721	GCACCAATGCGCTGCAACAGCCTTGACATGACCGGACCTTCAGACATATGCCGCTCTT	780

[illegible]

RESULT 2

BZ730996/c 825 bp DNA linear GSS 03-MAR-2003
 LOCUS OGEDJ377M ZM 0.7-1.5 KB Zea mays genomic clone ZMMBma237H02,
 DEFINITION genomic survey sequence.
 ACCESSION BZ730996
 VERSION BZ730996.1 GI:28704535
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 825)
 White, C.A., Quackenbush, J., Van Aken, S., Utecher, T., Resnick
 A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek
 R.W., Numborg, A., Robbins, D. and Lakey, N.
 R.W., Numborg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 TITLE Unpublished
 JOURNAL Other GSSs: OGEDJ377C
 COMMENT Contact: Cathy White, Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitec@maizegenomics.org
 Seq primer: TR
 Class: sheared ends.
 FEATURES
 source Location/Qualifiers
 1..825
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBma237H02"
 /clone_1lb="ZM 0.7-1.5 KB"
 /note="Vector: pBESK-; Site 1: HindIII; 0.7-1.5 kb
 methylation filtered genomic DNA library"
 BASE COUNT 245 a 221 c 191 g 168 t
 ORIGIN
 Query Match 37.6%; Score 662.4; DB 29; Length 825;
 Best Local Similarity 98.5%; Pred. No. 1.4e-105;
 Matches 701; Conservative 0; Mismatches 6; Indels 5; Gaps 3;
 1041 ATTGGGGAGAGGGGCGGCTTTGCTTTCAGCTTCACATTCGCGGATTCAGC 1099
 813 AATGGGGAGAGGGGCGGCTTTGCTTTCAGCTTCACATTCGCGGATTCAGC 754
 1100 GTCAATTGCTGCTGAACCACT--TCTGCTCGACGTATGTGCGGCGACCAAGG- 1155
 753 GTCCAAATTTGCTGCTGAACCACTTTCTTCTCCGACGTATGTGCGGCGACCAAGG- 694
 1156 CAATGACTGCTTTGAGAACAGACGCGCAGGACGCTCGACATCTCTGCTCTTGGAT 1215
 693 CAATGACTGCTTTGAGAACAGACGCGCAGGACGCTCGACATCTCTGCTCTTGGAT 634
 1216 GATTTGCTTCCAGCGTGGCTTCAAGTTGAGCAATCTGTTTCCCGGCTTACC 1275
 633 GATTTGCTTCCAGCGTGGCTTCAAGTTGAGCAATCTGTTTCCCGGCTTACC 574
 1276 TCGGTGCGCACTTTCGCAAGTTGACCGGCGGCTGCGGCACTTTGCAAGACATGGGCT 1335
 573 TCGGTGCGCACTTTCGCAAGTTGACCGGCGGCTGCGGCACTTTGCAAGACATGGGCT 514
 1336 CACTAATTTGCAAGCACAATTTGCGGCTCAATGCTTACATGAGAACATCAAGGCG 1395
 513 CACTAATTTGCAAGCACAATTTGCGGCTCAATGCTTACATGAGAACATCAAGGCG 454
 1396 TCGTGCATTCGAGCGGACGCGCTCAAGTGTGTCTCCGAGAAATTTGGTATGGGA 1455
 453 TCGTGCATTCGAGCGGACGCGCTCAAGTGTGTCTCCGAGAAATTTGGTATGGGA 394
 1456 GGCTGTGAACACCATGATTAATGGAGTGAAGATACGGGCTAATGGCAACTTCTGGTCT 1515

|||||
 393 GGCTGTGAACACCCATGATTAATGGAGTGAACGCGGCTAATGCGCAACTTCTGGTCT 334
 1516 TCAGCTTGCTGCGCCATGATGATGCTGATGCTGCTTCACTTTAGATATGATGCT 1575
 333 TCAGCTTGCTGCGCCATGATGATGCTGATGCTGCTTCACTTTAGATATGATGCT 274
 1576 TCAACCTGCTGAGTCAGGTTGGAATTTTCCGTTGACAGTGGCTGCTATCCAGTTGG 1635
 273 TCAACCTGCTGAGTCAGGTTGGAATTTTCCGTTGACAGTGGCTGCTATCCAGTTGG 214
 1636 AGAGTTCACTGCTTAATGATGCTGCTGTTTACAGGAGTGTCTCTCCATACAGGTA 1695
 213 AGAGTTCACTGCTTAATGATGCTGCTGTTTACAGGAGTGTCTCTCCATACAGGTA 154
 1696 ACTATATGATGATGATCTCTGCTTAAATTCATGAACACTGTTTCAAGTTA 1747
 153 ACTATATGATGATGATCTCTGCTTAAATTCATGAACACTGTTTCAAGTTA 102
 RESULT 3
 CD463185 744 bp mRNA linear EST 04-JUN-2003
 LOCUS ETH1_42_C07_01_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
 DEFINITION clone ETH1_42_C07_A002 5', mRNA sequence.
 ACCESSION CD463185
 VERSION CD463185.1 GI:31384453
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 744)
 Cordomier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein
 R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chua Tan
 N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O.,
 Baerman, A. and Pratt, L.H.
 An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
 (ACC)-treated seedlings
 TITLE Unpublished
 JOURNAL Other ESTs: ETH1_42_C07_01_A002
 COMMENT Contact: Cordomier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yuraka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University,
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seq primer: Sugs (CTTGTGCTTAAAGCTGCG).
 FEATURES
 source Location/Qualifiers
 1..744
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultiVar="BTK623"
 /db_xref="taxon:4558"
 /clone="ETH1_42_C07_A002"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_1lb="Ethylene-treated seedlings"
 /note="Vector: pME18S-PL3; Site 1: XhoI; Site 2: XhoI; The
 library was prepared from polyA+ RNA from seedlings grown
 in hydroponic culture. At 8 days of age, medium was
 supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
 acid (ACC) to induce endogenous ethylene (ETH) production.
 Roots and shoots were harvested after 27 and 72 hr and

material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pHE18S-PL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

BASE COUNT 102 a 325 c 201 g 116 t

Query Match 33.4%; Score 588.8; DB 14; Length 744;
Best Local Similarity 91.6%; Pred. No. 9,4e-93;
Matches 636; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

71 CCAGAGCCAGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCCCGC-----124
4 CCCCCTCGGGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCCCGCAGAGGA 63
125 GACGCGCGCGCGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCTCCAGAGAGCTCCGCGCTCAAGCT 184
64 GACGCGCGCGCGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCTCCAGAGAGCTCCGCGCGCAAGCG 123
185 TCGCGCGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCTCCAGAGAGCTCCGCGCTCAAGCT 244
124 TCGCGCGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCTCCAGAGAGCTCCGCGCTCAAGCT 183
245 CCCCACACCGCGCGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 304
184 CCCCACACCGCGCGCGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243
305 GCGCTTCG 364
244 GCGCTTCG 303
365 GCGCTTCG 424
304 GCGCTTCG 363
425 CTAATCTCG 484
364 CTAATCTCG 423
485 ATGCG 544
424 ATGCG 483
545 CACTCTCTCG 604
484 CACTCTCTCG 543
605 GACTCG 664
544 GACTCG 603
665 TCCGCGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
604 TCCGCGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 663
725 CACTCTCTCG 758
664 CACTCTCTCG 697

RESULT 4
BI075898 634 bp mRNA linear EST 20-JUN-2001
LOCUS BI075898
DEFINITION IPI 22.F11.b1 A002 Immature panicle 1 (IPI) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BI075898
VERSION BI075898.1 GI:14514555
KEYWORDS EST,
Sorghum bicolor (sorghum)
SOURCE Sorghum bicolor
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt
"L.H." database from Sorghum: developing preanthesis panicles
Unpublished
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions
below phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with POLYTAIL or 17
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 598
POLYA=No.

FEATURES
source
Location/Qualifiers
1..634
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature panicle 1 (IPI)"
/note="Organ: Developing preanthesis panicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

BASE COUNT 71 a 297 c 171 g 95 t

Query Match 31.7%; Score 559.4; DB 12; Length 634;
Best Local Similarity 94.1%; Pred. No. 1.3e-87;
Matches 594; Conservative 0; Mismatches 31; Indels 6; Gaps 1;

72 CGAGCCAGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCCCGC-----G 125
4 CGAGCGCGCGCGCGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 63
126 ACG 185
64 ACG 123
186 CCGCGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245
124 CCGCGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 183
246 CCGAGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305
184 CCGAGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243
306 CCGAGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 365
244 CCGAGAGAGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303
366 GCGCTCTACTAGAGCGCGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 425
304 GCGCTCTACTAGAGCGCGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 363
426 TATCTCTCGCGCGCGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 485
364 TATCTCTCGCGCGCGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 423
486 TGGCGCTCTCTTTTACGCGCGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCG 545
424 TGGCGCTCTCTTTTACGCGCGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCG 483
546 ACTCTCTCGCGCGCGCTCTGTGATGCAATGCCGCTCTGTGATGCAATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 605

|||||
 Db 484 ACCCTCGGGGGGGGCTCATCGGCTTGTGATTCAGTCCGGCTGATGGGACAG 543
 QY 606 ACTCGGGGCCACACCGGCATACCGGCTCTCTCGACCGCGTCTGTCAGAGTCTCT 665
 Db 544 ACTCGGGGCCACACCGGCATACCGGCTCTCTCGACCGCGTCTGTCAGAGTCTCT 603
 QY 666 CCGGGAAGTCTCTACCGGCTCTGATGAGTGC 696
 Db 604 CCGGCAACTGCTCTACCGGCTCTGATGAGTGC 634

RESULT 5
 BM322472 609 bp mRNA linear EST 04-JAN-2002
 LOCUS PIC1_5_C04.b1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
 DEFINITION bicolor cDNA, mRNA sequence.
 ACCESSION BM322472
 VERSION BM322472.1 GI:18059465
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 609)
 Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R.,
 Sudman,M. and Pratt,L.H.
 An EST database from Sorghum: plants infected with a compatible
 pathogen
 Unpublished
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@arches.uga.edu

SEQUENCES HAVE BEEN TRIMMED TO EXCLUDE POLYA, VECTOR, AND REGIONS
 BELOW PHRED QUALITY 16. THE THRESHOLD FOR HIGHEST QUALITY SEQUENCE
 IS 20. THREE-PRIME SEQUENCES, WHICH ARE OBTAINED WITH POLYT/MIX OR
 T7 SEQUENCING PRIMER, ARE PRESENTED AS THE REVERSE COMPLEMENT.
 Seq primer: JEN REV
 High quality sequence stop: 595
 POLYA=No.

FEATURES

source

1. 609
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /tissue_type="Leaves"
 /dev_stage="4-week-old seedlings infected with
 Colletotrichum graminicola"
 /clone_lib="Pathogen-infected compatible 1 (PIC1)"
 /note="Vector: pBluescript II SK(-) from lambda Zap II;
 Site1: XhoI; Site2: EcoRI; Four-week-old sorghum
 seedlings were sprayed with spore suspension prepared from
 3-week-old PM421, a sorghum isolate of the antheranose
 pathogen Colletotrichum graminicola. Inoculated plants
 were kept in a 25 C dark growth chamber with 100% relative
 humidity for 24 hr, followed by 12/12 hr of light/dark
 cycle at 25 C with 90% relative humidity for another 24
 hr. All leaves were harvested and quick frozen with liquid
 nitrogen and stored in a -80 C freezer. The library was
 made from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision.
 WARNING: While most or all ESTs are expected to derive
 from the host plant, no effort was made to eliminate ESTs
 deriving from the pathogen."

BASE COUNT

108 a 211 c 152 g 138 t

Query Match 31.0%; Score 546.6; DB 12; Length 609;
 Best Local Similarity 94.3%; Pred. No. 2,2e-85;
 Matches 567; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 694 CGCTGTGTGAAGTGTATCAACAACAGCAGCATATGCTGTGCAACAGCTTGACCATGA 753
 Db 9 CGCTGTGTGAAGTGTATCAACAACAGCAGCATATGCTGTGCAACAGCTTGACCATGA 68
 QY 754 CCGGACCTCCAGCAGATGCGCTTTTGGCGTCCCGCAAGCTGTTGGGCAACATATG 813
 Db 69 CCGGACCTCCAGCAGATGCGCTTTTGGCGTCCCGCAAGCTGTTGGGCAACATATG 128
 QY 814 GTCTTACTTCTACCAACAGCAGCTGCTGTGATGCGGCTCGAAATTTCTTACAGCTA 873
 Db 129 GTCTTACTTCTACCAACAGCAGCTGCTGTGATGCGGCTCGAAATTTCTTACAGCTA 188
 QY 874 CCAGCACTGAGACTTCTTACCCGGTATGTGATGTCATGCGCAGATTAATTTCTGCGCAGTC 933
 Db 189 CCAGCACTGAGACTTCTTACCCGGTATGTGATGTCATGCGCAGATTAATTTCTGCGCAGTC 248
 QY 934 CCGCTGTCTGTCTTCAAGAGAGAGGGTGCAGGCGGTTGCTTGAGATGCGGGGGGT 993
 Db 249 CCGCTGTCTGTCTTCAAGAGAGAGGGTGCAGGCGGTTGCTTGAGATGCGGGGGGT 308
 QY 994 CCGCACAATCTGAGGCTTGTGATACCGGTTGCTGCTTCCCTGCGAATTTGTGGAGAG 1053
 Db 309 CCGCACAATCTGAGGCTTGTGATACCGGTTGCTGCTTCCCTGCGAATTTGTGGAGAG 368
 QY 1054 GGTGGGTTTGTGCTTTTCACTTCAACATCTGCGGATTTACAGCAGTCCAAATTTGCTCT 1113
 Db 369 GGTGGGTTTGTGCTTTTCACTTCAACATCTGCGGATTTACAGCAGTCCAAATTTGCTCT 428
 QY 1114 GAACCACTTCTGTCTGCAAGTGTATGTCCGGCCACCCAGGCAATGACTGTTTGAAG 1173
 Db 429 CAACCACTTCTGTCTGCAAGTGTATGTCCGGCCACCCAGGCAATGACTGTTTGAAG 488
 QY 1174 GCAGACGAGCAGCAGCTGCAATCTGTGCTCTCTTGGATGATTTGTTCCAGCGTGG 1233
 Db 489 GCAGACGAGCAGCAGCTGCAATCTGTGCTCTCTTGGATGATTTGTTCCAGCGTGG 548
 QY 1234 CTTGCAATTCAGATTTGACACCATCTGTTTCCCGCTTACCTTGGTGCCACTTGGCAA 1293
 Db 549 TTTGCAATTCAGATTTGACACCATCTGTTTCCCGCTTACCTTGGTGCCACTTGGCAA 608
 QY 1294 G 1294
 Db 609 G 609

RESULT 6
 BQ281359 744 bp mRNA linear EST 13-MAY-2002
 LOCUS WHE3020.D06.H12S wheat unstressed seedling shoot normalized cDNA
 DEFINITION library Triticum aestivum cDNA clone WHE3020_D06_H12, mRNA
 sequence.

ACCESSION BQ281359
 VERSION BQ281359.1 GI:20548798
 KEYWORDS Triticum aestivum (bread wheat)
 SOURCE Triticum aestivum
 ORGANISM Triticum

REFERENCE
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
 P.S., Heia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
 Rauech,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

TITLE The structure and function of the expressed portion of the wheat
 genomes - Normalized shoot cDNA library

JOURNAL
 COMMENT Unpublished
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center

source
1. .499
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="ear"
/dev_stage="2 mm"
/lab_host="E. coli XL0LR"
/clone_1lb="3529 - 2 mm ear tissue from Schmidt and Hake
labs"
/note="Organ: ear; Vector: PAD-GAL4-2.1; Site_1: EcoRI;
Site_2: XhoI; RNA isolated by Hake lab. 1 million pfu
amplified. Ampicillin is the selection marker."

BASE COUNT 150 a 131 c 112 g 106 t

ORIGIN

Query Match 27.9%; Score 492.8; DB 14; Length 499;
Best Local Similarity 99.6%; Pred. No. 5.4e-76;
Matches 494; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1252 GCACCACTGTTCCCGCTACCTGCGGCCACCTTCGGAAGTTGCAACCGCGCTCCG 1311
DB 499 GCACCACTGTTCCCGCTACCTGCGGCCACCTTCGGAAGTTGCAACCGCGCTCCG 440
QY 1312 CGACCTTTCGAGAAGAGATGGGCTCACTTATTCGACGACCACTTCGGGGTCAATGT 1371
DB 439 CGACCTTTCGAGAAGAGATGGGCTCACTTATTCGACGACCACTTCGGGGTCAATGT 380
QY 1372 GCTTAACATGAGACACTCAGGCTGTGCTATTCAGGCGGACGAGCAAGTGTGG 1431
DB 379 GCTTAACATGAGACACTCAGGCTGTGCTATTCAGGCGGACGAGCAAGTGTGG 320
QY 1432 TGCTCCGAAGATTTGGTATGGAGAGCTGGAACACCCATGATTAATGGAGTAAGA 1491
DB 319 TGCTCCGAAGATTTGGTATGGAGAGCTGGAACACCCATGATTAATGGAGTAAGA 260
QY 1492 CGGGCTAATGGCAACTTCTGGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 1551
DB 259 CGGGCTAATGGCAACTTCTGGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 200
QY 1552 CAGTTAATTAAGATATTTGATTCATTCACCTGCTGAGTCAAGTTCAGTTCAGTTC 1611
DB 199 CAGTTAATTAAGATATTTGATTCATTCACCTGCTGAGTCAAGTTCAGTTCAGTTC 140
QY 1612 ACAAGTGGCTGTATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1671
DB 139 ACAAGTGGCTGTATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 80
QY 1672 TGATTCGTTCTCCCTATCAAGTACTATATGATGATGATCTTGTTCATTCAGTA 1731
DB 79 TGATTCGTTCTCCCTATCAAGTACTATATGATGATGATCTTGTTCATTCAGTA 20
QY 1732 ACTTGTTCAGATTA 1747
DB 19 GCTTGTTCAGATTA 4

RESULT 10
CD484487 497 bp mRNA linear EST 04-JUN-2003
LOCUS 3529.1.115.1 A01.Y.1 3529 - 2 mm ear tissue from Schmidt and Hake
DEFINITION lab's Zea mays cDNA, mRNA sequence.
ACCESSION CD484487
VERSION CD484487.1 GI:31405755
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 497)
AUTHORS Walbot V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University
COMMENT Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529.1.115.1 row: A column: 01.
Location/Qualifiers

FEATURES
source
1. .497
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="ear"
/dev_stage="2 mm"
/lab_host="E. coli XL0LR"
/clone_1lb="3529 - 2 mm ear tissue from Schmidt and Hake
labs"
/note="Organ: ear; Vector: PAD-GAL4-2.1; Site_1: EcoRI;
Site_2: XhoI; RNA isolated by Hake lab. 1 million pfu
amplified. Ampicillin is the selection marker."

BASE COUNT 78 a 197 c 123 g 99 t

ORIGIN

Query Match 27.6%; Score 486; DB 14; Length 497;
Best Local Similarity 99.8%; Pred. No. 8.3e-75;
Matches 497; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 413 CTCCTCGGAGATATCTCCGGGGCTCTTCGGAAGCGGTGGGCCCAACCCCAAGTTC 472
DB 1 CTCCTCGGAGATATCTCCGGGGCTCTTCGGAAGCGGTGGGCCCAACCCCAAGTTC 59
QY 473 CAGCTGCTCTGATGAGCGCTCTCTTCTTCAAGCGGCTGTACCTGCTCTGATGAGCG 532
DB 60 CAGCTGCTCTGATGAGCGCTCTCTTCTTCAAGCGGCTGTACCTGCTCTGATGAGCG 119
QY 533 AGGCGCTGGGGCGCACTCTCTCGGGGGGCTCTATTCGCTTGTCTGATTCAGTCCGG 592
DB 120 AGGCGCTGGGGCGCACTCTCTCGGGGGGCTCTATTCGCTTGTCTGATTCAGTCCGG 179
QY 593 TGGATGGGCGAGACTCGGGGCAACCGCATCACCGGCTCGGCTCTCGACCGGCTC 652
DB 180 TGGATGGGCGAGACTCGGGGCAACCGCATCACCGGCTCGGCTCTCGACCGGCTC 239
QY 653 GTGCAAGTCTCTCCGGGAATGCTTCAACCGGCTTCAAGTCTTCAAGTCTTCAAG 712
DB 240 GTGCAAGTCTCTCCGGGAATGCTTCAACCGGCTTCAAGTCTTCAAGTCTTCAAG 299
QY 713 CACACACGACCACTGCTGCAAGAGCTGAGACATGACCCGGAAGCTTCCAGCAGT 772
DB 300 CACACACGACCACTGCTGCAAGAGCTGAGACATGACCCGGAAGCTTCCAGCAGT 359
QY 773 CGGCTCTTGGCGGTCCCGCAAGCTTGGGCAACATATGAGTCTTCAACCAAGG 832
DB 360 CGGCTCTTGGCGGTCCCGCAAGCTTGGGCAACATATGAGTCTTCAACCAAGG 419
QY 833 ACCCTGGCTGTGATGCGGCTCGAATTCCTTCAATGATGATGATGATGATGATGAT 892
DB 420 ACCCTGGCTGTGATGCGGCTCGAATTCCTTCAATGATGATGATGATGATGATGAT 479
QY 893 CGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910
DB 480 CGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497

RESULT 11
BH785221 489 bp DNA linear GSS 28-MAR-2002
LOCUS fzm013f038h1k0 fzm013f038h1k0 fzm013f038h1k0 fzm013f038h1k0
DEFINITION fzm013f038h1 5', genomic survey sequence.

ACCESSION BH785221 GI:19789571
 VERSION BH785221.1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 489)
 Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D. Gene shreshner methylation filtered genomic sequences from maize
 Unpublished
 Contact: Bedell JA
 Orlon Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6879
 Fax: 314 615 5975
 Email: jbedell@oriolongenomics.com
 Plate: f2mb013f038 row: h column: 11
 Seq primer: SK reverse
 Class: shotgun
 High quality sequence stop: 489.
 Location/Qualifiers
 1..489
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /culivar="MO17"
 /db_xref="taxon:4577"
 /clone="f2mb013f038h11"
 /note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into E. coli cells."
 BASE COUNT 87 a 156 c 130 g 116 t
 ORIGIN
 Query Match 26.2%; Score 462.8; DB 28; Length 489;
 Best Local Similarity 99.0%; Pred. No. 9.1e-71;
 Matches 487; Conservative 0; Mismatches 2; Indels 3; Gaps 2;
 QY 724 CCACATGCGCTGCAAGAGCTGAGACCTGACCGGACCTGACAGATGCGCTTTGCG 783
 DB 1 CCACATGCGCTGCAAGAGCTGAGACCTGACCGGACCTGACAGATGCGCTTTGCG 58
 QY 784 CGTTCCTCCCAAGCTGTTGCGCAACATATGCTCTTACCAACGACCTGCGCTT 843
 DB 59 CGTTCCTCCCAAGCTGTTGCGCAACATATGCTCTTACCAACGACCTGCGCTT 117
 QY 844 CGATGCGCTGCAAGATTTCTTATCAGCTACAGCACTGACCTTTACCCGCTATATG 903
 DB 118 CGATGCGCTGCAAGATTTCTTATCAGCTACAGCACTGACCTTTACCCGCTATATG 177
 QY 904 CATGCGCAGATTAATCTTCTGCGCAGTCCGCGCTGTTGTTCTGACGGAAGAGGT 963
 DB 178 CATGCGCAGATTAATCTTCTGCGCAGTCCGCGCTGTTGTTCTGACGGAAGAGGT 237
 QY 964 GCGGACGCGTTGCTGAGATCGCGGGGCTGCGCAATTCGCGCTTGATCCGTTGCT 1023
 DB 238 GCGGACGCGTTGCTGAGATCGCGGGGCTGCGCAATTCGCGCTTGATCCGTTGCT 297
 QY 1024 GGTGGCTTCCCTGCGCAATTTGTTGGAAGAGGTGCGGTTGTTGCTTTACGCTTACCAT 1083
 DB 298 GGTGGCTTCCCTGCGCAATTTGTTGGAAGAGGTGCGGTTGTTGCTTTACGCTTACCAT 357
 QY 1084 CTGCGGATTCAGACGCTCAATTTGCTGGAACACTTCTGTCGAGGTATGTCG 1143
 DB 358 CTGCGGATTCAGACGCTCAATTTGCTGGAACACTTCTGTCGAGGTATGTCG 417
 QY 1144 GCCACCCAGAGGCAATGATGTTTGAAGACAGACGCGGACGCTGACATCTCTG 1203
 DB 418 GCCACCCAGAGGCAATGATGTTTGAAGACAGACGCGGACGCTGACATCTCTG 477

QY 1204 CTCTCCTTGAT 1215
 DB 478 CTCTCCTTGAT 489
 RESULT 12
 BJA65389
 LOCUS
 DEFINITION BJA65389 691 bp mRNA linear EST 23-MAY-2002
 BJA65389 K. Sato unpublished cDNA library, cv. Haruna Nijo
 germination shoots Hordeum vulgare subsp. vulgare cDNA clone
 bag339K05 5', mRNA sequence.
 BJA65389
 ACCESSION BJA65389.1 GI:21143896
 VERSION BJA65389
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
 1 (bases 1 to 691)
 Sato, K., Saitoh, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished
 Contact: Tadao Shin-1
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1..691
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 /culivar="Haruna Nijo"
 /db_xref="taxon:112509"
 /clone="bag339K05"
 /tissue_type="shoots"
 /dev_stage="germination"
 /clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots"
 BASE COUNT 118 a 224 c 183 g 165 t 1 others
 ORIGIN
 Query Match 26.2%; Score 462.6; DB 12; Length 691;
 Best Local Similarity 80.9%; Pred. No. 8.8e-71;
 Matches 551; Conservative 0; Mismatches 129; Indels 1; Gaps 1;
 QY 431 TCCGGGGGCTTGAAGCGCTGCGCCCGACCCCAAGCTCAGCTGCTGATGGCC 490
 DB 12 TCCGGACAGGCTTGAAGCGCTGCG-CCACCCCAAGTCTGCTGCAATGTG 70
 QY 491 GTCTCTTCAAGCGCGCTGTAAGCTGCTGATGCGGACGCGCTGCGCACCTC 550
 DB 71 GTCTCTTCAAGCGCGCTGTAAGCTGCTGATGCGGACGCGCTGCGCACCTC 130
 QY 551 CTGCGGGGGGTCTCATTTGCTTGTCTGATTCAGTCCGCTGATGGCCACGACTG 610
 DB 131 TTGCGCGGGGCTCATTTGCTTGTCTGATTCAGTCCGCTGATGGCCACGACTG 190
 QY 611 GGCACACCGGATACCGGCGCATCCGCTTCGACACCGGCTGTGCAAGTGTCTCCGG 670
 DB 191 GGCACACCGGATACCGGCGCATCCGCTTCGACACCGGCTGTGCAAGTGTCTCCGG 250
 QY 671 AACTGCTCAAGCGGCTGAGATCGCTGTTGAAGTGAACCAACACGACCAATC 730
 DB 251 AACTGCTCAAGCGGCTGAGATCGCTGTTGAAGTGAACCAACACGACCAATC 310
 QY 731 GCTGCAACGCTGACCATGACCCGACCTTCAGACATCCGCTTTTCCGCTTCC 790
 DB 311 TCTGCAACGCTGACCATGACCCGACCTTCAGACATCCGCTTTTCCGCTTCC 370

Qy	791	CCCAAGCTGTTGGGACATATGGCTCTACTCTTACACAGGACCCTGGCTTCATGCC	850
Db	371	ACCAAGCTCTTCAACAACTTTGGTCACTGTGCTACGAGCGGACCTTGCGCTGCATGCC	430
Qy	851	GCCCTCGAAATTTCTTCATCAGCTACACAGACTCGACCTTCTACCCGGTAAATGCAATGCC	910
Db	431	ATTATCCAAAGTTCTTGCTCAGCTACACAGACATGGACATTTTACCCGATATGGAAATTGCA	490
Qy	911	AGGATTAATCTTCTCGCGCAGTCCGCCCTGTCTCGTTCTCACGAGAAAGGGTCCGCAG	970
Db	491	AGGATTAATCTTCTTAGTGCAGTCAATCGTGTCTTCATCACAAAGAGGTGGGCAG	550
Qy	971	CGGTTGCTTAGATCGCGGGGGTGGCCACATTTGCGGCTGTGGTACCCGTTGCTGGTGGCT	1030
Db	551	CGTTGGCTGGAGATCGCCGGTGTGGCCGCGTTCGTGGGTTTGGTACCCCTTGTGTGTCT	610
Qy	1031	TCCCTGCGGAATTTGGTGGAGAGGGTTCGCGTTTGTGCTTTTCAGCTTTCACCATTCGCGGG	1090
Db	611	TGCTTCGCGGAATTTGGTGGAGAGGGTGTGCTTTTGTGCTTGCACAGCTTTGTGATCACGGGG	670
Qy	1091	ATTGACGACGTTCCAAATTCTGC	1111
Db	671	ATTGACGATGTGCATTTCTGC	691

RESULT	13
LOCUS	CD230348
DEFINITION	CD230348 562 bp mRNA linear EST 21-MAY-2003
DESCRIPTION	SSI_43_D08_b1_A012 Salt-stressed seedlings Sorghum bicolor CDNA clone_SSI_43_D08_A012 3', mRNA sequence.

ACCESSION	CD230348	
VERSION	CD230348.1	GI:30973782
KEYWORDS	EST	
SOURCE	Sorghum bicolor (sorghum)	
ORGANISM	Sorghum bicolor	

REFERENCE
AUTHORS

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 562)

Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein

TITLE
JOURNAL
COMMENT

R., R., Liang, C., Sun, F., Sullivan, R., Shah, M., Summer, B. J., Eastman, A. and Paetz, L. H.
An EST database from Sorghum: salt-stressed seedlings
Unpublished
Other ESTs: SSI_43_D08_g1_A012

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel.: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=yes.

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FEATURES
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                /lab_host="DH10B-T1 phage-resistant E. coli"
                /clone_lib="Salt-stressed seedlings"
                /note="Vector: pME18-FUJ, Site_1: XhoI, Site_2: XhoI. The
library was prepared from polyA+ RNA from 9-day-old

```

BASE COUNT 115 a 135 c 154 g 158 t
ORIGIN
seedlings grown in hydroponic culture. Seedlings were transferred to a 150 mM NaCl solution and harvested at 3, 6, 12 and 24 hr following transfer. Roots and leaves were pooled from all time points and RNA isolated. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pMD18-FL3 vector (5'-prime DraIII site is CACTGTGTG, 3'-prime DraIII site is CACCATGTG).

Query Match	25.9%	Score 456.8	DB 14	length 562
Best Local Similarity	90.7%	Pred. 0.9, 6e-70		
Matches 510; Conservative	0	Mismatches 47	Indels 5	Gaps 2

QY 1149 CCAAGGGCAATGACTGGTTTGAGAGACGACGACGACGCTGCACATCCGTGTCTC 1208

Db 1 CCAAGGCAATGACTGCTTTGAGAAGACGCGAGGACGCTGCATCTGTGCCCTC 60

Db 61 CCTGATGATGTTGGTTCATGTGGTCTGCAATTCAGATTGAGCACCATCTGTTCCCC 120

1269 GCCTACCTCGGTGCCACTTTCGCAAGTTGCACCGGCCGTCGCACTTTGCAAGAAGC 1328

Db 121 GCCTACTCGGTGCCACTTTCGCAAGGTGCGCGCGCGCTGCGTACACTTTGCAACAAAGC 180

Db 181 ATGGCTCACTTATTCGAGCTCATTCGGGCGCAATGTCTTACATGGAAACAC 240

1389 TCAGGAGCTGCTGCATTGCAAGGCCAGACCGCTACAGTGTGTGCTCCGAGAAGATTTCG 1448

241 TCAGGCTGCTGCATTGCAGGCCAGGAGCGCCACAGGCGGTGCCGCCCCCGAAGAAATTTGG 300

Dbb 301 TCTGGAGAGGCTTTGAAACACCCATGTGATGATGGGATATATGAACCTGAAGCGACG 360

1507 TTCTGGTTCAGCTTGCTGGGCCCATGTGATTCCTGGATGCCCTTCAGTTATTAGAGA- 1565

Db 361 TTGTGGTTTCAGCTTGTGTGCCATGCGATTGCTGATTGCTTTCAGTATTAGAGAT 420

Db	421	ACTATTGATCA	TTTAA	CCCGACTGAG	TGCGGGTGG	AAATTTTCG	TGTCGTGACA	GTGACTGT	480
Oy	1566	--TATGATCA	TTCAAC	CTGCGCTGAG	TCAGGTGG	AAATTTTCG	TGTCGTGACA	GTGAGTCGT	1623

1624 C T A T C A G T T G A G A C T T C A T C C T T C A T A T A G T C G T T G T T C A C G G A T G T T C G T T C T C 1683

Db 481 CTATCAGTTGAAGAGTTGATGCTTCAATTGCTGGTGTTCGCCGCGCTGTCTCTC 540

QY 1684 CCTATCAGGTAACATAATGAT 1705
 ||||| ||||| ||||| ||
 Db 541 CCTATCATGGTAACATAATAT 562

[illegible]

LOCUS	679 bp	mrna	linear	EST 26-JUL-2002
BQ788546				
RESULT 14				

Accession	Definition
U078864	WHE4151_B02_C03ZS wheat CS whole plant cDNA library Triticum aestivum cDNA clone WHE4151_B02_C03, mRNA sequence.

ACCESSION BQ/00210
 VERSION BQ788546.1 GI:2197018
 KEYWORDS EST.

SOURCE	ORGANISM
Triticum aestivum (bread wheat)	
Triticum aestivum	
Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:	

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.

REFERENCE
AUTHORS
1 (cases 1 to 6/9)
Anderson, O.D., Akhuncov, E., Chao, S., Crossman, C., Deal, K., Dvorak, J., Lazo, G.R., Rausch, C.U., Wilson, C. and Woo, J.

TITLE. The structure and function of the expressed portion of the wheat

JOURNAL
COMMENT

genomes - Chinese Spring whole plant cDNA library
Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: canderse@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.

FEATURES

source

Location/Qualifiers

1..679

/organism="Triticum aestivum"

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/cultivar="Chinese Spring"

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/tissue_type="Roots, leaves, crown, stem and sheath"

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/lab_host="E. coli SOLR"

/clone_lib="Wheat CS whole plant cDNA library"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plant
tissues from wheat cv. CS grown to full tillering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
RNA was prepared from leaves (young leaf and third leaf),
whole roots, crown, stem and sheath tissues, and then
equal quantities of RNA were pooled from the these
samples. PolyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo excised
to give pBluescript SK(-) phagemids in U. Dvorak's lab (E.
Akhunov, J. Dvorak) at the University of California,
Davis. Colony plating, plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."

BASE COUNT 95 a 300 c 176 g 107 t 1 others
ORIGIN

Query Match 25.8%; Score 455.8; DB 13; Length 679;
Best Local Similarity 81.4%; Pred. No. 1,4e-69;

Matches 542; Conservative 0; Mismatches 118; Indels 6; Gaps 1;

QY 27 CTTCCCGGCTCCCTCCCAATCAGACACCAAGGCGCATCCGACGACGCGCG 86
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QY 87 CAATGCGGCTCTGTGATGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCG 146
DB 80 CAACGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 133

QY 147 TGGCGATGATCTCTCCAGAGGCTCCGCGCTACAGCTTCGCGCGAGCAGCTTGTGATCT 206
DB 134 TCGGAGATCTCCACAGAGGTGAGGCGGCGCGCGCGCGCGCGAGCAGCTTGTGATCT 193

QY 207 CCACTTCGCGGAGGTGATGAGCTCAGCGCTTCGCTCCCGCACCAAGCGGCGCGGCGAGC 266
DB 194 CCANCTCCGCGGAGGTGATGAGCTCAGCGCTTCGCTCCCGCACCAAGCGGCGGCGAGG 253

QY 267 TCCGCGCTTCACCGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 326
DB 254 TCCGCGCTTCACCGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 313

QY 327 CTTCCGCGGCGGCGGCTTCCTCCGCGCTTCCTTCGTTGCGCGCGCTTCGTTGATAGCGCGCTCT 386
DB 314 CTTCCGCGGCGGCGGCTTCCTCCGCGCTTCCTTCGTTGCGCGCGCTTCGTTGATAGCGCGCTCT 373

QY 387 CCGCGCGGCTTCGCGGAGTACCGCGCGCTTCCTTCGTTGCGCGCGCTTCGTTGATAGCGCGCTCT 446
DB 374 CCGCGCGGCTTCGCGGAGTACCGCGCGCTTCCTTCGTTGCGCGCGCTTCGTTGATAGCGCGCTCT 433

QY 447 AACGCGTCCGCCCCCACCACCCCAAGTCCAGCTCTCTGTATGCGCGCTCTTTACGCCG 506
DB 434 AGCGCGTCCGCCCCCACCACCCCAAGTCTCTGTATGCGCGCTCTTTACGCCG 493
QY 507 CGTTGATCT 566
DB 494 CCCTTACTGCGCT 553
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DB 554 TTGGCTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 613
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DB 614 CCGGCGATCCGCT 673
QY 687 TCAGCA 692
DB 674 TCGGCA 679

RESULT 15
A1691910 575 bp mRNA linear EST 02-FEB-2000
LOCUS
DEFINITION
mays cDNA, mRNA sequence.
ACCESSION
A1691910 GI:4967237
VERSION
A1691910.1
KEYWORDS
EST.
SOURCE
Zea mays
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
1 (bases 1 to 575)
REFERENCE
Walbot, V.
TITLE
Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY

JOURNAL
COMMENT

Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 606012 row: P column: 04.
Location/Qualifiers
1..575

FEATURES

source

1..575

/organism="Zea mays"

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/db_xref="taxon:4577"

/tissue_type="mixed"

/dev_stage="ear length from 0.5 cm - 2.0 cm"

/lab_host="XLOLR (Stratagene)"

/clone_lib="606 - Ear tissue cDNA library from Schmidt
lab"/note="Organ: immature ear; Vector: pBK-CMV; Site 1: EcoRI
Site 2: XhoI; Mixed ear tissue cDNA library from Schmidt
lab"

BASE COUNT 180 a 143 c 108 g 142 t 2 others
ORIGIN

Query Match 25.0%; Score 441; DB 9; Length 575;
Best Local Similarity 99.8%; Pred. No. 5,4e-67;

Matches 441; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 575 CGTCCGCGACCTTTGCAAGACATGCGCTCACTATTTCAGAGCCACATTTCTGGGCTGC 516

QY 1366 AATGTGCTTACATGGAAGACACTCAGGCGCTCTGATTCAGGCGACGAGACCGCTTACAG 1425

Db	515	AAATGCTTACATGAGAGACACTCAGGAGCTGCTGCATTGCAGGCGCAGACCGCTACACAG	1485
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Db	455	TGTTGTTGCTCCGAAGAAATTTGGATATGGAGAGCTGTGAAACCCATGATATAATGGATG	396
Qy	1486	AAGATACGGGCTAATGSCAACCTTCTGTGTTTCAGCTTGTTGCCCATGTGATTTGCTGGAT	1545
Db	395	AAGATACGGGCTAATGSCAACCTTCTGTGTTTCAGCTTGTTGCCCATGTGATTTGCTGGAT	336
Qy	1546	GCCTTTCAGTTATTTAGAGATATTGATCATTTCAACCTGCTGAGTCAGGTTGGAATTTTC	1605
Db	335	GCCTTTCAGTTATTTAGAGATATTGATCATTTCAACCTGCTGAGTCAGGTTGGAATTTTC	276
Qy	1606	GTTGTTGACAAAGTGGCTGTCTATCCAGTTGGAGAGTTCACTGCTTCAATATGTCTGGTTGTC	1665
Db	275	GTTGTTGACAAAGTGGCTGTCTATCCAGTTGGAGAGTTCACTGCTTCAATATGTCTGGTTGTC	216
Qy	1666	AACGGATGTTCTGTTCTCCCTATCACCGGTAATCTATATGATATGATCCTTGCTTAAATTC	1725
Db	215	AACGGATGTTCTGTTCTCCCTATCACCGGTAATCTATATGATATGATCCTTGCTTAAATTC	156
Qy	1726	ATGAACACTTGTTTCAAGATTA	1747
Db	155	ATGAACACTTGTTTCAAGATTA	134

Search completed: December 31, 2003, 23:59:17
Job time : 2693.35 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:49:12 ; Search time 87.5326 Seconds
(without alignments)
8894.970 Million cell updates/sec

Title: US-09-857-524B-3

Perfect score: 1764
Sequence: 1 gcagcgagctccctctctc.....tcaaaaaaaaaaaaaa 1764

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491.2	27.8	1702	4	US-08-934-254-26 Sequence 26, Appl
2	365.4	20.7	1684	2	US-08-831-570-1 Sequence 1, Appl
3	365.4	20.7	1684	2	US-08-831-575-1 Sequence 1, Appl
4	365.4	20.7	1685	1	US-08-366-779-4 Sequence 4, Appl
5	365.4	20.7	1685	1	US-08-789-936-4 Sequence 4, Appl
6	365.4	20.7	1685	4	US-08-934-254-4 Sequence 4, Appl
7	275.6	15.6	221	4	US-09-313-294A-1966 Sequence 1266, Ap
8	215.8	12.2	266	4	US-09-313-294A-3256 Sequence 3256, Ap
9	120	6.8	1926	4	US-09-249-585A-4 Sequence 4, Appl
10	120	6.8	1931	2	US-09-130-114-2 Sequence 2, Appl
11	77.6	4.4	7218	1	US-08-232-463-14 Sequence 14, Appl
12	77.2	4.4	1221	1	US-08-343-428-1 Sequence 1, Appl
13	75.6	4.3	1221	6	5212296-16 Patent No. 5212296
14	75.6	4.3	1879	6	5212296-5 Patent No. 5212296
15	72.8	4.1	4411529	3	US-09-103-840A-1 Sequence 1, Appl
16	72.6	4.1	4403765	3	US-09-103-840A-2 Sequence 2, Appl
17	71.6	4.1	1249	4	US-09-674-741-7 Sequence 7, Appl
18	71.6	4.1	4466	4	US-09-410-551B-20 Sequence 20, Appl
19	71.6	4.1	4478	4	US-09-410-551B-16 Sequence 16, Appl
20	71.6	4.1	4547	4	US-09-410-551B-22 Sequence 22, Appl
21	71.6	4.1	4571	4	US-09-410-551B-18 Sequence 18, Appl
22	71.6	4.1	77536	4	US-09-410-551B-1 Sequence 1, Appl
23	71.6	4.1	77536	4	US-09-410-551B-1 Sequence 1, Appl
24	71.2	4.0	1248	3	US-09-105-537-7 Sequence 7, Appl
25	70.4	4.0	13613	3	US-09-105-537-3 Sequence 3, Appl
26	70.4	4.0	1671	4	US-09-252-991A-8261 Sequence 8261, Ap
27	70.4	4.0	1944	4	US-09-252-991A-8062 Sequence 8062, Ap

28	70	4.0	1717	4	US-09-048-888-2 Sequence 2, Appl
29	69.6	3.9	4689	3	US-09-105-537-34 Sequence 34, Appl
30	69.6	3.9	36778	3	US-09-105-537-5 Sequence 5, Appl
31	69.6	3.9	38506	3	US-09-320-878-19 Sequence 19, Appl
32	69.6	3.9	38506	4	US-09-141-908-1 Sequence 1, Appl
33	69.6	3.9	38506	4	US-09-657-440-19 Sequence 19, Appl
34	69.4	3.9	320	3	US-09-165-264-13 Sequence 13, Appl
35	68.6	3.9	1926	4	US-09-249-585A-2 Sequence 2, Appl
36	68.6	3.9	1926	4	US-09-410-399-3 Sequence 3, Appl
37	68.6	3.9	1965	3	US-09-178-252-26 Sequence 26, Appl
38	68.6	3.9	2580	3	US-09-050-863-2 Sequence 2, Appl
39	68.6	3.9	2580	4	US-09-359-081-2 Sequence 2, Appl
40	68.6	3.9	5452	2	US-09-130-114-1 Sequence 1, Appl
41	68.6	3.9	8705	4	US-09-647-344A-14 Sequence 14, Appl
42	68.6	3.9	9600	3	US-08-910-647-1 Sequence 1, Appl
43	68.6	3.9	9600	4	US-09-620-925-1 Sequence 1, Appl
44	68.6	3.9	10596	1	US-07-884-811-15 Sequence 15, Appl
45	68.6	3.9	10596	1	US-07-885-971-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-934-254-26
Sequence 26, Application US/08934254
Patent No. 6155861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSES: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
US-08-934-254-26
Query Match 27.8%; Score 491.2; DB 4; Length 1702;
Best Local Similarity 62.0%; Pred. No. 1.2e-96;

Matches 833; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

QY 155 ATGCTCCCAAGAGGCTCCGGCTCAAGCTTCCGCGCAGACCTGAGATCCATCTCC 214
 DB 72 ATCAGCGGAGGAGCTCCCGCGCCAGACAGTCCGCGATCTTGATCTCCATCCAG 131
 QY 215 GGGCAGCTGATCAGACTCAGCCCTGAGCTCCCGCAGCAGCGGAGGAGCTCCGCTT 274
 DB 132 GGGAGGCTGATCAGCTGCTCTCGGTGGCGCGAGAGACCCCGCGCGAGGTCCCGCTC 191
 QY 275 CTCACCTGGCGGGGAGAGAGCCAGCGCTTGGCGCGCTACACACCGCGCTCGGCG 334
 DB 192 CTCAGTCTGGCGCGGCGAGAGCTCAGCGAGCTTCAATGGGTGACACCGCGGAGCGG 251
 QY 335 CGCGCGCTCTCCCGCGCTCTGCTGG-----CGCGCTCTGATGAGCGCTCTCC 388
 DB 252 TGGGGGAGCTGATCTGCTCTTCAAGGCTACTACTCAAGGAGCTTGAAGTGTG 311
 QY 389 CCGCGCTCCGCGCAGCTACCGCGCTCTGCGAGCTATCTCGCGGCGCTCTTGA 448
 DB 312 GAGATCTCAAGAGCTACCGAGGCTTTGAAGAGATGTGCGGTCCGGATCTTGA 371
 QY 449 CGGCTCGGCCCAACCCCAAGTCCAGCTGTCTGATGGCGCTCTCTTCTAAGCGCG 508
 DB 372 AAGAGGGCCACCATCATGTGAGCGTGTGCGGTGCGATGATGCGCGCATC 431
 QY 509 CTGACTCTGCTCGATCGGAGCGCGCTGCGCGAGCTCTCGCGGGGGGTCTCAT 568
 DB 432 GTCTACGGCGGTGGGGGTGGAGTCCGTGGAGTTCAATGCTGCGGAGCATCTG 491
 QY 569 GGGCTTCTGATTCAGTCCGCGGTGATGGGCGCAGACTCGGCGCAGCAGCGCATCC 628
 DB 492 GGGTGTGTGGATTCAGAGCGCGTATGTGGGCGCATCTCGGCGCTTACAGGTATG 551
 QY 629 GGGCAGCTGCTCTGAGCGCGGTGTCAGAGTGTCTCTCGGGAATGCTCTCAAGCGCTC 668
 DB 552 CCAACCGTGGATTCACAGATTCACGCACTCATAGCAGCAACATCTTAAACGGAATC 611
 QY 689 AGCATGCGCTGGTGGAGTGTATACACAGCAGACCATCGCTGCAACAGCTTGAG 748
 DB 612 AGATCGCGGTGGAGTGTAGCCAGACCCAGCAGCAGCTCGCTGCAAGCTGAGC 671
 QY 749 CATGACCGGAGCTCCAGCAGATCCGCTTTGCGCTCTCCCGCAAGCTTGGGCAAC 808
 DB 672 TAGAGCCCGGAGCTCCAGCAGATCCGCTATGCGCGCTCTCAACCGCATCTTCACTCC 731
 QY 809 ATATGCTCTACTTCTTCAACAGGAGCTTGGCGGTGAGCGCGCTGGAATTTCTTATC 868
 DB 732 ATCACTCGGTCTTCTATGCGCGAGTCTGAATTTGACGAGAGTGACAGGTCTCTAGTC 791
 QY 869 AGCTACCGAGCTGGAGCTTCTACCGCGTATGTGCAATCGCGAGATMAATCTTCTGCG 928
 DB 792 AGCTACCGAGCTGGAGCTTCTACCGCGTATGTGCAATCTTGGCGAGCACTCTTCTATC 851
 QY 929 CAGTCCCGCTGTTGTTCTCAAGGAGAGAGGGTGGCGAGCGGTGTTGATGAGTGGCG 988
 DB 852 CAGACCTTTTATGCTCTCTCAAGGCGGAGCTCTCTGACCGCGCTTAACTTATG 911
 QY 989 GGGGTGCCACATTTGCGGCTTGTGACCTGTTGCTGAGCTTCCCTGCGAATGTGTG 1048
 DB 912 GGTATCGCGGTTTCTGAGAGTGTGCTCCGCTCTTCTATCTGTCTCCGAACTGGCGCT 971
 QY 1049 GAGAGGCTCGGTTTGTGCTTTTCAAGCTTCAAGCTTGGGAGATTCAGCATTC 1108
 DB 972 GAAAGGTTGGGTTGCTCTATCAGCTTGTGCGGTCAAGGAGATTCAGCATTC 1031
 QY 1109 TGCCTGAGCACTTCTGCTCGAGCTGTATGTGGGAGCAACCAAGGAGCAATGATGTTT 1168
 DB 1032 ACGCTACCACTTCTCTCGGAGACATACGTGGGCGCCCGCAAGGAGCACTGATGTTT 1091
 QY 1169 GAGAGGAGAGCGGAGGAGCTGAGCATCTGTGCTCTCTTGGATGATGTTGGTTCCAC 1228
 DB 1092 GAGAGGAGAGCGAAGGAGGAGTATATACAGTGGCCAGCGTGGATGAGCTGGTTCTTT 1151

QY 1229 GGTGGCTGAGTGTCCAGATTGAGACCACTGTTTCCCGCTTACTCGGTGCACTT 1288
 DB 1152 GGTGGCTGAGTGTCCAGATTGAGACCACTTGTTCCTAGAGCTGCGCGGTGGGCACTT 1211
 QY 1289 CGCAAGTTGACCGGCGCTCGGAGCTTTGCAAGAGAGTGGCTCACTTATTTCTGA 1348
 DB 1212 AGGAGATTGCGGCTTGGCTCGGAGCTTGTGTAAGAGAGCAGGAGTGCCTGATAGGAGC 1271
 QY 1349 GCCACATTTCTGG--GCTGCAATGTGCTTACATGAGAGCACTCAGGGCTGTGATTTG 1405
 DB 1272 TTGGGTTTGGGAGCAGACGCTAATGTCAAGACATTTGAGCGCTGAGGGATGCGCGGTT 1331
 QY 1406 CAGGCGAGAGCGGCTCAAGTGTGTTGCTCCGAGATTTGTTAT--GGAAGGCTGTG 1462
 DB 1332 CAGGCGGCTGACCTTATTTGCGCGCGCGCTTAAAGAACTGGGTATGGGAGACTTAT 1391
 QY 1463 AACCCCATGATMAATGGGAT 1484
 DB 1392 AACCCCATGATGATGTTGTT 1413

RESULT 2
 US-08-831-570-1
 ; Sequence 1, Application US/08831570
 ; Patent No. 5959175
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Numbert, Andrew N.
 ; APPLICANT: Beremand, Phillip D.
 ; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
 ; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; City: Garden City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Releasee #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/831,570
 ; FILING DATE: 09-Apr-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digililo, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 10545
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 743-4366
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1684 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..1387
 ; US-08-831-570-1

Query Match 20.7%; Score 365.4; DB 2; Length 1684;
 Best Local Similarity 55.8%; Pred. No. 1.2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCCGCGCTCAGCGTTCGCGCAGACCTCTGATCTCATCTCC 214
 DB 67 ATTACTCTGAGATGAATCAAGAAACACGATTAACCCGAGATCTATGATCTCGATTCAA 126
 QY 215 GGGGAGGTGATGAGAGCTCAGCGCTTGGCTTCCGACACCCGGGCGGCACTTCCGCTT 274
 DB 127 GGGAAAGCCTATGATTTTCGATTTGGATGGAAGAACATCAGTGGGAGCTTTCCTTTG 186
 QY 275 CTCACCTGGCGGGGAGAGACGCGACCGAGCTTGGCGGCTACCAACCGGCTGGGG 334
 DB 187 AAGAGCTTGTGCTGTAAGAGGTATGATGATGATTTGTCATTCATCTGCTCTTAA 246
 QY 335 CGCCGCTCTCCGCGCTTCTTCTGTTG---CGGCTCTGATACAGCCGCTCTCCG 391
 DB 247 TGGAAAGATCTGATTAAGTTTTCAGTGGTATATCTTAAAGATTAATCTGTTCTGAG 306
 QY 392 GCGTCCGCGACTACCGCGGCTCTCGGCGAGCTATCTCGGCGGCTCTTTCGAGCC 451
 DB 307 GTTCTTAAAGATTAAGAAAGCTTGTGTTGATTTTAAAGGTTGATGACAAA 366
 QY 452 GTGCGCCCAACCCCAAGCTCCAGCTGCTGCTGATGGCGCTCTCTTACGCGCGCTG 511
 DB 367 AAGAGTATATATATATGTTTGAATTTGCTTTATAGCAATGCTGTTGCTATGAGTGT 426
 QY 512 TACCTGCTCCTCGCATGCGCAGCGCTGGGCGCACTCTCGCGGGGGTCTCATTTGCG 571
 DB 427 TATGGGTTTGTGTTTGTAGGGTGTGTTGTATGATTTGTTTCTGGGTTTGTATGGG 486
 QY 572 TTGCTGTGATTCAGTCCGCTGATGGGCGACAGCTGGGCGCACCGCATCACCGCG 631
 DB 487 TTTCTTTGATTCAGAGTGGTGTGATTTGACATGATGCTGGGCAATATATGATGCTCT 546
 QY 632 CATCCGCTCTCGACCGCGCTGCGAGTGTCTCCGGGAACCTGCTACCGGCTCAGC 691
 DB 547 GATTCAAGGCTTAATATAGTTTATGAGTATTTTGTGCAAAATGCTTTTCAAGAAAT 606
 QY 692 ATGCGCTGTGTAAGTGAACCAACACGACCAATGCGCTGCAAGAGCTTGACAT 751
 DB 607 ATTGTTGTTGTAAGTGAACCAATATGACATCAATGCTGTTATAGCTTGATAT 666
 QY 752 GACCGGAGCTCCAGACATGCGCTTGTGCGCTTCCGCAAGCTGTTGCGCAATAT 811
 DB 667 GACCTGATTTACAAATATATACATCTTGTGTGCTTCCAAAGTTTGTGTTGCTACGC 726
 QY 812 TGTCTCTACTTCTACCAAGAGAGCTGGGCTTGAAGCGGCTCGAATTTCTATCAGC 871
 DB 727 ACCTTCTATTTCTATAGAAAGAGTGAATTTGATCTTTTATCAAGATTTCTTGAAGT 786
 QY 872 TACCAAGCTGAGCTTCTACCGGTAATGTCATGCGCAGATTAATCTTCCGGCAG 931
 DB 787 TATCAACATTTGACATTTTACCTTATGCTGCTGCTAGGCTCAATATGATGATCAA 846
 QY 932 TCCGCGCTTCTCTCAGAGAGAGGAGTCCGACAGGCTTGAATTCGCGGG 991
 DB 847 TCTCTATATATGTTGTAACAGAAAGATGTCCTATGAGCTCAGAGAACTTTGGGA 906
 QY 992 GTGCGCAATTTGCGCTTGTATACCGGCTGCTGCTGCTTCCCTGCGAATGTTGGAG 1051
 DB 907 TGTCTAGTGTCTGATTTGTGTTGCTGCTGCTTGTGTTGCTTATGAGGCTGAA 966
 QY 1052 AGGGTGGGCTTGTGCTTTTACGCTTACCATCTGGGGGATTCAGACGTTCAATCTGCG 1111
 DB 967 AGAATATGTTGTTATGCAAGTTTATACGTAATGGAATGCAACAGTCTCTCC 1026
 QY 1112 CTGAACCACTTCTGTCGACGTATGTCGGGCGACCCAGAGGCAATGATGTTTGAAG 1171
 DB 1027 TTGAACCACTTCTCTTCAAGTGTATATGTTGAAAGAACTAAAGGAATATGTTTGAAG 1086
 QY 1172 AAGCAAGCGGAGGAGCGCTGACATCTGTGCTCTCTTGTGATGATGTTTTCACGCT 1231
 DB 1087 AAAAACAACGATGAGGAGCACTTGTGATTTCTGCTCTGATGATGATGTTTCAATGCT 1146
 QY 1232 GCGCTGAGTTTCAAGTTGAGCAATCTGTTTCCCGGCTACTGAGTGGCCACTTCCG 1291

DB 1147 GGAATGCAATTCGAATGAGATCATTTGTTCCAGAGATGCTAGATGCAACCTTAGG 1206
 QY 1292 AAGTTGACCGGCGCTCCGAGCTTGTGCAAGAGCAATGGGCTCATATTTCTGAGCC 1351
 DB 1207 AAAATCTGCGCTTACGTTATGATGATGATGCAAGAAACATTAATTTGCTTACATTAATGCA 1266
 QY 1352 ACATCTGGGGGTCGAATGCTGCTTACATGAAAGACACTCAGGCTGCTGATTTGAGCGCC 1411
 DB 1267 TCTTTCTCCAGGCGCAATGAATGACACTCAGAACATTTGAGGAACACAGCATTTGAGGCT 1326
 QY 1412 AGACCGCTACAGTGTGCTGCTCGAAGAAATTTGATGAGGAGCTGTGACACCAT 1471
 DB 1327 AGG---GATATTAACCAAGCGGCTCCGAAAGATTTGATGGAAGCTTTCACACTGAT 1383
 QY 1472 GGAATAA 1478
 DB 1384 GGTAA 1390

RESULT 3
 US-08-831-575-1
 ; Sequence 1, Application US/08831575
 ; Patent No. 5977436
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/831,575
 ; FILING DATE: 09-APR-1997
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digilio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4346
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1684 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..1387
 ; US-08-831-575-1

Query Match 20.7%; Score 365.4; DB 2; Length 1684;
 Best Local Similarity 55.8%; Pred. No. 1,2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCCGCGCTCAGCGTTCGCGCAGACCTCTGATCTCATCTCC 214
 DB 67 ATTACTCTGAGATGAATCAAGAAACACGATTAACCCGAGATCTATGATCTCGATTCAA 126

QY 215 GCGAGCTGTACAGCTCAGCCCTGGCTCCCCACCAACCAGGCGGCGACCTCCGCTT 274
 DB 127 GGGAAAGCTATATATGTTTGGATTTGGTAAAGACATCAAGTGGCAGCTTCCCTTG 186
 QY 275 CTACACCTGGCGGGGCGAGAGCCAGAGCTTCCGCGCTACACCCGCTCGGGG 334
 DB 187 AAGAGCTTCTGTGTCAAGAGTAACTGATGCAATTTGTGCAATTCCTGCTCTACA 246
 QY 335 CGCCCGCTCCCGCGCTTCTTGGTGG---CGGCTCTGTGCTAGCGCGCTCCGCC 391
 DB 247 TGGAGATCTTGAATTAAGTTTCTAGTGGATTAATCTTAAGATTAAGTCTTCTGAG 306
 QY 392 GCGCTCCGCGACATACCGCGCTCTCGCGAGCTATCTCCGCGGCTCTTGAAGCG 451
 DB 307 GTTCTTAAGATTAAGAGAGCTTGTGTGAAGTTTCTAAGAGGTTTGTATGAAGAA 366
 QY 452 GTGCGCCCAACCCCAAGTTCAGCTGTCTGATGCGCGCTCTTCTACGCGCGCTG 511
 DB 367 AAGGCTATATATGTTTGGCAATTTGTGCTTTATACCAATGCTGTTGCTATGAGT 426
 QY 512 TACCTGCTCCGCTCGAGCGGCGCTGGCGGAGCTCTCGGCGGGGGCTTCATGGC 571
 DB 427 TATGGGTTTTTTTGTGAGGGTGTGTGATGATTTTCTGAGTGTGATGGG 486
 QY 572 TTGCTGTGATTCAGTCCGCTGATGAGCGACATCGGCGCACACCGCATCACCGCG 631
 DB 487 TTTCTTTGATTCAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGAT 546
 QY 632 CATCGGCTCTCGACCGCGCTGTGAGTGTCTTCGCGGAACTGCTTCACCGGCTCAGC 691
 DB 547 GATTCAGAGCTTAATTAAGTTTATGAGTTTGTGCTCAAAATGCTCTTACGAGATAGT 606
 QY 692 ATGCGCTGTGAGATTAACCAACACGACACACATGCTGCAACAGCTGAGACAT 751
 DB 607 ATGCTTGTGAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 666
 QY 752 GACCCGAGCTTCAGACATGCGCTCTTTCGCTCTCCCAAGCTGTTGCGGACATA 811
 DB 667 GACCTGATTTAGAT 726
 QY 812 TGTCTACTTCTACCAACGAGACCTGCGCTGATGATGATGATGATGATGATGATGAT 871
 DB 727 ACCTCTATTTCTATGAGAAAGTTGACTTTTATGATCTTATGATCTTATGATCTT 786
 QY 872 TACAGAGCTGAGACCTTACCGCGTATGATGATGATGATGATGATGATGATGATGAT 931
 DB 787 TATCAACATTTGACATTTTATCCCTATATATGATGATGATGATGATGATGATGATGAT 846
 QY 932 TCCGCTGTTCTGTTCTACGAGAAAGAGGAGCGGAGCGGTTGTTGATGATGCGGG 991
 DB 847 TCTCTATATATGTTTGAACCAAGAAATGATGATGATGATGATGATGATGATGATGAT 906
 QY 992 GTGCGACATTTGCGGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1051
 DB 907 TGCTAGTGTCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
 QY 1052 AGGCTGCGGTTTGTGCTTTTACGCTTACCATGCGGAGATGAGAGCTGCAATTTGCG 1111
 DB 967 AGAATTAATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
 QY 1112 CTGAACCACTTCTGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1171
 DB 1027 TTGAACCACTTCTTCAAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 1086
 QY 1172 AAGGAGCGGAGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1231
 DB 1087 AAACAAACGATGAGACATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1146
 QY 1232 GCGCTGAGTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291
 DB 1147 GGAATGCAATTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
 QY 1292 AAGGTGACAGCGGCTGTCGAGATTTGCAAGAAAGATGAGGCTCACTTATTTGAGCC 1351

DB 1207 AAAATCTCCCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1266
 QY 1352 ACATTCGAGGTCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1411
 DB 1267 TCTTTTCCAGGCGCATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1326
 QY 1412 AGGACGCTACAGTGTGTGCTCCGAGAAATTTGATGAGAGCTGTAACACCAT 1471
 DB 1327 AGG---GATTAACAGAGCGGCTCCGAGAAATTTGATGAGAGCTTTCACACTCAT 1383
 QY 1472 GGTATAA 1478
 DB 1384 GGTATAA 1390

RESULT 4
 US-08-366-779-4
 ; Sequence 4, Application US/08366779
 ; Patent No. 5614393
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/366,779
 ; FILING DATE: 30-DEC-1994
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXX
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-366-779-4

Query Match 20.7%; Score 365.4; DB 1; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 1,2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAAAGAGCTCCGCGCTTCAGCGCTTCGCGAGAGCTCTGATATCTCATCTCC 214
 DB 68 ATTAACCTCAGATTAATCTCAAGAACACAGATAACCCGAGATCTATGATCTGATTCAA 127
 QY 215 GCGAGCTGTACAGCTCAGCGCTTGGCTTCCCGACACCCGCGGCGGACCTCCGCTT 274
 DB 128 GGAAGAGCTATGATGTTTCGATTTGGGTGAAGAACATTCAGGTGGCAGCTTCCCTTG 187

QY 275 CTCACCTGCGGGGAGAGAGCGCCACCGAGCGCTTGGCGGCTACCGACCGCGGCGG 334
 DB 188 AAGAGCTGCTGCTGTAAGAGGTAAGTACGATGCTTGTGCAATTCATCTGCTTAA 247
 QY 335 CGCGCGCTCCCGCGCGCTTCTGTTGG---CGCGCTCTGATGATGCGCGCTCTCC 391
 DB 248 TGGAGAAATCTGATTAAGTTTTCACCTGGGATTAATCTTAAGATTAATCTGTTCTGAG 307
 QY 392 GCGTCCGCGGATCAACCGCGCGCTCTCGGAGAGTAATCTCCGCGGCGCTTTCGACCG 451
 DB 308 GTTCTTAAGATTAAGAACTTGTGTTGATGTTTCTAATAATGGGTTGATGACAA 367
 QY 452 GTGCGGCCACCGCCCAAGGTCAGCTGCTGTAAGGCGGCTCTCTTACCGCGGCTG 511
 DB 368 AAGAGCTAATTAATGTTTGCATCTTGTGCTTAATGCAATGCTTGTGTAATGATGTT 427
 QY 512 TACCTGCTCTGCAATGCGCAGCGCGCTGGCGCACCTCTCGCGGGGCTCATTTGCG 571
 DB 428 TATGGGTTTTTGTGTTGAGGGTGTGTTGTAATTTGTTTCTGGGTTTGAATGGG 487
 QY 572 TTGCTGATGATGATGCGCGCTGATGGGCGACGATCGGGCGACACCGCATCACCGC 631
 DB 488 TTTCTTGAATCAGAGTGGTGTGATGATGATGATGATGATGATGATGATGATGATG 547
 QY 632 CATCGGCTCTGACCGCGCTGCGAGGCTCTCGCGGAACTGCTCAACCGGCTCAGC 691
 DB 548 GATTAAGGCTTAATTAATGTTTATGAGGTAATTTTGTGCAATGTTCTTCAAGAAATAG 607
 QY 692 ATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
 DB 608 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
 QY 752 GACCGGAGCTCTGACGATGCGCTCTTGTGCGCTCTCCCGAAGCTGTTGGCAATG 811
 DB 668 GACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 727
 QY 812 TGGTCTACTTCAACGAGAGCGCGCTGATGATGATGATGATGATGATGATGATGATG 871
 DB 728 ACTCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 787
 QY 872 TACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
 DB 788 TATCAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
 QY 932 TCGCGCTGTTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
 DB 848 TCTCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 907
 QY 992 GTGCGCAATTTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
 DB 908 TGCCTAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967
 QY 1052 AAGGTCGCGTTTGTGCTTTCAGCTTCAACATCTGGGAGATGAGCAAGCTCAATCTG 1111
 DB 968 AGAATTAATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1027
 QY 1112 CTGACCACTTCTGCTCGAGCGTATGATGATGATGATGATGATGATGATGATGATG 1171
 DB 1028 TTGAACACTTCTCTCAAGTGTGTTATGTTGAAGAGCTTAAGGATTAATGTTTGA 1087
 QY 1172 AAGCAAGCGGAGGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1231
 DB 1088 AAGCAAGCGGATGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1147
 QY 1232 GCGCTGAGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1291
 DB 1148 GGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1207
 QY 1292 AAGGTCGACCGGCGCTGCGGAGCTTGGCAAGAGATGAGGCTCAATTAATTCGAGCC 1351
 DB 1208 AATATCTCGCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1267

QY 1352 ACATTTGCGGATGCAATGCTTACATGAGACATCAGGCGCTGCTGATTCAGCGCC 1411
 DB 1268 TCTTTCTCCAGCGCAATGAATGATGATGATGATGATGATGATGATGATGATGATG 1327
 QY 1412 AGACCGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1471
 DB 1328 AGG---GATATTAACCAAGCGCTCCCGAAGATTTGATGGAAGCTTCTCACTCAT 1384
 QY 1472 GGATAAA 1478
 DB 1385 GGTTAAA 1391
 RESULT 5
 US-08-789-936-4
 ; Sequence 4, Application US/08789936
 ; Patent No. 5789220
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freybelnet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/789,936
 ; FILING DATE: 28-JUN-1997
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/366,779
 ; FILING DATE: 30-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383ZYXW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-789-936-4
 Query Match 20.7%; Score 365.4; DB 1; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 1.2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 275 CTACCCCTGGGGGAGAGAGCCACCGACCTTCGCGCTACACCGCCCTCGGGC 334
 DB 188 AAGAGCTTCTGTGTCAAGAGTACATGATTTTGTGATTCATCTGCTCTACA 247
 QY 335 CGCCCTCTCTCGCGCGCTTCCTGTTG--CGGCTCTCTGACATACCGCTTCGCC 391
 DB 248 TGAAGAGATCTGATTAAGTTTTCATGCGATATATCTTAAGATTAATCTGTTTGA 307
 QY 392 GCGTCCGCGACATACCGCGCTTCGCGAGATATCTTCGCGCGCTTCGAGCC 451
 DB 308 GTTCTAAGATTAAGAGAGCTGTGTGAGTTTCTAAGATTAAGATTAAGAGAG 367
 QY 452 GTGCGCCCAACCCCAAGTTCAGCTGCTGATGAGCGCTCTCTACGCGCGCTG 511
 DB 368 AAGAGCTATATATATTTGACATCTTGTGCTTATACATGCTGTGTGATGAGT 427
 QY 512 TACCTGCTCTCGATCGCGAGCGCTGCGCGACCTCTCGCGCGCGCTCTCATTTGC 571
 DB 428 TATGCGGTTTGTGTTGAGGAGTTTGTGATCATTTGTTTCTGCGGTGTTGATGGG 487
 QY 572 TTGCTCTGATCCAGTCCGCTGATGAGCGACATCTCGCGCGACACCGCATACCGC 631
 DB 488 TTTCTTGTGATGAGAGTGTGATGAGATGATGCTGCGCATATATATGATGATCT 547
 QY 632 CATCCGCTCTCGACCGCGCTGTCAGAGTGTCTCGCGAGAACTGCTCACCGCGCTG 691
 DB 548 GATTCAAGCTTAAATAGTTTATGAGTATTTTGTGCAATTTGCTTTCAGAGATTA 607
 QY 692 ATGCGCTGTGAGAGTGTAAACACACGACGACCATGCTGCGACACGCTGAGCAT 751
 DB 608 ATGCTGTGTGAGAAATGAGACATATAGACATACATGCTGCTGATTAATGAT 667
 QY 752 GACCGGAGCTCCAGACATGCGCTCTTGTGCGCTCTCCGCAAGCTGTTCGCAATA 811
 DB 668 GACCTGATTTACATATATATACATCTTGTGTGTCTTCAAGTTTGTGTTCACTC 727
 QY 812 TGTCTACTTCTACCAAGAGACCTGCGCTGATGCTGCGCTGCAATTTCTCATGAG 871
 DB 728 ACCTCTATTTCTATGAGAAAGTGTACCTTTTATACATCTTTATGATTTGAT 787
 QY 872 TACAGAGCTGAGACCTTCTACCGGTAATGTGATCGCGAGATTAATCTTCTCGCGAG 931
 DB 788 TATCAACATTTGACATTTTACCTATATATGTCGTGAGGCTCATATATATGATCA 847
 QY 932 TCGCGCTGTCTCTCAAGAGAGAGAGGTGCGGAGGCTTGTGATGCGCGG 991
 DB 848 TCTCTATATATGTTGTGACCAAGAGATGTCTTATGAGCTCAGGAATCTTGGGA 907
 QY 992 GTGCGCACATTTGCGGCTGTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
 DB 908 TGCCTAGTGTCTGATTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967
 QY 1052 AGGAGTGGCTTGTGCTTTCAGCTTACCATGCGGATTCAGACGTCATTTCTGC 1111
 DB 968 AGATTAATGTTTGTATTTGAGATTTATCAATGATGAGATTAAGATTAAGTTCTC 1027
 QY 1112 CTGAGACATTTCTGCTGCGAGCTGATGTCGCGCACACCGGCAATGCTGTTGAG 1171
 DB 1028 TTAAGACATCTTCTCAAGTGTATGTTGAGAAAGCTTAAGGAGATTAATGCTTGG 1087
 QY 1172 AAGAGAGGAGGAGGAGCTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1231
 DB 1088 AAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1147
 QY 1232 GGCCTGAGTTCAGATTTGAGACATCTGTTCCCGCTACTCGGTCGACCTTCGC 1291
 DB 1148 GAGTGTGATTTCAAAATTTGAGACATTTGTTTCCAAAGATGCTTAATGCAACTT 1207
 QY 1292 AAGGTTGACCGGCGCTGCGGACCTTTGCAAGAGATGAGGCTCACTTATTCGAGCC 1351
 DB 1208 AAGATCTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1267

QY 1352 ACATCTGGGTCGCAATGCTTACATGAGAGACATGAGGCTGCTGATTCAGGCC 1411
 DB 1268 TCTTCTCCAGGCGCATGATTAATGACATCAGAACTTGAAGAACAGCATTCAGGCT 1327
 QY 1412 AGGAGCGCTACAGTGTGTGCTCCGAAAGATTTGATGAGAGCTGTGAACCCAT 1471
 DB 1328 AGG---GATATACCAAGCGCTCCGAAAGATTTGATGAGAGCTTTCACACTCAT 1384
 QY 1472 GGATAAA 1478
 DB 1385 GGTTAAA 1391

RESULT 6

US-08-934-254-4

; Sequence 4, Application US/08934254
 ; Patent No. 635861
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,254
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832XXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-934-254-4

Query Match 20.7%; Score 365.4; DB 4; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 1.2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCGCGCTCAAGCTTCGCGCGAGACCTGTGATCTTCATCTCC 214
 DB 68 ATTAAGCTGAGATTAATCAAGAAACAGATTAACCGAGATGATGATGATGATGATG 127
 QY 215 GCGAGGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 274
 DB 128 GGGAAAGCTATATATTTTGTGATTTGGTGAAGACATTCAGTGTGAGCTTTCCTTG 187
 QY 275 CTACCCCTGGCGGGGAGAGCGCACGAGCGCTTGGCGCGCTACACCGCGCTCGGGG 334
 DB 188 AAGAGCTTGTGCTGTAAGAGGATGATGATGATGATGATGATGATGATGATGATG 247
 QY 335 CGCCCTCTCTCGCGCGCTTCTGTTG--CGGCTCTCTGACATACCGCTTCGCC 391

Db 248 TGAAGATCTTGTATAGTTTTCACCTGGTATTTATCTTAAAGATTAATCTGTTTCAG 307
 QY 392 GCGTCCGCGACATACGCGCCCTCTCGCGACATACCTCCGCGCCCTCTTGCAGACG 451
 Db 308 GTTTCATAAAGATTATAGGAAGCTTGTGTGATTTTCTAAAAATGGGTGTATGACAAA 367
 QY 452 GTGCGCCCGCCCGCCCAAGGTCAGCTGCTGATGGCCGCTCTCTTCTACGCGCGCTG 511
 Db 368 AAGGTCATATTATGTTTGCACATTTTGTCTTATAGCAATGCTGTTGTATGAGCTT 427
 QY 512 TACCTGCTCTCGCATGCGCAGCGCTGGCGCAGCTCTCGCGGGGGCTTCATTTGCG 571
 Db 428 TATGGGATTTGTTTGTGAGGGGTGTTGTATGATTTGTTTCTGGGTGTTGATGGGG 487
 QY 572 TTGCTGTGATTCAGTCCGCTGATAGGGCCAGACTCGGGCCACCAAGCCGATCACCGGC 631
 Db 488 TTTCTTTGATTCAGAGTGTGATTTGACATGATGCTGGGATTAATATAGTAGTCTT 547
 QY 632 CATCCGGTCTCGACCGCGTGTGAGAGTGTCTCCGGGAATGCTCACGCGCTGAGC 691
 Db 548 GATTCAAGGCTTATTAATGTTATAGGTAATTTTCTGCAATTTCTCTTACGAAATAGT 607
 QY 692 ATCGCTGTGAGATGTAAACAACAGCAGCAGCAGCAGCTGCGCAAGCTTGACCAT 751
 Db 608 ATTTGTTGTGGAATGGAACATTAATGACATACATGCTGCTGTAATAGCTTTGAATAT 667
 QY 752 GACCCGAGCTCCAGCAGCATGCGCTCTTTGCGCTCTCCCGCAAGCTGTTGGCAATA 811
 Db 668 GACCCGTATTTACATATATATACCATCTTGTGTGCTTCCAGATTTTGTGCTCATC 727
 QY 812 TGGTCTACTTTTACCAAGGACCCGTGCGATGCGCGCTGGAATTTTCATCAGC 871
 Db 728 ACCTCTATTTTCTATGAGAAAGTTGACTTTTATCACTTTTATCAATTTCTTTGTAAT 787
 QY 872 TACCAGACATGACCTTTCTACCCGTAATGTGATGCGCAGATTAATCTTCTCGCAG 931
 Db 788 TATCAACATTTGACATTTTACCTATATGTTGCTGCTAGGCTCATATGATGATCAAA 847
 QY 932 TCGCGCTGTCTTCTACGAGAAAGAGGTGCGCAGCGGTGCTTGAATGCGCGGG 991
 Db 848 TCTCTCAATATGTTGTGACCAAGAAATGTCTATGAGTCAAGGAACTCTTGGGA 907
 QY 992 GTGCGCACATTTCTGGGCTGGTATACCCGTGCTGTGCTTCCCTGCGAAATTTGGTGGAG 1051
 Db 908 TGCTTAGTGTCTGATTTGTTGTAACCGTGTGTTTCTTGTGCTTAATGGGAGTGA 967
 QY 1052 AGGCTGCGTGTGTCTTTTCAAGCTTCAACATCTGCGGATTCAGACGTTCATTTGCG 1111
 Db 968 AGAATTATGTTTGTATTTGCAAGTTTATCACTGATGGAATGCAACAAGTTCACTTCTCC 1027
 QY 1112 CTGAACCACTTCTGTCGAGAGTATGTGCGGCCACCAAGGCAATGACTGTTTGGAG 1171
 Db 1028 TTGAACCACTTCTTCAAGTGTATGTTGAAAGGCTTAAAGGAATTAATTTGTTGAG 1087
 QY 1172 AAGCAGACGAGCAGCAGCTGACATCTGTGCTCTCTTGGATGGAATTTGGTTCAAGGT 1231
 Db 1088 AAACAAACGATGAGACACTTGAATTTCTGTCTCTCTTGGATGGAATTTGGTTCAAGGT 1147
 QY 1232 GGCCTGCAATTCAGATTTGACACATCTGTTTCCCGCCTACCTCGGTGCGACCTTGC 1291
 Db 1148 GGATTTGCAATTTCAATTTGACATCTTGTTCCTTCCAAAGATGCTAGATGCACTTGAAG 1207
 QY 1292 AAGTTGCAACGCGCGCTGCGACCTTTGCAAGAGCATGGGCTCATTTATTCGAGCC 1351
 Db 1208 AAAATCTGCGCTTACGTATGATGATGCAAGAAATTAATTTGCTTAAATTTATGCA 1267
 QY 1352 ACATTTCTGGGTGCAATGTGCTTATCAGGAAGACATCAGGGCTGCTGATTCAGAGCC 1411
 Db 1268 TCTTTTCTCAAGGCAATGAATGACATCTGAAACATTTGAGAAACAGCATTTGAGGCT 1327
 QY 1412 AGGACCGCTACAGTGTGTGCTCGAAGAAATTTGTATGAGAGCTGTGAACACCCAT 1471
 Db 1328 AGG---GATATATACCAAGCCGCTCCGAAAGATTTGTATGGAAGCTCTTCAACATCAT 1384

QY 1472 GGATAAA 1478
 Db 1385 GGTTAAA 1391
 RESULT 7
 US-09-313-294A-1966
 ; Sequence 1966, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalauadi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1966
 ; LENGTH: 291
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Inocyte ID No. 6476212 700551823H1
 ; NAME/KEY: unsure
 ; LOCATION: 256
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-09-313-294A-1966
 Query Match 15.6%; Score 275.6; DB 4; Length 291;
 Best Local Similarity 98.2%; Pred. No. 1.5e-50;
 Matches 278; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1014 ACCCGTTGTGTGTGCTGCTTCCCTGCGCAATTTGTGTGGAAGAGGTGCGGTTGCTTTTCA 1073
 Db 1 ACCCGTTGTGTGTGCTGCTTCCCTGCGCAATTTGTGTGGAAGAGGTGCGGTTGCTTTTCA 60
 QY 1074 GCTTCAACATCTGCGGGATTCAGACATGCTTCCCAATTTGCTGCGGAGC 1133
 Db 61 GCTTCAACATCTGCGGGATTCAGACATGCTTCCCAATTTGCTGCGGAGC 120
 QY 1134 TGTATGTCGGGGCCACCAAGGCAATGACTGTTTGAAGAGGAGGCGACGCTCG 1193
 Db 121 TGTATGTCGGGGCCACCAAGGCAATGACTGTTTGAAGAGGAGGCGACGCTCG 180
 QY 1194 ACATCTGTGCTCTCTTGTGATGATTTGTTCCAGCGTGGCTGCAATTCAGATTGAGC 1253
 Db 181 ACATCTGTGCTCTCTTGTGATGATTTGTTCCAGCGTGGCTGCAATTCAGATTGAGC 240
 QY 1254 ACCATCTGTTTCCCGGCTTACCTCGGTGCTGCACTTGGCAAGGT 1296
 Db 241 ACCATCTGTTTCCCGGCTTACCTCGGTGCTGCACTTGGCAAGGT 283
 RESULT 8
 US-09-313-294A-3256
 ; Sequence 3256, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalauadi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 3256
 ; LENGTH: 266

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? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: misc feature
? OTHER INFORMATION: Incyte ID No. 6476212 700611205H
? NAME/KEY: unsure
? LOCATION: 262
? OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3256

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Query Match	12.2%;	Score 215.8;	DB 4;	Length 266;
Best Local Similarity	90.9%;	Pred. No. 1e-37;		
Matches 240; Conservative	0;	Mismatches 23;	Indels 1;	Gaps 1;

QY	1164	GGTTTGAGAACACAGACGGCAGCAGCAGCATCTGTGCTCTCTTGATGATGATGAT	1222
Db	1	GGTTTGAGAACACAGACGGCAGCAGCATCTGTGCTCTCTTGATGATGATGAT	60
QY	1224	TCACGGTGCCCTGCAGTTCCAGATTGAGACCAATCTGTTTTCCCGCTACCTGGTGCC	1283
Db	61	TCCATGGCGGGCTGCAGTTCCAGATTGAGACCAATCTGTTCGCCCGCTT - GCTCGATGCC	119
QY	1284	ACCTTCGCAAGSTTGCACCGGCGCCGCGACCTTTGGAAGAAGATGGCGTCATTTAT	1343
Db	120	ACCTTCGCAAGSTTGCAGCGCGCGGTGCTGACCTTTTGCAGAGCATGGCTGACCTTAT	179
QY	1344	CTGCAGCCCAATCTGGGGTCCAAATGCTTACATGGAAGCACTCAGGGCTGTGCAT	1403
Db	180	CCGACGACTCTCTTCTGGGACGCAAAATGCTTACATGGAAGCACTCAGGGCTGCCAT	239
QY	1404	TGCAGGCCAGGACCGGCTTCAAGTG	1427
Db	240	TGCAGGCCAGGACCGCACAAGG	263

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RESULT 9
US-09-249-585A-4
: Sequence 4, Application US/09249585A
: Patent No. 6417002
: GENERAL INFORMATION:
: APPLICANT: Horlick, Robert
: TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
: FILE REFERENCE: 0867/0D905
: CURRENT APPLICATION NUMBER: US/09/249,585A
: CURRENT FILING DATE: 1999-02-11
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 4
: LENGTH: 1926
: TYPE: DNA
: ORGANISM: Epstein Barr Virus
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1926)
: OTHER INFORMATION: template strand of EBNA-1 DNA
:US-09-249-585A-4

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Query Match	6.8%;	Score 120;	DB 4;	Length 1926;
Best Local Similarity	48.4%;	Pred. No. 6.1e-17;		
Matches 333;	Conservative 0;	Mismatches 355;	Indels 0;	Gaps 0;

Qy	193	CGACCTTCGATCTCAATCTCCGGGAGATGTACAGACTCAGCCCTAGCTCCCAACA	252
Db	307	CGTCTGATCTCCGCCGCTCTGCTCTCTCCCGCTCCGCCGCTCTCCCGCT	366
Qy	253	CCGGGGGCGGACCTCCCGCTTCTCAACCTGAGCGGAGGAGAGACGACGAGCTTGGC	312
Db	367	CCCGTCTCTGATCTCTCTCCCGCTCTGCTCTCTCCCGCTCTCCCGCTCTCCCGT	426
Qy	313	CGCTTACACCGCGCTCTGAGCGCGCGCGGCTCTCTCGCGCTTCTTGTGTGCGCGCTCTC	372
Db	427	CTGTGCTCTCTCCCGCTCTGATCTCTCTCCCGCTCTCTCCCGCTCTGATCTCTCTCC	486

Oy	373	GGACTACGCGCTCTCCCCGCGGTCCGCGCACTACCGCGCTCTCGCGAGTATCTC	432
Db	487	CGTCTCCCCGCTCTCCCCGCTCTGCTCTCTCCCCGCTCTGCTCTCTCCCCGCTCT	546
Oy	433	CGCGGCGCTTTCGACGCGTCCGCGCCGACCCCGAAGTCCAGTCTGCTCGATGCGGT	492
Db	547	CCCGGTCTTGCTCTCTCTCCCCGCTCTCCCCGCTCTCCCCGCTCTGCTCTCTCCCCG	606
Oy	493	CCTCTTCACGCGCGCTGTACTCTGCTCTCGCATGCGCGAGCGCTTGCGGCGCACTCT	552
Db	607	CCTCGTCTCCCCGCTCTCCCCGCTCTCCCCGCTCTGCTCTCCCCGCTCTGCTCTCT	666
Oy	553	CGCGGGGGGTCTCATTTGGCTCTGTTGGATCCAGTCCGCGTGGATGGGCGACAGACTCGG	612
Db	667	CCCCCTCTCCCCGCTCTCCCCGCTCTGCTCTCCCCGCTCTGCTCTCCCCGCTCTGCT	726
Oy	613	CCACGACGCACTACCGGCGCATCCGGTCTCTGACCGCGTCCGAGTCCGCGGAA	672
Db	727	CCTCCCCGCTCTGCTCTCCCCGCTCTCCCCGCTCTGCTCTCCCCGCTCTCCCCGCTCT	786
Oy	673	CTGCTCAACGGGCTTCAGACATCGCCTGTGGAAGTAAACCAACAGCACACACATCGC	732
Db	787	CGTCTCCCCGCTCTCCCCGCTCTGCTCTCTCTCCCCGCTCTCCCCGCTCTGCTCTCT	846
Oy	733	CTGCAACGCGCTGAGCCATGACCCGGACCTTCGACACATGCGCTCTTTGGCGTCTCCC	792
Db	847	CCCGGCTCTCCCCGCTCTGCTCTCCCCGCTCTCCCCGCTCTGCTCTCCCCGCTCTCCC	906
Oy	793	CAAGCTGTTGGGCAACATATGCTCTACTTTCTACCAAGGAGCCCTGAGCTTGGATGCCG	852
Db	907	CGTCTCTGCTCTCCCCGCTCTCCCCGCTCTGCTCTCTCTCCCCGCTCTGCTCTCCCCG	966
Oy	853	CTCGAAATTTTCATCAGCTACAGACAC	880
Db	967	CCTGCTCTTCACCTTCGCGCCCACTC	994

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RESULT 10
US-09-130-114-2
: Sequence 2, Application US/09130114
: Patent No. 5976807
: GENERAL INFORMATION:
: APPLICANT: HOTLICK, Robert A.
: APPLICANT: DamaJ, Bassem B.
: APPLICANT: Robbins, Alan K.
: TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
: TITLE OF INVENTION: From Multiple Transfected Epibosomes
: FILE REFERENCE: 0867/1D903US1
: CURRENT APPLICATION NUMBER: US/09/130,114
: CURRENT FILING DATE: 1998-08-06
: NUMBER OF SEQ. ID NOS: 16
: SOFTWARE: PASTESEQ for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 1931
: TYPE: DNA
: ORGANISM: EBNA
US-09-130-114-2

```

Query Match	6.8%;	Score 120;	DB 2;	Length 1931;
Best Local Similarity	48.4%;	Pred. No. 6.1e-17;		
Matches 333;	Conservative 0;	Mismatches 355;	Indels 0;	Gaps 0;

Qy	193	CGACCTTGAGATCTCAATCTCCGGAGAGGTATAGACGTCAAGGCTTGGTCTCCCAACA	252
Db	307	CGTCTCGTCTCTCCCGGCTCTGATCTCTCTCCCGGTCTGCCCGGCTCTCCCGTCT	366
Qy	253	CCCGGGGCGAGACCTCCCGCTTCTCAACCCTGGGGAGAGACGGCAACGGACCTTGGC	312
Db	367	CCCCGTCTGATCTCTCTCCCGGCTCTCTCTCTCCCGTCTCCCGGCTCTCTCCGT	426
Qy	313	CGCCTACCAACGCGCTCTGGAGGCGCGCGCTCTCTCCGCGCTTCTTGGTGGCGGCTCTC	372
Db	427	CGTGTCTCTCTCCCGGCTCTGATCTCTCTCCCGTCTCTCCCGGCTCTGATCTCTCTCC	486

QY	37	TAGTAAAGCGGCTCTCCCGCGCGATCAACGCGCGCTCCGTGGGAGAGTAACTTC	433
Db	487	CGTCTCTCCCGTCTCTCCCGTCTGTGCTCTCTCCCGTCTCTGTCCTCTCCCGTCT	546
QY	433	CGCGGCGCTTTTGAAACGCGTGGGCGGCCACCCCAAGGTCAAGCTCGTCTGATGAGCGT	492
Db	547	CCCCGCTCTGTCTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTGCTCTCTCCCGT	608
QY	493	CCTCTTTCAAGCGCGCTGTACCTGTCTGTGATGAGCGCAAGCGCTTGAGGAGCACTCT	552
Db	607	CTCGTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCGTCTCGTCTCTCTCTCTCTCT	666
QY	553	CGGGGGGGGTCTATAGGCTTGTCTGTGATTCAGTCTGGCTGATGAGGCAAGCTGGG	612
Db	667	CCCCGCTCTCCCGTCTCTCCCGTCTGTGCTCTCTCCCGTCTGTGCTCTCTCCCGTCTGT	728
QY	613	CCACACACGATCATCCGGCATCCGGCTCTGACCGCGCTGAGAGGCTCTCCGGGAA	672
Db	727	CTCTCCCGTCTGTCTCTCTCCCGTCTCTCCCGTCTCTGCTCTCTCCCGTCTCTCCCGTCT	786
QY	673	CTGCTTCACCGGCTCAGCATGCGCTGTGAGTGAAGTAAACAACAAGCAACAATGCG	732
Db	787	CGTCTCTCCCGTCTCTCCCGTCTGTGCTCTCTCCCGTCTCTCCCGTCTCTGCTCTCT	846
QY	733	CTGCAACAGCTGGACCATGACCCGAGCTCTCAGAGCATGCGGCTTTTGCGCTCTCCC	792
Db	847	CCCCGCTCTCCCGTCTGTGCTCTCCCGTCTCTCCCGTCTCTCGTCTCTCCCGTCTCTCC	906
QY	793	CAAGCTGTTTGGGACATATGCTCTACTTCTAACAAAGAACCTGGGCTTGTATGCCGC	852
Db	907	CGTCTCTGTCTCTCCCGTCTCTCCCGTCTCTGCTCTCTCCCGTCTGTCTCTCCCGT	966
QY	853	CTGGAATCTTTCATCAGCTACGACAC	880
Db	967	CTCTGCTCTCACTCTCGGCGCCAGCTC	994

RESULT 11
 US-08-232-463-14
 Sequence 14, Application US/08232463
 Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STANDARDS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ19-pc-Fls
US-08-232-463-14

US-08-232-463-14

Query Match	4.4%;	Score 77.6;	DB 1;	Length 7218;
Best Local Similarity	4.9%;	Pred. No. 1.1e-07;		
Matches 20;	Conservative 242;	Mismatches 146;	Indels 0;	Gaps 0;

[illegible]

US-08-343-428-1
; Sequence 1, Application US/08343428
; Patent No. 5665586
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Etsuo
; APPLICANT: Tezuzuki, Hiroshige
; APPLICANT: Kitadokoro, Kengo
; APPLICANT: Shin, Naasaru
; APPLICANT: Teraoka, Hiroshi
; TITLE OF INVENTION: No. 5665586e1 Protease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720KB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS Dos 5.0
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,428

FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/J93/00592
FILING DATE: 30-APR-1993
APPLICATION NUMBER: JAPAN 4-126511
FILING DATE: 19-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
REFERENCE/DOCKET NUMBER: SHGN-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE: Streptomyces fradiae
ORGANISM: Streptomyces fradiae
FEATURE:
NAME/KEY: -35 signal
LOCATION: 359..364
IDENTIFICATION METHOD: by experiment
NAME/KEY: -10 signal
LOCATION: 378..383
IDENTIFICATION METHOD: by experiment
NAME/KEY: CDS
LOCATION: 435..1505
IDENTIFICATION METHOD: by experiment
NAME/KEY: sig peptide
LOCATION: 435..944
IDENTIFICATION METHOD: by experiment
US-08-343-428-1

Query Match 4.4%; Score 77.2; DB 1; Length 2064;

Best Local Similarity 43.6%; Pred. No. 9.7e-08; Matches 394; Conservative 0; Mismatches 508; Indels 2; Gaps 1;

QY 11 CCTCTCTCTCCCAATCTCCCGCTCCCGCTACCAATACAGACCAAGCGCAT 70
DB 460 CCGGTCTGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 519
QY 71 CCGAGCCAGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 128
DB 520 CCGAGCGCGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 579
QY 129 CCGCGCGCGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 188
DB 580 CCGCGCGCGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 639
QY 189 CCGAGCACTCTGATCTCCATCTCCGCGAGCGTACGAGTACGCGCTGAGTCCC 248
DB 640 CCGGCAACCGCGCAATCTGTGTACGAGTACGAGTACGCGCTGAGTCCC 639
QY 249 ACCACCGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 308
DB 700 CCGCGCGCGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 759
QY 309 TCGCGCGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 368
DB 760 CCGCGCGCGCGCGCATGCGCGCTCTGTGATGCAATGCG--GCCCGCGGAG 819
QY 369 TCTCTGACTACGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 428
DB 820 ACCGAGTCTCGGTGAGGCGCATCTCTCTCTCTCTCTCTCTCTCTCTCT 879
QY 429 CTTCTCGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 488
DB 880 AGGTCTCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939

QY 489 CCGTCTCTTTTACGCGCGCTGTACTCTGTCATGCGGACGCGCTGCGGAC 548
DB 940 GCGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 999
QY 549 TCTCTCGCGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 608
DB 1000 AGGTCT 1059
QY 609 CCGGCG 668
DB 1060 CCG 1119
QY 669 GGAAGTCT 728
DB 1120 CCG 1179
QY 729 TCG 788
DB 1180 ACCGTCT 1239
QY 789 CCG 848
DB 1240 CCG 1299
QY 849 CCG 908
DB 1300 TCG 1359
QY 909 CCGG 912
DB 1360 CCGG 1363

RESULT 13

5212296-16

PATENT NO. 5212296

APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
TEPPERMAN, JAMES M.

TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
CYTOCHROMES

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781

FILING DATE: 23-AUG-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499

FILING DATE: 12-JAN-1990

APPLICATION NUMBER: 405,605

FILING DATE: 11-SEP-1989

SEQ ID NO: 16

LENGTH: 1221

5212296-16

Query Match 4.3%; Score 75.6; DB 6; Length 1221;

Best Local Similarity 44.1%; Pred. No. 1.9e-07; Matches 315; Conservative 0; Mismatches 399; Indels 0; Gaps 0;

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DB 369 CCG 428
QY 187 CCG 246
DB 429 CCG 488
QY 247 CCG 306
DB 489 CCG 548
QY 307 CTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366

Db 549 CACGAGACGAGGCGCTCAACGAGGAAACACTCGGGATTACTGAGCGGCT 608
QY 367 CCTCTGACTACGCGCTTCCCCCGCTCCGACACTACGCGCTCTCTCGCGAGCT 426
Db 609 CATACCCAGATTCCAGACCAACCGGCGCGGCGCTGGGCGCTTGTCTCCACCA 668
QY 427 ATCTCCGCGGGCTCTTGAACGCGTGGCCCAACCCCAAGTTCAGTCTCGTAT 486
Db 669 GCTGGCCAAAGGAGATGACGTTGAGAACTGATTTCCACCGCATGCTGCTCAT 728
QY 487 GGCCTCTCTTCTACGCGCGCTGTATCTGTCTTCGATGCGACAGCGCTGGGCGCA 546
Db 729 CGCGGCGACAGAACACCGCTCTGATGATCTCCCTAGCGTATACCTCTGAGACA 788
QY 547 CTTCTTCGCGGGGGTCTATTGGCTTCTGTGATCACTCCGGCTGATGGGCGACA 606
Db 789 CCCCAGCATAGCGCCGCTGCGCGCGACCGAGCTGTGCGCGCGCGGTGGAGGA 848
QY 607 CTGGGGCACACCGCATACCGGCGCATCGGCTCTGACCGGCGTGGAGGTCTTC 666
Db 849 ACTGCTCGTACTCTGCGCATCGCCGACATCGCGGCGCGCGCTCCACCGCGACAT 908
QY 667 CGGGAATGCTCTACCGGCTCTGACATCGCTGTGAGTGAACCAACACGACCA 726
Db 909 CGAGTTCGAGGGGACCTCATTCGGGCGGCGAGGGGCTGATGCTGTAACCTGATAGC 968
QY 727 CATGCTTCGAACAGCTTGACCATGACCGGACCTTCAGACATACGCGCTTTGGCGT 786
Db 969 CAACCGGAGCGGACGCTGTACGAGACCGGACGCTTCGACATCCACCGCTCGGCGG 1028
QY 787 CTCCCCAAGCTGTTCGGCAACATATGTCCTTCTTACCAACGAGCCCTGGC 840
Db 1029 CCACCACTTCGCTTGGCTTGGCGGTGACCAAGTGTGCGGCGAGACTTCG 1082

RESULT 14
5212296-5
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE, HARDER, PATRICIA A., LENO, KENNETH
; J. O'KEEFE, DANIEL P., OMER, CHARLES A., ROMESSER, JAMES A.
; TEPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
; CYTOCHROMES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/569, 781
; FILING DATE: 23-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 464,499
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO: 5
; LENGTH: 1879
5212296-5

Query Match 4.3%; Score 75.6; DB 6; Length 1879;
Best Local Similarity 44.1%; Pred. No. 2,1e-07;
Matches 315; Conservative 0; Mismatches 399; Indels 0; Gaps 0;
QY 127 CGCGCGCGCGCGCGCGACGTCGCGCATGATCTCTCCAGAGAGTCCGCGCTCAACGCTTC 186
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QY 187 CGCGGACGACCTCTGATCTTCATCTCCGCGGACGTCGACGTCACGCGCTGGCTCC 246
Db 556 CGCGGACCTGCTAGTGTAGTTCGCGCTCCGCGTCCCTCCATGATGATTCGCGACTCT 615
QY 247 CCACCAACCGCGGCGGACCTTCGCTTCTGACCTTCGCGGCGGACGACGCGACCGAC 306
Db 616 CGGCGTGCCTTACCGCGGACGAGTCTTCCAGAGACGAGGCGGCTGTGACGTC 675
QY 307 CTTGGCGGCTTACCAACCGCGGCTCGGCGCGCGCTCTCTCGCGGCTTCTTCTTGGCG 366

Db 676 CACGAGCGGAGAGCGGCTCACCGCGGAAACGACCTTCGCGGTTACTGAGCGGCT 735
QY 367 CCTCTGACTACGCGCTTCCCCCGCTCCGACACTACGCGCTCTCTCGCGAGCT 426
Db 736 CATACCCAGATTCCAGACCAACCGGCGCGGCGCTGGGCGCTTGTCTCCACCA 795
QY 427 ATCTCCGCGGGCTCTTGAACGCGTGGCCCAACCCCAAGTTCAGTCTCGTAT 486
Db 796 GCTGGCCAAAGGAGATGACGTTGAGAACTGATTTCCACCGCATGCTGCTCAT 855
QY 487 GGCCTCTCTTCTACGCGCGCTGTATCTGTCTTCGATGCGACAGCGCTGGGCGCA 546
Db 856 CGCGGCGACAGAACGAGGCTGATGACCTCCCTAGCGTATACCTCTGAGACA 915
QY 547 CTTCTTCGCGGGGGTCTATTGGCTTCTGTGATCACTCCGGCTGATGGGCGACA 606
Db 916 CCCCAGCATAGCGCCGCTGCGCGCGACCGAGCTGTGCGCGCGCGGTGGAGGA 975
QY 607 CTGGGGCACACCGCATACCGGCGCATCGGCTCTGACCGGCGTGGAGGTCTTC 666
Db 976 ACTGCTCGTACTCTGCGCATCGCCGACATCGCGGCGCGCGCTCCACCGCGACAT 1035
QY 667 CGGGAATGCTCTACCGGCTCTGACATCGCTGTGAGTGAACCAACACGACCA 726
Db 1036 CGAGTTCGAGGGGACCTCATTCGGGCGGCGAGGGGCTGATGCTGTAACCTGATAGC 1095
QY 727 CATGCTTCGAACAGCTTGACCATGACCGGACCTTCAGACATACGCGCTTTGGCGT 786
Db 1096 CAACCGGAGCGGACGCTGTACGAGACCGGACGCTTCGACATCCACCGCTCGGCGG 1155
QY 787 CTCCCCAAGCTGTTCGGCAACATATGTCCTTCTTACCAACGAGCCCTGGC 840
Db 1156 CCACCACTTCGCTTGGCTTGGCGGTGACCAAGTGTGCGGCGAGACTTCG 1209

RESULT 15
US-09-103-840A-1/C
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 441529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 4.1%; Score 72.8; DB 3; Length 441529;
Best Local Similarity 46.2%; Pred. No. 5.8e-06;
Matches 279; Conservative 0; Mismatches 322; Indels 3; Gaps 1;
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Db 1218147 CGTACAGCAACCGCGGAGTGGCGCGCTTCCGCAATGCGGCAATGCGCGCTTGGCCG 1218088
QY 145 CGTGGCATGATTCCTTCAAGAGAGTCCGCGGTACAGCTTCCGCGGAGACCTCTGAT 204
Db 1218087 CATTTGCGCGCTTCCGCGGACCGCGGCTTGGCGCGGCGCGCGCGCGG 1218028
QY 205 CTCATCTCGCGGAGATGACAGCTGACGCGCTTGTCTTCCCAACACCGGCGCGCA 264

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Db 1218027 CCCCgcggtTccGcCAGcccccGATGcGAAcAGcCAccGgGcGgGccGgGcCC 1217968
QY 265 CcTccCGcCTTcTAcCCcCTGgGgGgGAGAGcGcCAcGgAcGcCTTccGccGcTAcCAcc 324
Db 1217967 GgCccCGcGcGcTAcCAcCgCgTgCAcCGcTgCcGccCGcGcGcCAcGgCgGcCAcGc 1217908
QY 325 GcCCTcGgGcGcGcCgCgCgTcCTcGcGcGcCTTcTtGgTtGcCgGcCCTcTGAcTAcGcGcT 384
Db 1217907 CgGcGATgCccCGTgCccGcGcGcGcGcCccGcGcTAcCgCccCTTgAcCgGcGcGcGcG 1217848
QY 385 CTcCccCGcGcTcGcGcGcTAcCgCgCgCCTcCTcGcGcAcGcTAcCTcGcGgGcCTT 444
Db 1217847 CccGcCgTAcCgCgCgTgCccGcGcGcGcCgCgCgCgCgCgCgCgCgCgCgCgCgC 1217788
QY 445 GgAAcGcGTgGgGcCccCAcCccCAAGTcCAgCT--cGTcTGAATgGcCGTcCTcTAc 501
Db 1217787 GgCgGgGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGcGc 1217728
QY 502 GcCgCgCgCTGAcCTcGTcCTGcATGcGcCAGcGcGcCTGgGcGcGcAcCTcCTcGcGgGgG 561
Db 1217727 GgCTGAGgGcCAGAGcCccCTTtGcGcGcGcGcCccGcGcGcCAcCGTccCgCgGcCC 1217668
QY 562 TcTcATTgGcTtGcTcGATcCAgTcGgCgTgATgGcCAcGAcTcGgGcCAcCAcCG 621
Db 1217667 GcCgGgGcCAGcCAcGcCccCAcGcCTgGgGcTtGcCTcCgGcCccGcGcGcCAcCGT 1217608
QY 622 CATcAcCGGcCATcCGcTcCTcGAcCgCgTgTgGcAGcTcTcCgGgAAcTgCCTAc 681
Db 1217607 CccCAcCGcGcCccGcGcGcTcCAcCGcGcCgCgCgCgCTgCTGAcGcCAcTAc 1217548
QY 682 CgGc 685
Db 1217547 CcGc 1217544

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Search completed: January 1, 2004, 00:05:24
 Job time : 99.5326 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 21:04:45 ; Search time 439.973 Seconds
(without alignments)
13877.414 Million cell updates/sec

Title: US-09-857-524B-3

Sequence: 1 gacagagccctctctc.....tcaaaaaaaaaaaaaa 1764

Scoring table: IDENTITY_NIC
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Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/prodata/2/pubpna/PCF_NEW_PUB.seq:*
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- 11: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
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- 16: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
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- 18: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491.2	27.8	1702	14	US-10-029-756-26 Sequence 26, Appl
2	439.2	24.9	1350	10	US-09-938-842A-558 Sequence 558, Appl
3	365.4	20.7	1685	14	US-10-029-756-4 Sequence 4, Appl
4	237.8	13.5	265	9	US-09-923-876-5116 Sequence 5116, Ap
5	237.8	13.5	265	12	US-09-923-876-5116 Sequence 5116, Ap
6	203.8	11.6	657	9	US-09-770-149-494 Sequence 494, Appl
7	152.4	8.6	287	10	US-09-878-574-3260 Sequence 3260, Ap
8	150.2	8.5	1098	12	US-10-369-493-27824 Sequence 27824, A
9	129	7.3	476	9	US-09-770-444-39 Sequence 39, Appl
10	120.6	6.8	1095	15	US-10-156-761-2285 Sequence 2285, Ap
11	120.6	6.8	9025608	15	US-10-156-761-1 Sequence 1, Appl
12	115.2	6.5	480	10	US-09-924-035A-370 Sequence 370, Appl
13	114	6.5	263	10	US-09-878-574-9255 Sequence 9255, Ap
14	112	6.3	1360	10	US-09-967-477B-7 Sequence 7, Appl
15	100.4	5.7	12733	15	US-10-032-393-47 Sequence 47, Appl

16	100.4	5.7	12739	15	US-10-032-393-8 Sequence 8, Appl
17	94.8	5.4	1059	15	US-10-156-761-1580 Sequence 1580, Ap
18	91.4	5.2	3163	13	US-10-292-798-1513 Sequence 1513, Ap
19	91.4	5.2	3163	13	US-10-017-161-1857 Sequence 1857, Ap
20	91.4	5.2	3133	13	US-10-292-798-1191 Sequence 1191, Ap
21	91	5.2	3133	12	US-10-017-161-1483 Sequence 1483, Ap
22	90.4	5.1	1117	12	US-10-292-798-1141 Sequence 1141, Ap
23	90.4	5.1	1117	13	US-10-017-161-1403 Sequence 1403, Ap
24	88.4	5.0	1362	13	US-09-769-863-13 Sequence 13, Appl
25	88.4	5.0	1362	13	US-10-054-534B-13 Sequence 13, Appl
26	88.4	5.0	1362	13	US-10-431-952-13 Sequence 13, Appl
27	88.2	5.0	5452	12	US-10-292-798-1189 Sequence 1189, Ap
28	88.2	5.0	5452	13	US-10-017-161-1481 Sequence 1481, Ap
29	87.2	4.9	1320	13	US-09-769-863-28 Sequence 28, Appl
30	87.2	4.9	1320	13	US-10-054-534B-28 Sequence 28, Appl
31	87.2	4.9	1320	13	US-10-431-952-28 Sequence 28, Appl
32	83.6	4.7	1815	10	US-09-758-269-13 Sequence 13, Appl
33	82	4.6	239	9	US-09-923-876-3376 Sequence 3376, Ap
34	82	4.6	239	12	US-09-923-876-3376 Sequence 3376, Ap
35	80.8	4.6	1687	15	US-10-163-198-40 Sequence 40, Appl
36	79.4	4.5	1329	13	US-09-804-682-29 Sequence 29, Appl
37	76.8	4.4	1064	10	US-09-804-682-29 Sequence 29, Appl
38	76.4	4.3	1574	12	US-10-324-316-11 Sequence 11, Appl
39	76.2	4.3	1221	13	US-10-214-446-1 Sequence 1, Appl
40	76	4.3	720	14	US-10-101-487-74 Sequence 74, Appl
41	76	4.3	720	14	US-10-101-487-74 Sequence 74, Appl
42	75.8	4.3	1320	10	US-09-967-477B-3 Sequence 3, Appl
43	75.4	4.3	1041	15	US-10-156-761-1188 Sequence 1188, Ap
44	75	4.3	1695	15	US-10-156-761-3949 Sequence 3949, Ap
45	74.2	4.2	1125	15	US-10-156-761-5034 Sequence 5034, Ap

ALIGNMENTS

RESULT 1
US-10-029-756-26
Sequence 26, Application US/10029756
Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thoma, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029, 756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934, 254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19, 827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANG UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 1702 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 48..1406
 NAME/KEY: CDS
 LOCATION: 48..1406
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 us-10-029-756-26

Query Match 27.8%; Score 491.2; DB 14; Length 1702;
 Best Local Similarity 62.0%; Pred. No. 2,5e-124;
 Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

155 ATCTCTCAAGAGCTCCGCGCTCAGCTTCCGCGCAGCACTCTGGATCTCCATCTCC 214
 Db ATACGGCGGAGAGACCTCCGCGCCACACAAGTCCGGCATCTCTGATCTCATCCAG 131

215 GGGAGCTGTACGACGTACGCGCTGCTCCCAACACCGCGCGGACCTCCGCTT 274
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275 CTCACCTCTGCGGGGAGAGCGCACGAGCGCTTCCGCGCTACACCGCGCTCGGGC 334
 Db CTCAGTGTGGCGCGGAGAGAGTACCGACGCTTTCATTTGGTACACCGGGGACGGCG 251

335 CGCGCGCTCTCCGCGCGCTTCTTCTGTTG-----CGGCTCTCTGACTACGCGCTCC 388
 Db TGGGGGATGTGATCTCGGCTTTTACCGGCTACTACTCAAGACTTCCGAAGTCTG 311

389 CCGCGCTCGCGGAGCTACCGCGCGCTCTCGCGGAGCTATCTCCGCGGCTCTTGGAA 448
 Db GAGATCTCCAGAGACTACCGGAGGCTTTGAGACGAGATGTGCGGATCTCGGATCTGAG 371

449 CGGCTGGCGGCGGCGGCGGAGTCTCACTGCTCTGATGCGCGCTCTCTTCTACGCGCG 508
 Db AAGAGGGGCGGCGGCGGAGTCTGATGCGCTGCGCGCTTCCGCGGCTGATGAGCGCGCATC 431

509 CTGTACTCTGCTCTCGCATCGCGAGCGCGCTGGCGGCGGAGCTCTCTCGCGGGGCTCAT 568
 Db GTCTACGCGGCTGCTGCGGTGAGATCGGTGGAATTCATGCTCTCTCGCGGCGGCTCTG 491

569 GGGCTTCTGTGATTCAGTCTCGGTGATGGGCGGAGCTCTGGCGGCGGAGCGGATACC 628
 Db GGGCTTCTGTGATTCAGTCTCGGTGATGGGCGGAGCTCTGGCGGCGGAGCGGATACC 551

629 GGGCATCCGGTCTCTCGAGCGCGGTCTGTCAGAGTGTCTCTCGGGAATGCGCTCACCGGCTC 688
 Db CCAACCGGTGATTCAGAGATTCAGCACTCATAGCAGGCGGAGATCTCAACCGGATC 611

689 AGCATGCTCTGTGAGAGTGTAAACAACAAGCGGAGCGGAGTCTCTGCAACAGCTGGAG 748
 Db AGCATGCTCTGTGAGAGTGTAAACAACAAGCGGAGCGGAGTCTCTGCAACAGCTGGAG 671

749 CATGACCGGAGCTCTGAGACATGCGGCTTCTGCGGTCTCCCAAGCTCTTGGGCAAC 808
 Db TAGGACCGGAGCTCTGAGACATGCGGCTTCTGCGGTCTCCCAAGCTCTTCAACTCC 731

809 ATATGCTCTACTTCTTACCAAGGAGCGCTGCGGTGATGCGCGCTGGAATTTCTTATC 868
 Db ATGACCTCTGCTTCTTATGCGCGAGTCTGAAATTCAGCAAGGAGCGGATCTTATGTC 791

869 AGCTACAGGAGCTGAGACTTCTACCGGCTATGTCATGCGGAGGATTAATTTCTTCCGC 928
 Db AGCTACAGGAGCTGAGACTTCTACCGGCTATGTCATGTCGCGGAGTCAACTTTTATC 851

929 CAGTCCGCGCTGTCTCTTCAAGGAGAGAGGTTGCGGAGGCTTCTTGAATGCGG 988
 Db CAGACCTTTTATTTGCTCTCAAGGAGGAGGTTCTCTGACCGGCTTAAACTTATG 911

QY 989 GGGATCGCCACATTTCTGGGCTTGATACCCGTTGCTGAGCTTCCCTGCGGAAATGGTGG 1048
 Db 912 GGTATCGCGGTTTCTGAGAGTGTTCGCGCTCTTGTATCTTGTCTCCGAACTGGCCT 974

QY 1049 GAGAGGTGCGGTTTGTGCTTTTCACTTTCACATCTGCGGAGTTCAGCACTTCAATTC 1108
 Db 972 GAACGTTGGGTTGCTGCTCATCAGCTTTCGCGTACCGGAGTTCAGCACTGAGTTTC 1031

QY 1109 TGCCTGACCACTTCTCTGCGGAGTATGTCGCGGAGCGGAGGAGGAGTTCAGTCTGTT 1168
 Db 1032 ACCTCAACCACTTCTCTGCGGAGTATGTCGCGGAGCGGAGGAGGAGTTCAGTCTGTT 1091

QY 1169 GAGAGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1228
 Db 1092 GAGAGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1151

QY 1229 GGTGGCTGTGAGTTCAGATTCAGCACTTGTTCCTCCGCTTACCTTGGTGGCACTT 1288
 Db 1152 GGTGGCTGTGAGTTCAGATTCAGCACTTGTTCCTCCGCTTACCTTGGTGGCACTT 1211

QY 1289 CGAAGGTTCACCGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348
 Db 1212 AGGAGAGTTCGCGCTTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1271

QY 1349 GGCACATTCCTG--GATGCAATGTGCTTACATGGAAGACACTCAGGCGTGTGCAATTG 1405
 Db 1272 TTTGGGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1331

QY 1406 CAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1462
 Db 1332 CAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1391

QY 1463 AACACCATGATGATTAATGGAT 1484
 Db 1392 AACACCATGATGATTAATGGAT 1413

RESULT 2
 US-09-938-842A-558
 ; Sequence 558, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 558
 ; LENGTH: 1350
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-558

Query Match 24.9%; Score 439.2; DB 10; Length 1350;
 Best Local Similarity 59.8%; Pred. No. 4.4e-110;
 Matches 773; Conservative 0; Mismatches 513; Indels 6; Gaps 2;

QY 189 CCGACGACCTCTGGATCTCCATCTCCGCGAGCGTGAAGAGTCAAGCGCTTGGCTCCCC 248
 Db 62 CTGAGATCTATGATGCGGATTCAGGCAAGGTCTAACAAGCTCTCGATTGGATTAAAA 121

QY 249 ACCACCCGGGCGGCGACCTCCCGCTTCTACCTTCGGGGGAGAGCCGACCGACCT 308
 Db 122 CTCATCCCGGAGGCGACAGGATGATTCGAATCTCGTGGTGAAGAGTCACCGATGCTT 181
 QY 309 TCGCCGCTTACACCC---GCCCTCGGCGGCGGCTCTCCGCGGCTTCTGTTGGCC 365
 Db 182 TCTATCCATTTTCAATCCGGAACGCTTGGACCATCTCGACATCTCTTCAACGCGTTAC 241
 QY 366 GCTCTCTGACTAGGCGGCTCCCGCGGTCGCGGATACCGGCGGCTCTGCGGCGAG 425
 Db 242 ACATCAGAGATTTTCAAGTCTCCGAAGTCTCAGCGATTAACGCTGATGCGTCCGAGT 301
 QY 426 TATCTCTCGGCGGCTCTTCGAAAGCGTCGCGGCCACCCCAAGTCCAGCTGCTCTGA 485
 Db 302 TTGTAACCTCGGCTCTTCGAAAACAAAGTACGTTACTCTTCACTACCTTACGCTTGG 361
 QY 486 TGGCGCTCTCTTCAAGCGCGGCTGACTGCTCTCGATGCGGACGCGCTGGGCGG 545
 Db 362 TCGCCGCTATGTTCTCGAGTCTCTACGAGTCTTGGCTTGTACCTCGTCTTGGCTC 421
 QY 546 ACCTCTCGGCGGCTCTTCTGAAAGCGTCGCGGCCACCCCAAGTCCAGCTGCTCTGA 605
 Db 422 ACCAAATCGCGCGGCTCTCTGCTCTCTGATCCAGAGCGCTTACATAGTCTCAG 481
 QY 606 ACTCGGCGCACACCGCATACCGGCTCCGCTCCGACGCGTCTGTCAGAGTCTCT 665
 Db 482 ATTCTGTGATTAAGTATATCATATCGAACAAATCTTATTAAGATTCGCTGAGCTTCT 541
 QY 666 CCGGGAAGTCTCTACCGGCTGAGCTGCTGCTGAGTGAAGTGAACCAACACGAC 725
 Db 542 CCGGTAAGTCTCTACCGGAACTCAATCGTGGTGAATGAGCTCAACAAATGCTCANT 601
 QY 726 ACATCGCTGCAACAGCTGAGCAATGAGACCGGACCTCCAGGACATGCGGCTTGGCG 785
 Db 602 ATCTACTGTGTAACAGCTGATAGATCAATCAACATCCCTGCTTGGCGG 661
 QY 786 TCTCCCAAGCTGTTGCGGAATATAGTCTACTTCAACGAGACCGTGGCGGCT 845
 Db 662 TCTCCACCAATCTCTCTCTCATTTGACCTGAGATTTCTACGATCCGAAATCACTTGG 721
 QY 846 ATGCGGCTGGAATTTCTGATGAGTACGACGACGACGACCTTCTACCGGTAATGGA 905
 Db 722 ATCAGTCCGGAATTTCTGATGAGTATCAACATTTACTTATTAATCCAGTATGCT 781
 QY 906 TCGCCAGATTAATCTTCTGCGGAGTCCGCTGCTTCTGCTCAGAGAGAGAGGCTG 965
 Db 782 TTGGAAGATCAATCTCTTCAATCAACGTTTCTGCTCTTCAACGTAAGTAC 841
 QY 966 CGGAGGCTGCTTGAATGAGTGGGAGGAGGAGCAATTTGCGGCTGATCCGCTGCTG 1025
 Db 842 CAGATGCTGTTAACTTCCGGAATCTTACTTCTGAGCTTGGATTCCTCCACTTTAG 901
 QY 1026 TGGCTTCCCTGCGGAATTTGTTGAGAGAGGAGTCCGTTTGTCTTTTCACTTCCACT 1085
 Db 902 TCTCATGTGTAAGAACTGGCTGAGAGATTTCTTCTGCTTCAAGATTCACGCTCA 961
 QY 1086 GCGGGAATTAAGACGTTCAATTTGCTGAACCACTTCTGCTGAGAGTATGTCGGG 1145
 Db 962 CGCGGCTTCAACATTTCAATTCACGTTAACATTTGCTGATGCTAGTGTGTC 1021
 QY 1146 CACCAAGGCAATGAGTGGTTTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205
 Db 1022 CACCAAGGCAATGAGTGGTTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1081
 QY 1206 CTCCTTGAATGAGTGGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1265
 Db 1082 GATCATATCAATGAGTGGTTTCTTGGAGATTTACAGTTTGAAGTTCAGATTTTCTTC 1141
 QY 1266 CCGGCTTCTGAGTGGTCACTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1325
 Db 1142 CTGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1201
 QY 1326 AGCATGGGCTCACTTATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1385

Db 1202 AGCATATCTTCCGATAGAGATATGTCGTTGGAAGCAATGTTGACCATTAACA 1261
 QY 1386 CACTCAGGCTGCTCTTATTCAGGCGGAGACCGCTCAAGTGTGTGCTCCGAAGAT 1445
 Db 1262 CTTTGAAGCAGACCTTATCAAGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1318
 QY 1446 TGGTATGGAGGCTGTGAACCCATGATTA 1477
 Db 1319 TGGTTGGAGAGCTTGAATACTCATGGCTAA 1350

RESULT 3
 US-10-029-756-4
 ; Sequence 4; Application US/10029756
 ; Publication No. US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; DELTA 6-DESATURASE
 ;
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/029,756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
 ;
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4366
 ; TELEFAX: (516) 742-4366
 ; TELEBOX: 230 901 SANS UR
 ;
 ; INFORMATION FOR SEQ ID NO: 4:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: DNA (genomic)
 ;
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-029-756-4
 Query Match 20.7%; Score 365.4; DB 14; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 8.9e-90;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGCTCCGCTCAGCGCTTCCGCGAGACCTTGTGATCTTCATCTCC 214
 Db 68 ATTACTCAGAGTGAATCAAGAACCAAGATAACCCGAGATCTATGATCTCGATTCAA 127
 QY 215 GCGAGCTGTAGAGTCAAGCGCTCCGCCACCAACCGGCGGAGGAGGAGGAGGAGGAGG 274
 Db 128 GGAAGAGCTATGATGTTTGGATTGGGTAAGACATTCAGGTGGAGCTTCTCTTG 187
 QY 275 CTCACCTTGGCGGCGGAGAGCGACGAGAGGCTTGGCGGCTTACACCGGCTCGGCG 334
 Db 188 AAGAGCTTCTGCTGCTCAAGAGTACTGATGATTTGTTGATTCATCTGCTCTTACA 247

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Qy 335 CGCCCGCTCCCGCCGCTCTTGTG--CCGCTCTGACGAGCGCTCCCC 391
Db 248 TGGAAGATCTGATAGATTTTACCTGGGATATATTAAGATTAATCTGTTTCGAG 307
Qy 392 GCGTCGCGCACTACCGCCGCTCTGCGGAGTATCTCCGCGGCTCTTGAAGC 451
Db 308 GTTCTTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 367
Qy 452 GTGCGCCCAACCCCAAGCTGCTGCTGATGAGCCGCTCTTACGCGCGCTG 511
Db 368 AAGGATATATATATATATATATATATATATATATATATATATATATATAT 427
Qy 512 TACCTGCTCTGCGAGCGCGCTGCGGAGCGAGCTCTGCGGAGGCTCATGAGC 571
Db 428 TATGGGTTTGTGTTGTGAGGCTTTGTGATATTTGTTGAGGTTGATGAGG 487
Qy 572 TTGCTGATGATGCTGCGCTGATGAGGCGAGCTGCGGCGACACCGCATCCG 631
Db 488 TTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547
Qy 632 CATCCGCTCTGACCGCGCTGCGAGGCTCTCCGGAATGCTTACCGGCTGAGC 691
Db 548 GATTCAAGCTTAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 607
Qy 692 ATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
Db 608 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
Qy 752 GACCGGAGCTCTGACGATGCGCTCTTGGCGCTCTCCCGAAGCTTTCGCGACA 811
Db 668 GACCGTATTAATATATATATATATATATATATATATATATATATATATAT 727
Qy 812 TGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 871
Db 728 ACCTCTATATATATATATATATATATATATATATATATATATATATAT 787
Qy 872 TACGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
Db 788 TATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
Qy 932 TCCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 991
Db 848 TCTCTATATATATATATATATATATATATATATATATATATATATAT 907
Qy 992 GTGCGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1051
Db 908 TGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 967
Qy 1052 AGGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1111
Db 968 AGAATATATATATATATATATATATATATATATATATATATATATAT 1027
Qy 1112 CTGAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1171
Db 1028 TTGAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1087
Qy 1172 AAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1231
Db 1088 AAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1147
Qy 1232 GAGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1291
Db 1148 GAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1207
Qy 1292 AAGGCTGACGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1351
Db 1208 AAGATCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1267
Qy 1352 ACATCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1411
Db 1268 TCTTCTCAAGGCGCAATGAAATGACACTGAGAACATGAGGAGGAGGAGG 1327

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Qy 1412 AGGACCGCTACAGATGATGATGATGATGATGATGATGATGATGATGAT 1471
Db 1328 AGG--GATATACCAAGCGGCTCCGAGAAATTTGATGAGGAGCTTTCACAT 1384
Qy 1472 GATATAA 1478
Db 1385 GATATAA 1391

```

RESULT 4

```

US-09-923-876-5116
; Sequence 5116, Application US/09923876
; Patent No. US2002013958A1
; GENERAL INFORMATION:
; APPLICANT: laljudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (lco)
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 5116
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2002013958A1 700456385H1
US-09-923-876-5116

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Query Match 13.5%; Score 237.8; DB 9; Length 265;
Best Local Similarity 93.6%; Pred. No. 4.6e-55;
Matches 248; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy 728 ATGCGCTGCAACGCTGGAACATGACCGGAGCTCTCAGACATGCGCGCTTGGCCG 787
Db 1 ATGCGCTGCAACGCTGGAACATGACCGGAGCTCTCAGACATGCGCGCTTGGCCG 60
Qy 788 TCCCGCAAGCTGTCGCAACATATGCTCTACTTCTACCAAGGACCTGCGCTGAT 847
Db 61 TCCCGCAAGCTGTCGCAACATATGCTCTACTTCTACCAAGGACCTGCGCTGAT 120
Qy 848 GCGCGCTGCAAAATCTTCAACAGCTACAGCACTGAGCTTCAACCGGATATGTCATC 907
Db 121 GCGCGCTGCAAAATCTTCAACAGCTACAGCACTGAGCTTCAACCGGATATGTCATC 180
Qy 908 GCCAGATTAATCTTCTGCGGAGTCCGCGCTGTTGTTCTCAGGAGAGAGGTCGCG 967
Db 181 GCCAGATTAATCTTCTGCGGAGTCCGCGCTGTTGTTCTCAGGAGAGAGGTCGCG 240
Qy 968 CAGCGGTTGCTTGAATCCGCGGCG 992
Db 241 CAGCGGCTGCTTGAATCCGCGG 265

```

RESULT 5

```

US-09-923-876-5116
; Sequence 5116, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: laljudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (lco)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06

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; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program

; SEQ ID NO 5116
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
 US-09-923-876-5116

Query Match 13.5%; Score 237.8; DB 12; Length 265;
 Best Local Similarity 93.6%; Pred. No. 4,6e-55;
 Matches 248; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 728 ATGCGCTGCAACAGCTGACATGACCCGAGACCTCCAGACATGCGCGTCTTGCGCGTC 787
 Db 1 ATGGCTGCAACAGCTGACATGACCCGAGACCTCCAGACATGCGCGTCTTGCGCGTC 60
 QY 788 TCCCCCAAGCTGTTCCGCAACATATGCTCTTCTTACCAAGGACCTGCGGTTGAT 847
 Db 61 TCCCCCAAGCTGTTCCGCAACATATGCTCTTCTTACCAAGGACCTGCGGTTGAT 120
 QY 848 GCGCGCTCGCAATTTCTTATCATGACATGACATGACATGACATGACATGACATGAC 907
 Db 121 GCGCGCTCGCAATTTCTTATCATGACATGACATGACATGACATGACATGACATGAC 180
 QY 908 GCCAGATTAATCTTCTGCGAGTCCGCGCTGTTCTTCAAGGAGAGAGGTCGCG 967
 Db 181 GCCAGATTAATCTTCTGCGAGTCCGCGCTGTTCTTCTGCTGACCGAGAGAGGTCGCG 240
 QY 968 CAGCGGTTGCTTGAATCGCGGCG 992
 Db 241 CAGCGGTTGCTTGAATCGCGGCG 265

RESULT 6
 US-09-770-149-494/C
 ; Sequence 494, Application US/09770149
 ; Patent No. US20020059663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorlach, Jörn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Matthew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Woessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Kricker, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurdan, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2024 (PABA-013PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770,149
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,506
 ; PRIOR FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 494
 ; LENGTH: 657
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-770-149-494

Query Match 11.6%; Score 203.8; DB 9; Length 657;
 Best Local Similarity 62.2%; Pred. No. 1.5e-45;
 Matches 338; Conservative 0; Mismatches 202; Indels 3; Gaps 1;

QY 984 TCGCGGGGTCGCCACATTTCTGGCTTGGTACCCGTTGCTGCTGCTTCCGCAATT 1043
 Db 642 TCGCGGGAATCTTAGCTTCTGCACTTGGTCCCATCTTAGCTCATGCTCAACAACT 583
 QY 1044 GGTGGAGAGGTCGCGTTTGTCTTTCAGCTTCAACATCTCGGGATTACAGACTCC 1103
 Db 582 GGTGGAGAGGTCGCGTTTGTCTTTCAGCTTCAACATCTCGGGATTACAGACTCC 523
 QY 1104 AATTCTGCTGAACCACTTCTGTCGACGCTGATGTGCGGCAACCAAGGCAATGACT 1163
 Db 522 AATTCAAGCTTAACCACTTCTGTCGATGTGCTGATGTGCTGATGTGCTGATGTG 463
 QY 1164 GGTGGAGAGGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1223
 Db 462 GGTGGAGAGGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 403
 QY 1224 TCCAGGTGCTGCAATTTCTTCAATGATGACATCTGTTTCCCGCTTACCTGCGTCC 1283
 Db 402 TCTTGGTGAATTAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCA 343
 QY 1284 ACCTTGCAAGGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1343
 Db 342 ATCTCGGAAAGTTTCTCGGCTGTTCAAGACTTTGCAAGAGCAATATCTTCCGTA 283
 QY 1344 CTGACAGCAATTTCTGAGGTGCAATGCTTACATGAGAGCACTCAGGCTGCTGAT 1403
 Db 282 GAGATATGCTGAGGTGCAATGCTTACATGAGAGCACTTACATGAGAGCACTTAC 223
 QY 1404 TCGAGGCCAGAGCGCTTCAAGTGTGCTTCCGAAATTTGATGAGAGGCTGTGA 1463
 Db 222 ATCAAGCTGAGAGCGGCTTAACTCCGTTGTT---AAGAACTTGTGAGAGGCTTTGA 166
 QY 1464 ACACCCATGATTAATGAGATGAGTACGGGCTATAGGCACTTGTGTTACGCTTG 1523
 Db 165 ATACTAGCTTAATGATTTTAACTAAACAAATATCTTTGTTGGTTAAATTTG 106
 QY 1524 GTG 1526
 Db 105 ATG 103

RESULT 7
 US-09-878-574-3260
 ; Sequence 3260, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 3260
 ; LENGTH: 287
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure

LOCATION: (1)..(287)
 OTHER INFORMATION: unsure at all n locations
 OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-H6
 US-09-878-574-3260

Query Match 8.6%; Score 152.4; DB 10; Length 287;
 Best Local Similarity 72.0%; Pred. No. 1.4e-31;
 Matches 198; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1001 TTTCGGCTTGTATCCCGCTTGTGCTGCTTCCCTGCGAATTTGTGGAGAGGTGCG 1060
 DB 2 TTTTGGATTTGGTTCCTCTATGATCTCATCTGCGAATTTGGAGAGGTATG 61
 QY 1061 TTTGTGCTTTACGCTTACCATTTGCGGGATTGAGACGCTCAATTTCTGTAACAC 1120
 DB 62 TTTGTTTGGCCAGTTTGTGCTTGTGCTCATCCAACTTCAATTTTGTGAACAT 121
 QY 1121 TTCTGTCGACGATGATGTGGGCAACCAAGGCAATGCTGTTGAGAACAGACG 1180
 DB 122 TTGCGACAGATGTATGAGGGCCCAAAATGGCAATGCTGTTGAGAACAACT 181
 QY 1181 GCAGGACGCTCGACATCTGCTGCTTGTGATGATGATGTTGCAAGTGGCTGACG 1240
 DB 182 GGTGGACATTTGACATCTTGTCTCAATGATGATGATGTTGCGGCTTCA 241
 QY 1241 TTCGATTTGACGACATCTGTTCCCGGCTTACC 1275
 DB 242 TTCGACTTGAACACATTTGTTCCCTAAGCTCCC 276

RESULT 8

US-10-369-493-27824
 Sequence 27824, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 PRIOR FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 27824
 LENGTH: 1098
 TYPE: DNA
 ORGANISM: Neurospora crassa
 US-10-369-493-27824

Query Match 8.5%; Score 150.2; DB 12; Length 1098;
 Best Local Similarity 50.4%; Pred. No. 9.6e-31;
 Matches 436; Conservative 0; Mismatches 408; Indels 21; Gaps 2;

QY 567 TTGGCTTGTGTGATCCAGTCCGGCTGATGGCCAGATCGGCGCACACCGCATCA 626
 DB 170 TCGGCTTGTGTGACAGCTAGTCTTCACTGCCCATGAGCGGACACATGGGATCA 229
 QY 627 CCGGCTATCGGCTCTGACCGGCTGTCAGGCTCTCGGGAATGCTTCAACGGCC 686
 DB 230 CGACCATTTTCATGATGATGCTGCTATCGGCAATCATGATCGGACTTTCATCGTGTGTC 289
 QY 687 TCAGCATGCGCTGTGAGATGTAACCAACACGACGACCATGCGTGGACAGCGCTGG 746
 DB 290 TCACTTATGATGTTGAGAGGACCAACAGCTTACCATATATATACCAACAGCCCTG 349
 QY 747 ACATGACCGGACCTCGACGACATGCGCTCTTGTGCTTCCCAAGCTGTTGCGCA 806
 DB 350 AGCAGATCGGACATGAGAACACTCCCTTCTTGGCATTTCCATGCTTTCTTCACTA 409

QY 807 ACATATGTCCTTACTTCTTACCAACGAGACCTGGCGTTCGATGCGGCTCGAAATCTTCA 866
 DB 410 ATCTGGGCTCCACATATCTATGACCGCTGTATGAGATGACACATCTTTCGCAATTTCTTG 469
 QY 867 TCAGCTACGACGACTGACCTTCTTACCCGGTATATGATGCTGCGAGATTAATCTTCTG 926
 DB 470 TCTCCCTCCAGCACTACTTCTATCATCATCATGATGATGCTGCGCCCTGAACTTAC 529
 QY 927 CGAGTCCCGCTTGTGCTTCTACGAGAGAG-----AGGTCGCGC 968
 DB 530 GTTCTGTTGGAGTACTTACTTAAGGAGGCGACGACCAAGACAGGCTCTGCTGTGCG 589
 QY 969 AGCGTTGCTTGAATGCGGAGGCTGCGCAATTTCTGAGCTTGGTAAACCGTGTGCTG 1028
 DB 590 ACCGCACTTCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
 QY 1029 CTTCCTGCGGAAATGTTGTTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088
 DB 650 TGTACAAAGCAATGATGCACTGGAACGCTTGTGTTTTCATGATCTCCACGCGG 709
 QY 1089 GATTTAGACGCTCAATTTCTGCTTGAACCACTTCTGCTGCTGCTGCTGCTGCTGCTG 1148
 DB 710 TCAACAGCCGTTGACGCTGCAATCATCTGTCACACTTGTGCTGCTGCTGCTGCTG 769
 QY 1149 CCAAGGCAATGATGCTGTTTGAAGACGACGCGCAGG---CACGCTGCAATCTGCTG 1205
 DB 770 TGGGCTTCAATGATGCTTCTTCCGACGCGATGCTGCGACACATGAGATGATGCTG 829
 QY 1206 CTCTTGAATGATGATGTTTCCAGGATGCGCTGCGATGCTGATGACATCTGTTT 1265
 DB 830 CCAAGTGGCTTGAATTTTTCACGCGGCTCAGTTCAGGCTTCAACATCTTAC 889
 QY 1266 CCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1325
 DB 890 CCGGCAATCTTCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949
 QY 1326 AGCATGGGCTCACTTATTTGACGACCAATTTGCGGCTCAATGCTTACATGAGAA 1385
 DB 950 ATTTGGATCTCTTATGCGCTGTATGAGATTTGTGAGAGCAACAAACATCATCGGA 1009
 QY 1386 CACTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1410
 DB 1010 GCTTACGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1034

RESULT 9

US-09-770-444-39
 Sequence 39, Application US/09770444
 Patent No. US2002023280A1
 GENERAL INFORMATION:
 APPLICANT: Gorlach, Jorn
 APPLICANT: An, Yong-Qiang
 APPLICANT: Hamilton, Carol M.
 APPLICANT: Price, Jennifer L.
 APPLICANT: Raines, Tracy M.
 APPLICANT: Yu, Yang
 APPLICANT: Rameaka, Joshua G.
 APPLICANT: Page, Amy
 APPLICANT: Mathew, Abraham V.
 APPLICANT: Ledford, Brooke L.
 APPLICANT: Moesener, Jeffrey P.
 APPLICANT: Garcia, Carlos A.
 APPLICANT: Krickler, Maya
 APPLICANT: Slater, Ted
 APPLICANT: Davis, Keith R.
 APPLICANT: Allen, Keith
 APPLICANT: Hoffman, Neil
 APPLICANT: Hurban, Patrick
 TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 FILE REFERENCE: 2027 (PABA-016PRV)

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; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-39

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Query Match      7.3%; Score 129; DB 9; Length 476;
Best Local Similarity 55.8%; Pred. No. 4.5e-25;
Matches 265; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

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QY 261 GGGACCTCCGCTTCAACCTGCGGGGAGAGCCGACCGCTTCGCGGCTTAC 320
DB 1 GGCACACGGTATTCATCTGTTGTCAGACGTCACCGATCTTTCATGCAATTC 60
QY 321 ACCC--GCCCTGCGCGCGCGCGCTCTCCGCGCTTCTGTTGCGCGCTCTGACT 377
DB 61 ATCCCGGAACCGTTTGACACATCTGACATCTTTCACCGGTACACATAGAGATT 120
QY 378 AGCCGCTTCCCGCGCTGCGGACCTACCGCGCTCTGCGGAGCTATCTCGCGG 437
DB 121 TCCAACTCTCCGAAGTCTCAACGAGTACCGGTGATGCTGCGGATTCGTAAC 180
QY 438 GCGCTTCCAGCCGCTGCGGCGGACCCCAAGCTCAGCTGCTGATGCGCTCTCT 497
DB 181 GTCTTTCGAAAACAAAGTCAGTTACTCTACCTTAAGCTTCTGTCGCGCATGT 240
QY 498 TCTACCGCGCTGATCTGCTGCTGCAATGCGCGCGCGCGCGCGCGCGCGCG 557
DB 241 TCTCGGAGTCTCTACGGGTGTTTGGCTTGTACCTCGCTTCTGCGCAATGCGG 300
QY 558 GGGGTCTCATTTGCTTGTGATCCAGTCCGCGCTGATGCGGCGCAAGCTCGGCG 617
DB 301 CGCGGCTTCTCGGCTCTCTCTGATCCAGAGCGCTTACATAGGTGCAAGATTG 360
QY 618 ACCGATACCGCGCATCGGCTCTGACCGCGCTGCGAGGCTCTCTCGGGAATGCC 677
DB 361 ACCTTATCATGTGGAACAATCTTATTAAGATTGCTCTCTTNNGGTAACTGTC 420
QY 678 TCACCGCGCTCAGATCGCGCTGAGAGGTAAACCAACAGCAACCAATGCG 732
DB 421 TCACCGGAATCTCAATGCGGTGGAGATGAGCTCAATGCTCATCTAAGC 475

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RESULT 10
; US-10-156-761-2285
; Sequence 2285, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02

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; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2285
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1095)
US-10-156-761-2285

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```

Query Match      6.8%; Score 120.6; DB 15; Length 1095;
Best Local Similarity 46.8%; Pred. No. 1.3e-22;
Matches 457; Conservative 0; Mismatches 484; Indels 36; Gaps 1;

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QY 385 CTCCCCCGGCTCGCGACTACCGCGCTCTCGCGGAGCTATCTCGCGGCGCTTT 444
DB 54 CACCGCGCTTGGCGGCGGCTGCGGACTGCTCAACGCGTCAAGCGGAGGCGCTTCT 113
QY 445 CGAAGCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 504
DB 114 CGACCTGATCCCGCTACTACATAGCGCGGCTGCGGCTGMAACACAGCTGCTGCT 173
QY 505 CGCGCTGATCTGCTCTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 564
DB 174 CGGCTTCCGCGGCTTCTGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 233
QY 565 CATGCTTCTGCTGATCCAGTCCGCTGATGCGGCGGCGGCGGCGGCGGCGGCGG 624
DB 234 GATGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 293
QY 625 CACCGGCGATCGGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 684
DB 294 GTTCCGAGACGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 353
QY 685 CCTCAGCATGCGCTGCTGAGTGAAGTGAACCAACACGACCAACATGCGCTGCA 744
DB 354 GGTACAGCTTCCGCTGCTGAGTGAAGTGAACCAACACGACCAACGCGGCGGCG 413
QY 745 GGAACATGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 804
DB 414 GGAACATGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 437
QY 805 CAACATGATGCTCTACTTCAACAGGACCGGCGGCGGCGGCGGCGGCGGCGGCGG 864
DB 438 GCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 497
QY 865 CATCAGCTACGACGATGACCTTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGG 924
DB 498 CGTGCGCTACGAGAGGCTGCTGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGG 557
QY 925 CGGCGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
DB 558 GAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 617
QY 985 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1044
DB 618 CCGCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 677
QY 1045 GTGGAGAGAGTCCGCTTGTGCTTTCAGCTTTCAGCTTTCAGCTTTCAGCTTTC 1104
DB 678 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 737
QY 1105 ATTGCTGCTGAACCACTTCTGCTGCGAGTGAATGCGGCGGCGGCGGCGGCGG 1164
DB 738 CTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 797
QY 1165 GTTGAAGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1224
DB 798 GCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 857
QY 1225 CCACGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1284
DB 858 CTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 917

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QY 1285 CCTTCGCAAGTTGCACCGGCGGCTTTCGACAGATGGGCTCACTTATTC 1344
 DB 918 CTTGGCGCGCGCCCGGTAACCTACCCGCGCTACTGCGCGCGGCGGTGCTGATCA 977
 QY 1345 TGCAGCCACATCTTGGG 1361
 DB 978 CGAGGTGCGGTTCTGGG 994

RESULT 11

US-10-156-761-1/c
 ; Sequence 1, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMR, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1
 ; LENGTH: 9025608
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermectilis
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4187715)
 ; OTHER INFORMATION: a, t, c, g, other or unknown
 ; US-10-156-761-1

Query Match 6.8%; Score 120.6; DB 15; Length 9025608;
 Best Local Similarity 46.8%; Pred. No. 6.1e-21;
 Matches 457; Conservative 0; Mismatches 484; Indels 36; Gaps 1;
 QY 385 CTTCCTCCGCTCCGCGCACTACCGCGCTCTCTGCGCGCACTATCTCTCGCGGCTCTT 444
 DB 2801106 CACCGCGCTTCGCGCACTGCTCCGCACTCAACCGGTCAGGCGGAGGCTTCT 2801047
 QY 445 CGAAGCGGTGGGCGCCCAAGGTCAGCTGCTCTGATGAGCGGCTCTCTTCTACGC 504
 DB 2801046 CGACTCGATCCCGCTACTACTAGGCGGCTGGCGCTTAACACACGCTGCTGCTGT 2800987
 QY 505 CGGCTGTACTCTGCTCTCGATGCGCGCAAGCGCTGGGCGCACCTCTCTCGCGGAGTCT 564
 DB 2800986 CGGCTTCCGCGGCTTCTTGGCGGCGCACTGCTGTGTCAGCTGCTGTGCGCTGTG 2800927
 QY 565 CATGGCTTCTGTGATGATGCTCGGCTGATGAGGCGCAAGCTCGGCGCAACCGCAT 624
 DB 2800926 GATGGGCTGTGCGGCGGTACGCTTCATGTGGCAGAGCGCGCGCAAGGCCAT 2800867
 QY 625 CACGGGCAATCGGCTCTCGACCGCGTCTGCAAGGTCTCTCTCGGGAATCGCTCACCGG 684
 DB 2800866 GTTCCGAGCAAGAGCGCGCTCTCGCGGTGATTTCTACGCCAATCTGTCAACGG 2800807
 QY 685 CTTACAGATCGCTGTGTGAAGTGAACCAACACGCAACGACATCGCTGCAACAGCT 744
 DB 2800806 GGTCACTTCTGCTGTGTGTGATCAACCAACACGCGACCAACAGCAACCACT 2800747
 QY 745 GAGCATGACCGGACCTTCAGACATGCGGCTTTTGGCTCTCCCAAGCTGTTGG 804
 DB 2800746 GGCATGACCGCGCATC-----GGCG 2800723

QY 805 CAACATATGGTCTTACTTCTACCAAGACCTTGCGGTTTCATGCGCGCTCGAATTCCT 864
 DB 2800722 GCGCACCGCATTTTGATCATGAAGATACCGACCGCGCGGACACAGATTCAT 2800663
 QY 865 CATACCTACACGACTGACCTTCTTACCGGTATGTGATGCGCAGATTAATCTTCT 924
 DB 2800662 CGTGGCTACAGAGGCTGTGTTCTTCCGCTGTGTACAGGATCTCTTCAAGATGCT 2800603
 QY 925 CGGCACTCGCGCTTGTCTCTCAAGAGAGAGGCGCGCACGCTTGTGAT 984
 DB 2800602 GAAGACGCGCTCTTCTTCAATGCGCCAGACCAAGCGCGCTCTGAGTCT 2800543
 QY 985 CGCGGGGCTCGCACATTTCTGAGCTTGTATACCGTGTGTGCTTCCCTGCGAATTG 1044
 DB 2800542 CTTGCTCTCGCGCGCGCGCGCTTATGACGCTGTGTTACCGCTCTCGCGCG 2800483
 QY 1045 GTGGAGAGGCTGCGTTGTGCTTTTACGCTTACCATCTGCGGATTCAGACCTCCA 1104
 DB 2800482 CTTGCGGCTCGCTTGTCTGCTTCCAGACAGCGCGCTGCGGCTTACTTCCGCTAT 2800423
 QY 1105 ATTCGCTGAACTTCTCTGCGACGATGATGCGGCGCACCCAGGGCAATGACTG 1164
 DB 2800422 CTTGCGCGGACCAAGGCGCATGAGGTGCGCGACGACGAGAGACCTGAGCTG 2800363
 QY 1165 GTTGAAGACAGACGCGACGCTCGACATCTGTGCTCTCTTGTGATGATGATTG 1224
 DB 2800362 GCTGAGCGCGCTGCTCTACCTCCGCAACATCGCGCTCTGTTATGACTTCT 2800303
 QY 1225 CACGGTGGCTGCACTTCAATGAGACCATCTGTTTCCCGCTACTCTGCTGCA 1284
 DB 2800302 CTACGCGGCTCTCACTACAGGTGAGACACACCTGTTCCGCGCATGCCAGAGAA 2800243
 QY 1285 CTTTCGCAAGTTGCACCGCGCTCGGACCTTTGCAAGAGAGGCTCACTATTC 1344
 DB 2800242 CTTGCGCGCGCGCGCTGAATCAACCGGCTTACTGCGCGAGCGGTGCTGATCA 2800183
 QY 1345 TGCAGCCACATCTTGGG 1361
 DB 2800182 CGAGGTGCGGTTCTGGG 2800166

RESULT 12

US-09-924-035A-370/c
 ; Sequence 370, Application US/09924035A
 ; Patent No. US20020142319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glaxo, Jm
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2011US
 ; CURRENT APPLICATION NUMBER: US/09/924,035A
 ; CURRENT FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: US 60/148,784
 ; PRIOR FILING DATE: 1999-08-13
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: FaastSeq for Windows Version 3.0
 ; SEQ ID NO 370
 ; LENGTH: 480
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-924-035A-370

Query Match 6.5%; Score 115.2; DB 10; Length 480;
 Best Local Similarity 61.0%; Pred. No. 2.8e-21;
 Matches 205; Conservative 0; Mismatches 128; Indels 3; Gaps 1;
 QY 1191 TGCATCTCTGCTCTCTCTGATGATGATGTTGTCACGCTGCGATTCAGATTG 1250
 DB 478 TCGATATCTCTTGTGATATATGATGATGTTGTTCTTGTGATTAAGTTTCACTTG 419
 QY 1251 AGCACCATCTGTTTCCCGCTTACTCTGCTGTCACCTTTCAGAGTTGACCGCGCTCC 1310
 DB 418 AGCATATTTGTTCCCGCTTACTCTGCTGTCATCTCGGAAAGTTTCTCCGGTGTTC 359

QY 1311 GCGACCTTTGGAGAAGAGATGGGGCTCACTTATTTCTGCAGCCACATCTTGGGGTGCAAATG 1370

Db 358 AAGAGCTTTGCAGAAGAGATATCTTCCGTATAGGAGATATGTCTGTGTTTAAAGCAATG 299

QY 1371 TGCCTTACATGGAAGACACTCAGGGCTGTCTGCAATTCAGAGCCAGGACGGCTACAGTGGTG 1430

Db 298 TGTTCACCATTTACCTTTGAAGACAGACCTTATCAAGCTTAGAGACCTGGCTAATCCGG 239

QY 1431 GTGCTCCGAAACAATTTGGTATGGAAGAGCTGTGAACACCCATGATTAATGGATGAAGAT 1490

Db 238 TGTGTT---AAACAATTGGTTTGGGAGAGCTTTGAATATCAATGGCTAATATGATTTTAATCA 182

QY 1491 ACGGGCTAATGCAACAATCTGTGGTTCACCTTGGG 1526

Db 181 AAACAAATATGCTTTTGTGTTGGGTTAAATTTGAATG 146

```

RESULT 13
US-09-878-574-9255
; Sequence 9255, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (15401) B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 9255
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102270H1
US-09-878-574-9255

```

Query Match	6.5%	Score 114;	DB 10;	Length 263;
Best Local Similarity	68.1%;	Pred. No. 4, 6e-21;		
Matches 173;	Conservative	0;	Mismatches 80;	Indels 1;
			Gaps 1;	
QY	641	CTCGACGCGCTGTGTCAGATGCTCTCCGGAACTGCTTCACCGCGCTCAGCATGCGCTGG	700	
Db	11	CTCGACGCGCTCGAGCAATCTTTGTGGCAATTGCAATGACGTGGGATAGCATTTGCATGG	70	
QY	701	TGGAAGTGTAAACAAACAGCACCAATTCGCTGCGAACAGCTTGACATGACCCGGAC	760	
Db	71	TGGAAGTGTGACTACAAATGCTTCACCAATCTCATGCAATGATCTTTGACTTAATGATCTTGA-129		
QY	761	CTCAGACATGCGCGCTCTTTGCCGTCCTCCCAAGCTGTTCCGCAACATATGAGTCTAC	820	
Db	130	TTTCAGGCACTAACCTGTCCTTTGGCGTGTGACAGCGTTCTTCAATGCAATGAATCTTGT	189	
QY	821	TTTACCAACAGGACCCCTGGCGTTGGATGATGCCGCTCGAAATCTTCATGACTTACCAAC	880	
Db	190	TTCTATGGAAGAAATATGTTGATTCATTATCAAGTTTCATATGCTTCACTACCAAGCAC	249	
QY	881	TGAGACTTTTACCC	894	
Db	250	TTTCACATTTTACCC	263	

RESULT 14
US-09-967-477B-7
; Sequence 7, Application US/0996477B
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Qiu
; APPLICANT: Haiping Hong

```

?
? TITLE OF INVENTION: PAD4, PAD5, PAD5-2, AND PAD6, NOVEL
? TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
? FILE REFERENCE: BMZ-001
? CURRENT APPLICATION NUMBER: US/09/967,477B
? CURRENT FILING DATE: 2002-04-16
? PRIOR APPLICATION NUMBER: 60/236,303
? PRIOR FILING DATE: 2000-09-28
? PRIOR APPLICATION NUMBER: 60/297,562
? PRIOR FILING DATE: 2001-06-12
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 7
?
? LENGTH: 1380
?
? TYPE: DNA
?
? ORGANISM: Thraustochytrium sp.
?
? FEATURE:
?
? NAME/KEY: CDS
? LOCATION: (1)...(1380)
?
US-09-967-477B-7

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Query Match	Local Similarity	6.3%	Score 112	DB 10	Length 1380
Best Local Similarity	47.0%	Pred. No. 3.3e-20			
Matches 612	Conservative	0	Mismatches 600	Indels 90	Gaps 5
QY	138	CCGAGCAGTGTGCGCATGATCTCTTCCAGAGAGCTCCGCGCTACACCTTCCCGCGAGCAC	197		
DB	17	CTGAGGTGAAGCGCTGTGTGAGCTGGAGAGATCTCCGAGACCGCAGCGCCCGAGCCG	76		
QY	138	TCTGATCTTCATCTTCGCGCAGCTGTACAGCTCAGCCCTGTGCTCCCAACACCCGG	257		
DB	77	CGTGATGTGTATTCACCAAGGCTCTCAGCATCTCCAAAGTGGAATCTGCACCCGGGT	136		
QY	258	GCAGGAGACTCCCGCTTCTCAACCTGGGAGGGGACGAGCCACCGACCTTCGCGCT	317		
DB	137	GCTCGT-----GATGCTACGACGAGCGCGGAGAGCCACGAGCCCTTCGCGGT	190		
QY	318	ACCACCGCGCTCGCGCGCGCGCTCTCTCGCGCTTCTTGTTGCGCGCTCTCTGACT	377		
DB	191	TCCACCGCTCTCGCGCGCTCAAGCTGCTCGAGCAGTTCTTAAGTGCGGACCTGGACGAAA	250		
QY	378	ACGCGG-----	383		
DB	251	CTTCACAGCGCGAGATGAGGGGAGCCGCGAGCAGACAGAGCGCGCGCGAGC	310		
QY	384	---TCTCCCCCGCTCCGCGCAGATACCGCGCGCTCTCGCGCAGTATCTCTCCGCGGCC	440		
DB	311	GCATCAAGAGATTATGCGCTCTCAGCTGTCTGCGCTTCAGAGTCAAGGGCATTGGGCG	370		
QY	441	TCTTGAAACGGCGTGCAGCCCAACCCCAAGTCCAGCTGCTCTGATGAGCGCTCTTCT	500		
DB	371	TCTACAGCGCAGCGCGCTCTACTACGCTGGAAAGCTGTGAGACGTTGGGATCCGCG	430		
QY	501	ACGCGGCGGTACCTGCTCTCTGSCATGCGCCAGCGCTGGCGCACCTCTCGCGGGG	560		
DB	431	TGCTCTGATGGCGATTGCTTCTTCTTCAACAGTTTGGCATGTATCATGTGCGCGCGC	490		
QY	561	GTCTCATTTGCTTCTGATGCACGTCCGCGTGAATGGGCGACAGACTCGGCGCACAC	620		
DB	491	TGATTATGGGGCTTCTTACACAGAGTCGGATGGCTGGCGCACAGACTTCTTGACACAC	550		
QY	621	GCAATACCGGCAATCCGCTCTTGACCGCGCTCGTGACAGTGTCTTCGGGAATGCTCTA	680		
DB	551	AGGTGTGCGGAACCGCACGCTCGGCAACTTATTCGGCTGCTCTGTGGGCAACGCTTGC	610		
QY	681	CCGCGCTCACATTCGCTGTGTGAAGGTAAACACAAACGACCAATTCGCTGCACAA	740		
DB	611	AGGGCTTACCGCTGCACTGTGTGAAGAAACAGACAACTGCACCA---CGCGTCCGA	667		
QY	741	GCTTGACCATGACCGCGACTTCACACATGCGCTTCTTTCGCTCTCCCGCAAGCTGT	800		
DB	668	ACCTGACACGCGCCAGAGAGAGGGCTTCATCGGCGACCCGGACATTCGACACCATTCGCG	727		
QY	801	TGCGCAACATATGTCTTACTTCTACCAACGACACTTGCGCTTTCGATGCGCGCTCGAAT	860		


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Db      728  TGCTGGCGGTGGCTCTAAGGAGATGGCGGCGCAAGGGCTTGAGTGGCGGACCGGCCG---T 784
Qy      861  TCTTCATCAGCTACCAAGCACTGGACCTTCTCTACCCGGTATATGTCATCGCCAGATPAATC 920
Db      785  TCTTCATCCGCAACCAAGCGCTTCCATATCTTCCCGCTCTGCTGCTCGCGCCCTGACCT 844
Qy      921  TTCTCGGCACTCCGCGCCCTGTTCGTTTCACGGAG-----AAGA 959
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RESULT 15
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; Sequence 47, Application US/10033393
; Publication No. US2003027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Daniel
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/255,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
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; SEQ ID NO 47
; LENGTH: 12733
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector pEPEF14
; US-10-032-393-47

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[illegible]

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Job time : 458.973 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:54:32 ; Search time 3928.96 Seconds
(without alignments)
14889.683 Million cell updates/sec

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Perfect score: 1764
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1764	100.0	1764	33	US-09-857-524B-3
2	1406.4	79.7	2067	55	US-10-612-783-1024
3	1349	76.5	1541	48	US-10-219-999-27869
4	1349	76.5	1541	52	US-10-425-114-14218

5	1333.8	75.6	2054	1	PCT-US03-07858-288	Sequence 288, App
6	1333.8	75.6	2054	1	PCT-US03-07858-288	Sequence 288, App
7	1333.8	75.6	2054	1	PCT-US03-07858-288	Sequence 288, App
8	1333.8	75.6	2054	2	PCT-US03-07858-288	Sequence 288, App
9	1333.8	75.6	2054	51	US-10-389-566-288	Sequence 288, App
10	1333.8	75.6	2054	53	US-10-613-520-288	Sequence 288, App
11	1175	66.6	1448	30	US-09-654-617-265928	Sequence 265928,
12	1175	66.6	1448	38	US-09-684-016-265928	Sequence 265928,
13	1091.4	61.9	1972	35	US-09-857-524B-9	Sequence 9, Appl1
14	1000.6	56.7	1944	53	US-10-437-963-83761	Sequence 83761, A
15	973.6	55.2	14392	51	US-09-702-134-25614	Sequence 25614, A
16	973.6	55.2	14392	34	US-09-815-264-72548	Sequence 72548, A
17	973.6	55.2	14581	27	US-09-620-392-30987	Sequence 30987, A
18	891.4	50.5	1407	86	US-60-312-544-3168	Sequence 3168, Ap
19	891.4	50.5	1408	48	US-10-219-999-13422	Sequence 13422, A
20	891.4	50.5	1408	52	US-10-425-114-17460	Sequence 17460, A
21	891.4	50.5	1485	54	US-60-391-781-446	Sequence 446, App
22	845.4	47.9	1069	65	US-10-110-784-8	Sequence 8, Appl1
23	829.8	47.0	1302	53	US-10-437-963-83759	Sequence 83759, A
24	609.6	34.6	1967	48	US-10-219-999-12725	Sequence 12725, A
25	609.6	34.6	1967	52	US-10-425-114-14991	Sequence 14991, A
26	608	34.5	2236	52	US-10-424-599-124471	Sequence 124471, A
27	602	34.1	1207	48	US-10-219-999-25017	Sequence 25017, A
28	539.4	30.6	684	28	US-10-425-114-28231	Sequence 28231, A
29	539.4	30.6	684	30	US-09-654-617-452235	Sequence 452235,
30	539.4	30.6	684	36	US-09-873-402A-43580	Sequence 43580, A
31	492.6	27.9	581	36	US-09-685-775-26	Sequence 26, Appl
32	491.2	27.8	1702	30	US-10-029-756-26	Sequence 26, Appl
33	491.2	27.8	1702	44	US-60-110-784-6	Sequence 6, Appl
34	486.6	27.6	514	65	US-10-219-999-12694	Sequence 12694, A
35	486.2	27.6	1828	48	US-10-425-114-14869	Sequence 14869, A
36	486.2	27.6	1828	52	US-10-424-599-36789	Sequence 36789, A
37	486.2	27.6	1940	52	US-09-857-524B-7	Sequence 7, Appl1
38	479.8	27.2	1934	35	US-09-865-419A-52475	Sequence 52475, A
39	464	26.3	615	36	US-09-534-859-381	Sequence 381, App
40	453.8	25.7	110149	23	US-09-803-736-381	Sequence 381, App
41	453.8	25.7	110149	34	US-09-513-996A-34823	Sequence 34823, A
42	452	25.6	1465	22	US-09-708-427-1024	Sequence 1024, Ap
43	452	25.6	1465	39	US-09-935-625-19394	Sequence 19394, A
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ALIGNMENTS

RESULT 1
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 ; Sequence 3, Application US/09857524B
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgar B. Cahoon
 ; APPLICANT: Rebecca E. Cahoon
 ; APPLICANT: William D. Hitz
 ; APPLICANT: Anthony J. Kinney
 ; TITLE OF INVENTION: Membrane-Bound Desaturases
 ; FILE REFERENCE: B01264
 ; CURRENT APPLICATION NUMBER: US/09/857, 524B
 ; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: 60/110,784
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 3
 ; LENGTH: 1764
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-09-857-524B-3

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 Best Local Similarity 100.0%; Pred. No. 0;
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Qy	121	CGGCGAGCGCGGGGGCGCGGCGAGATGCGATATCTCTCCAGAGATGCGCGCTCA 180
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Db	541	GAGGCACTCTCTGCGGGGGGTCTCATTTGCTTGTGATTCAGTCCGGCTGTAGTGG 600
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RESULT 2

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 ; Sequence 1024, Application US/10612783
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53373)A
 ; CURRENT APPLICATION NUMBER: US/10/612, 783
 ; CURRENT FILING DATE: 2003-07-02
 ; NUMBER OF SEQ ID NOS: 7098
 ; SEQ ID NO 1024
 ; LENGTH: 2067
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4577_136542C.1
 US-10-612-783-1024

Query Match 79.7%; Score 1406.4; DB 53; Length 2067;
 Best Local Similarity 90.2%; Pred. No. 3,1e-252;
 Matches 1588; Conservative 0; Mismatches 151; Indels 21; Gaps 7;

Qy 9 TCCCTCTCTTCCCAATCTTCCCGCTCCCTCAACA-AATACACACACCAAGGCG 67
 Db 82 TCTCCCACTTCCACAAATCTTCCCGCTCCCTCCCAATTCAGACACAC 141
 Qy 68 CATCCAGCCACGCGCGGCAATGCGGCTCTGTGATGCAATGCGGCGCGGCGAGC 127
 Db 142 CATAGGGGCGACGCGCGCAATGCGGCTCTGTGCGAGCAATGCGGCGCGGAGAC 201
 Qy 128 GCGCGGGGCGCGGCGAGTGGGCAATGATCTCTCAAGAGACTCGGCGCTTCC 187
 Db 202 GCGCGTGGCGGCGAGCTGGGCTGATCTCTCCAGAGACTCGGCGAGCGCTTC 261
 Qy 188 GCGAGACACTTGAATCTCATCTTCCGCGAGCTGTAAGAGTCAAGCTTGGCTCC 247
 Db 262 GCGCGGACCTTGATCTCATCTTCCGCGAGCTGTAAGAGTCAAGCTTGGCTCC 321
 Qy 248 CACACCGCGGCGGAGCTTCCGCTTCTACCTTGGCGGCGAGAGACCCACCGAGCC 307
 Db 322 CACACCGCGGCGGAGCTTCCGCTTCTACCTTGGCGGCGAGAGACCCACCGAGCC 381
 Qy 308 TTGCGCGCTTACACCGCGCTCGGCGGCGGCTCTCGGCGCTTCTGTTGGCGCG 367
 Db 382 TTGCGCGCTTACACCGCGCTCGGCGGCGGCTCTCGGCGCTTCTGTTGGCGCG 441
 Qy 368 CTCTCTGACTAGCGGCTTCCCGGCTCCGCGAGCTACCGCGGCTCTCTCGGCGAGCTA 427
 Db 442 CTCTCGAGTACACCGCTTCCCGGCTCCGCGAGCTACCGCGGCTCTCTCGGCGAGCTC 501
 Qy 428 TCTCTCGGCGGCTTCTGCAAGCGCTGCGGCCACCCCAAGGTCCAGTCTCTGATG 487
 Db 502 TCTCTCGGCGGCTTCTGCAAGCGCTGCGGCCACCCCAAGGTCCAGTCTCTGATG 561
 Qy 488 GCGGCTCTTCTTACCGCGCGCTGTAACCTGCTCTGCGATGGGCGAGCGGCTGGGCGAC 547
 Db 562 GCGGCTCTTCTTACCGCGCGCTGTAACCTGCTCTGCGATGGGCGAGCGGCTGGGCGAC 621
 Qy 548 CTCTCTCGCGGCGGCTTCTGATGGCTTCTGATGATCACTCGGCTGATGGGCGAGAC 607
 Db 622 ATCTCTGCTGGGCGGCTTCTGATGGCTTCTGATGATCACTCGGCTGATGGGCGAGAC 681
 Qy 608 TGGGCGACACCGCATCCGCGCATCCGCGCTTCTGACCGGCTCTGAGGCTCTCTCC 667
 Db 682 TGGGCGACACCGCATCCGCGCATCCGCGCTTCTGACCGGCTCTGAGGCTCTCTCC 741
 Qy 668 GGAAGTCTCTACCGGCTTCAAGCATCGGCTGTGGAATGTAACCAACACGACAC 727
 Db 742 GGAAGTCTCTACCGGCTTCAAGCATCGGCTGTGGAATGTAACCAACACGACAC 801
 Qy 728 ATGCGCTGACAGCGCTGAGCATGACCGGACCTTCAGACATGCGGCTTGTGCGCTC 787
 Db 802 ATGCGCTGACAGCGCTGAGCATGACCGGACCTTCAGACATGCGGCTTGTGCGCTC 861
 Qy 788 TCCCCCAAGCTTGGCAATATGCTCTACTTCTTACCAAGGACCTTGGGCTTGTAT 847
 Db 862 TCCCCCAAGCTTGGCAATATGCTCTACTTCTTACCAAGGACCTTGGGCTTGTAT 921
 Qy 848 GCGGCTTCAAAATTTCTTCACTACGTAACGACGACTGACCTTCAACCGGTAATGTGATC 907
 Db 922 GCGGCTTCAAAATTTCTTCACTACGTAACGACGACTGACCTTCAACCGGTAATGTGATC 981
 Qy 908 GCGAGATTAATCTTCTGCGGAGTCCGCGCTGCTGCTTCAAGGAGAAAGGAGGCGG 967
 Db 982 GCGAGATTAATCTTCTGCGGAGTCCGCGCTGCTGCTTCAAGGAGAAAGGAGGCGG 1041
 Qy 968 CAGCGGCTTGAATGCGGCGGCTGCGCACATTTCTGAGCTTGGATCCCGTGTGCTG 1027
 Db 1042 CAGCGGCTTGAATGCGGCGGCTGCGCACATTTCTGAGCTTGGATCCCGTGTGCTG 1101
 Qy 1028 GCTTCCCTTCCGAATTTGGTGGAGAGGCTGCGGTTTGTGCTTTTCAAGCTTCACTATGC 1087
 Db 1102 GCGTCTCTCCGAATTTGGTGGAGAGGCTGCGGTTTGTGCTTTTCAAGCTTCACTATGC 1161
 Qy 1088 GGGATTACAGAGTCCAAATTTGCGCTGAACCACTTCTGCTCGAGAGTGAATGTGGGCGCA 1147

Db	1162	GGGATCCAGCAGCTCCATTCTGCTGAGACCACTTCTGTCGATGTGTAGTGGGCGCA	1221
Qy	1148	CCCAAGGSCAAATGACTGTGTTTGAAGACAGACGAGGACCGCTTGACATCTGTGCTCT	1207
Db	1222	CCCAAGGCGCAACGACTGGTTCGAGAGACAGACGAGGACCGCTGACATCTGTGCGCTT	1281
Qy	1208	CCTTGATATGATTTGGTTTCCACCGTGGCCCTGACAGTTCCAGATTGAGACCACTGTGTTCC	1267
Db	1282	CCTTGATATGATTTGGTTTCCATGAGCGCGCTGACAGTTCCAGATTGAGACCACTGTGTTCC	1341
Qy	1268	CGCCCTACCTCGGTGCGACCTTTCGCAAGGTTGCGACGCGCGCTGCGGACCTTTGCAAGAG	1327
Db	1342	CGCCCTGCTCGGTGCGACCTTTCGCAAGGTTGCGCGCGGTGCGGACCTTTGCAAGAG	1401
Qy	1328	CATGGGCTCATTATTTCTGACAGCCACATTTGCGGGTGCAGAAATGCTTTACATGGAAGCA	1387
Db	1402	CATGGGCTCATTATTTCTGACAGCCCTCTTTCGGAACGCAATGCTTTACATGGAAGCA	1461
Qy	1388	CTCAGGGCTGCTGCAATTGACAGGCCAGACCGCTACA-----AGTGGTGGTCTCCGAG	1441
Db	1462	CTCAGGGCTGCTGCAATTGACAGGCCAGACCGCTACA-----AGTGGTGGTCTCCGAG	1521
Qy	1442	AATTTGGTATGGAGGAGGCTGTGAACCCCATG---GATAATGGGATGAAGATACG-----	1494
Db	1522	AATTTGGTCTGGAGGCGATTGAACCCCATGATATGAACGGAGCGAGATATGGCTGA	1581
Qy	1495	GCTAATGGCACTTCTGGTG-TTCACTTGGTGCCCATGTGATTTGTCTGATGC-----C	1548
Db	1582	GCGGAGGCAACTTCTGGTGTTTTCAGCTTTTGCGGAGCGCATTTGTCTGGTTCTTAA	1641
Qy	1549	TTTCACTTATTTAGA-GATATTTGATCATTAACACTGCTGATGACAGTTGGAATTTTCTG	1607
Db	1642	TCTCAGTTGTTTGAATTTGATTTGGTCATTTGAACCCGCTCGAGCTGGAAATTTTGT	1701
Qy	1608	GTTGACAAAGTGGCTGTATCATCAGTTGGAGATTGATGCTTCAATAGCTGGTTGTCAC	1667
Db	1702	GTTGACAAAGTACCGTCTATCATCAGTTGGAAGTTATCATCTTCAATAGCTGGTTGTCAC	1761
Qy	1668	GGGATGTTCTGTTCTCCCTATCAGCGGTAACTATATGATGATGATCCTTGAATTCAT	1727
Db	1762	GGGATGTTCTGTTCTCCCTATCAGCGGTAACTATATGATGATGATCCTTGAATTCAT	1821
Qy	1728	GAACTGTTTTCAGATTA	1747
Db	1822	GAACTGTTTTCAGATTA	1841

[illegible]

|||||
Db 961 GGGGTGCAATGATGCTTACATGAGAACATCGAGGCTGCTGATGACAGCCAGGACCG 1020
Qy 1419 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGAACACCCATGATATA 1478
Db 1021 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGAACACCCATGATATA 1080
Qy 1479 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGAGCTTGTGTGCTGATGATG 1538
Db 1081 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGAGCTTGTGTGCTGATGATG 1140
Qy 1539 TGTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGTGCTGAGCTTGG 1598
Db 1141 TGTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGTGCTGAGCTTGG 1200
Qy 1599 AATTTTCGTGTGACAGAGGCTGTATTCAGATTTGAGAGATTCATGCTTCAATGCTG 1658
Db 1201 AATTTTCGTGTGACAGAGGCTGTATTCAGATTTGAGAGATTCATGCTTCAATGCTG 1260
Qy 1659 GTTGTTCAGGAGATGTTCTGTCTCCCTATCACGATACATATGATGATGATCTTGTCT 1718
Db 1261 GTTGTTCAGGAGATGTTCTGTCTCCCTATCACGATACATATGATGATGATCTTGTCT 1320
Qy 1719 TTAATTCATGAACACTGTTTCAAGATTA 1747
Db 1321 TTAATTCATGAACACTGTTTCAAGATTA 1349

RESULT 4
US-10-425-114-14218
; Sequence 14218, Application US/10425114
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14218
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-051-G4_FLI
US-10-425-114-14218

Query Match 76.5%; Score 1349; DB 52; Length 1541;
Best Local Similarity 100.0%; Pred. No. 1.5e-241;
Matches 1349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Db 241 TCTCGACCGCGCTGCTGAGGTGCTCTCGGGAACATGCTCACCGGCTCACATGCGCT 300
Qy 699 GGTGAAGTGTAAACCAACAACGCAACCATATGCGCTGCAAGCGCTGACCAATGACCGCG 758
Db 301 GGTGAAGTGTAAACCAACAACGCAACCATATGCGCTGCAAGCGCTGACCAATGACCGCG 360
Qy 759 ACCCTCAGACATATGCGCGCTCTTGTGCGGTCTCCCAAGCTGTGCGCAATATGATGCTCT 818
Db 361 ACCCTCAGACATATGCGCGCTCTTGTGCGGTCTCCCAAGCTGTGCGCAATATGATGCTCT 420
Qy 819 ACTTTCACCAACGGAACCTTGCGGTGATGATGCGGCTCGAAATTTCTTATACATACCTACAC 878
Db 421 ACTTTCACCAACGGAACCTTGCGGTGATGATGCGGCTCGAAATTTCTTATACATACCTACAC 480
Qy 879 ACTGACCTTCTACACCGGATATGATGATGATGATGATGATGATGATGATGATGATGATG 938
Db 481 ACTGACCTTCTACACCGGATATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy 939 TGTGCTGCTCAACGGAAGAGAGGTGCGGACAGGCTGCTGATGATGATGATGATGATGATG 998
Db 541 TGTGCTGCTCAACGGAAGAGAGGTGCGGACAGGCTGCTGATGATGATGATGATGATGATG 600
Qy 999 CATTCGCGCTTGTGATACCGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 1058
Db 601 CATTCGCGCTTGTGATACCGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 660
Qy 1059 CGTTGTGCTTTCAGCTTACCATCTGCGGATTCAGACGCTCCATTTCTGCTTAAAC 1118
Db 661 CGTTGTGCTTTCAGCTTACCATCTGCGGATTCAGACGCTCCATTTCTGCTTAAAC 720
Qy 1119 ACTTCGCGCTGAGGTATGTCGCGGCAACCAAGGCAATGATGATGATGATGATGATGATG 1178
Db 721 ACTTCGCGCTGAGGTATGTCGCGGCAACCAAGGCAATGATGATGATGATGATGATGATG 780
Qy 1179 CCGCAGGCAAGCTGCAACATCTGTGCTCTCTTGTGATGATGATGATGATGATGATGATG 1238
Db 781 CCGCAGGCAAGCTGCAACATCTGTGCTCTCTTGTGATGATGATGATGATGATGATGATG 840
Qy 1239 AGTTCCAGATTGAGCAACATCTGTGCTCTCTTGTGATGATGATGATGATGATGATGATG 1298
Db 841 AGTTCCAGATTGAGCAACATCTGTGCTCTCTTGTGATGATGATGATGATGATGATGATG 900
Qy 1299 CACCGCGCTCGGCAACCTTTCAGAAAGAGAGGCTGCTATTTCTGAGCCATTTCT 1358
Db 901 CACCGCGCTCGGCAACCTTTCAGAAAGAGAGGCTGCTATTTCTGAGCCATTTCT 960
Qy 1359 GGGGTGCAATGATGCTTACATGGAAGACATCAGGCTGCTGATGATGATGATGATGATG 1418
Db 961 GGGGTGCAATGATGCTTACATGGAAGACATCAGGCTGCTGATGATGATGATGATGATG 1020
Qy 1419 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGAACACCCATGATATA 1478
Db 1021 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGAACACCCATGATATA 1080
Qy 1479 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGAGCTTGTGTGCTGATGATG 1538
Db 1081 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGAGCTTGTGTGCTGATGATG 1140
Qy 1539 TGTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGTGCTGAGCTTGG 1598
Db 1141 TGTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGTGCTGAGCTTGG 1200
Qy 1599 AATTTTCGTGTGACAGAGGCTGTATTCAGATTTGAGAGATTCATGCTTCAATGCTG 1658
Db 1201 AATTTTCGTGTGACAGAGGCTGTATTCAGATTTGAGAGATTCATGCTTCAATGCTG 1260
Qy 1659 GTTGTTCAGGAGATGTTCTGTCTCCCTATCACGATACATATGATGATGATGATGATG 1718
Db 1261 GTTGTTCAGGAGATGTTCTGTCTCCCTATCACGATACATATGATGATGATGATGATG 1320
Qy 1719 TTAATTCATGAACACTGTTTCAAGATTA 1747

Db 1321 TTAATTCGAGACCTGTTTCAGATTGA 1349

RESULT 5
PCT-US03-07858-288
Sequence 288, Application PC/TUS0307858
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
CURRENT APPLICATION NUMBER: PCT/US03/07858
PRIOR FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PatentIn version 3.2
SEQ ID NO 288
LENGTH: 2054
TYPE: DNA
ORGANISM: Zea mays
PCT-US03-07858-288

Query Match 75.6%; Score 1333.8; DB 1; Length 2054;
Best Local Similarity 88.4%; Pred. No. 1,1e-238;
Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

Qy 4 CGAGCTCCCTCTCTCTCCCAATCCTCCGCGCTCCCTCCCTCAACCAATCAGACCAACCA 63
Db CGATTCCTCTCTCTCCCAATCCTCCGCGCTCCCTCCCTCCCTCCCAATCAGACCAAC 137

Qy 64 GGGCATCCGAGCCAGCCGCGCGCAATGCGCCCTCTGTGATGCAATGCGCGCCCG 123
Db CACCCATAGGGGCGAGCGCGCGCAATGCGCCCTCTGTGATGCAATGCGCGCCCG 197

Qy 124 CGAGCGCGCGCGCGCGCGCGCAATGCGCGCGCTCTGTGATGCAATGCGCGCGCG 183
Db AGAGCGCGCGCGCGCGCGCGCAATGCGCGCGCTCTGTGATGCAATGCGCGCGCG 257

Qy 184 TTCGCGCGAGGAGCTCTGTGATGCTCATCTCCGCGAGGAGTGAAGAGTCAAGCGCT 243
Db GTCCGCGCGAGGAGCTCTGTGATGCTCATCTCCGCGAGGAGTGAAGAGTCAAGCGCT 317

Qy 244 CCCCACCAACCGCGCGCGCGCAATGCGCGCTCTGTGATGCAATGCGCGCGCGCG 303
Db TCCCAACCAACCGCGCGCGCGCAATGCGCGCTCTGTGATGCAATGCGCGCGCGCG 377

Qy 304 CGCTTTCGCGCGCGCGCGCGCGCGCAATGCGCGCGCTCTGTGATGCAATGCGCGCG 363
Db CGCTTTCGCGCGCGCGCGCGCGCGCAATGCGCGCGCTCTGTGATGCAATGCGCGCG 437

Qy 364 CCGCGCTCTGTGATGAGCGCTCTCCGCGCGTCCGCGAGTCAAGCGCGCGCTCCGCG 423
Db CCGCGCTCTGTGATGAGCGCTCTCCGCGCGTCCGCGAGTCAAGCGCGCGCTCCGCG 497

Qy 424 GCTATCTCTCGCGCGCGCTCTGTGAGCGCTCCGCGCGCGCAACCGCGCGCGCGCT 483
Db GCTATCTCTCGCGCGCGCTCTGTGAGCGCTCCGCGCGCGCAACCGCGCGCGCGCT 557

Qy 484 GATGCGCGCTCTCTGTGAGCGCGCGCTGTGATGCTCTGTGATGCGCGCGCGCGCG 543
Db GATGCGCGCTCTCTGTGAGCGCGCGCTGTGATGCTCTGTGATGCGCGCGCGCGCG 617

Qy 544 GCACTCTCTCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCGCGCG 603
Db GCACTCTCTCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCGCGCG 677

Qy 604 CGACTCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCGCG 663
Db CGACTCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCGCG 737

Db 678 CGACTCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCG 723
Qy 664 CTTCCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCG 723
Db CTTCCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCG 797

Qy 724 CCAATCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCG 783
Db CCAATCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCGCGCG 857

Qy 784 CGTCTCTCTCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCG 843
Db CGTCTCTCTCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCGCG 917

Qy 844 GATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCG 903
Db GATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCG 977

Qy 904 CATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCG 963
Db CATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCGCG 1037

Qy 964 GCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1023
Db GCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1097

Qy 1024 GGTGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1083
Db GGTGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1157

Qy 1084 CTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCG 1143
Db CTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCG 1217

Qy 1144 GCCACCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGAT 1203
Db GCCACCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGAT 1277

Qy 1204 CTTCTCTGTGATGAGTGTGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGAT 1263
Db CTTCTCTGTGATGAGTGTGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGAT 1337

Qy 1264 TCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCG 1323
Db TCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATGCG 1397

Qy 1324 GAAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1383
Db GAAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1457

Qy 1384 GACACTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1440
Db GACACTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1517

Qy 1441 GAATTTGATGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCT 1494
Db GAATTTGATGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCT 1577

Qy 1495 -GCTAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1547
Db -GCTAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGCGCGCGCTGTGATG 1637

Qy 1548 CTTTCAATGATTTAGA-GATATGATGATTTCAACCTGCGCGAGTCAAGTGTGAAATTT 1606
Db CTTTCAATGATTTAGA-GATATGATGATTTCAACCTGCGCGAGTCAAGTGTGAAATTT 1697

Qy 1607 TGTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1665
Db TGTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1757

Qy 1666 ACAGGATGTTCTGTTCT-----CCCTATCAGCGGTAATGATGATGATGATGATG 1718
Db ACAGGATGTTCTGTTCT-----CCCTATCAGCGGTAATGATGATGATGATGATGAT 1814

QY 1719 TTAATTCATGAACCTGTTTCA 1741
 Db 1815 CTAACTCATGAGACCTCGTTTAA 1837

RESULT 6
 PCT-US03-07858A-288
 ; Sequence 288, Application PC/TUS0307858A
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology, LLC
 ; APPLICANT: Laurie, Cathy C
 ; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 ; FILE REFERENCE: 38-77(52900)D
 ; CURRENT APPLICATION NUMBER: PCT/US03/07858A
 ; CURRENT FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: US 60/365,301
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/391,786
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/392,018
 ; PRIOR FILING DATE: 2002-06-26
 ; NUMBER OF SEQ ID NOS: 2459
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 288
 ; LENGTH: 2054
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; PCT-US03-07858A-288

Query Match 75.6%; Score 1333.8; DB 1; Length 2054;
 Best Local Similarity 88.4%; Pred. No. 1,1e-238;

Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

QY 4 CGAGTCCCTCTCTCTCCCAATCTCTCCGCTCCCTCCCAATTCAGACACCACCA 63
 Db 78 CGATCTCCCTCTCTCTCCCAATCTCTCCGCTCCCTCCCAATTCAGACACCAC 137
 QY 64 GGGGATCCGAGCAGCGCGCGCATGCGCCCTCTGTGAGCAATGCGGCCCCCG 123
 Db 138 CACCCATAGGGGCGAGCGCGCGCATGCGCCCTCTGTGAGCAATGCGGCCCCCG 197
 QY 124 CGAGCGCGCGCGCGCGCGCATGCGCATGCTCTCCAGAGACTCGGCGCTCAGC 183
 Db 198 AAGCGCGCGCGCGCGCGCATGCGCATGCTCTCCAGAGACTCGGCGCTCAGC 257
 QY 184 TTCGCGCAGCAGCTCTGATCTCAATCTTCGCGCAGAGTGTACAGCTCAGCCT 243
 Db 258 GTCGCGCGCGCAGCTCTGATCTCAATCTTCGCGCAGAGTGTACAGCTCAGCCT 317
 QY 244 CCCCCCAGCAGCGCGCGCGCATGCGCATGCTCTCCAGAGACTCGGCGCTCAGC 303
 Db 318 TCCCAACAGCAGCGCGCGCGCATGCGCATGCTTCGCGCGCAGAGCAGCAGCA 377
 QY 304 CGGCTTGCGCGCATGCGCGCGCATGCGCGCGCTCTCCGCGCTCTTGCTGTTG 363
 Db 378 CGGCTTGCGCGCATGCGCGCGCATGCGCGCGCTCTCCGCGCTCTTGCTGTTG 437
 QY 364 CGGCTTGCTGATGAGCGCGCTCTCCGCGCGCTTCGCGCAGTACCGCGCTCTCGCA 423
 Db 438 CGGCTTGCTGATGAGCGCGCTCTCCGCGCGCTTCGCGCAGTACCGCGCTCTCGCA 497
 QY 424 GCTATCTCTGCGCGCGCTCTTGAGAGCGTGGGCCCCAGCCCAAGTCAAGTCTGCT 483
 Db 498 GCTCTCTCTCGCGCGCGCTCTTGAGAGCGTGGGCCCCAGCCCAAGTCAAGTCTGCT 557
 QY 484 GATGCGCGCTCTCTTGAGAGCGCGCTGATGCTGCTGAGTGGGCGAGCGCTGGG 543
 Db 558 GATGCGCGCTCTCTTGAGAGCGCGCTGATGCTGCTGAGTGGGCGAGCGCTGGG 617
 QY 544 GCACTCTCTGCGCGCGCGCTCAATGAGCTTCTGATTCAGTCCGCGCTGATGGAGCA 603
 Db 618 GCACTGCTCTGCGCGCGCGCTCAATGAGCTTCTGATTCAGTCCGCGCTGATGGAGCA 677

QY 604 CGACTCGGGCCACACACCGCATCACGGCCATCCGGTCTTCGACCGCGTGTGAGGTGCT 663
 Db 678 CGACTCGGGCCACACACCGCATCACGGCCATCCGGTCTTCGACCGCGTGTGAGGTGCT 737
 QY 664 CTCGCGGAACTGCTTACCGGCTTACGATCGCTGTGTGAAAGTGTAAACACACAGCA 723
 Db 738 CTCGCGGAACTGCTTACCGGCTTACGATCGCTGTGTGAAAGTGTAAACACACAGCA 797
 QY 724 CCAATCGGCTGCAACAGCTGAGCATGACCGGACCTCCAGCAATCCGCTCTTTC 783
 Db 798 CCAATCGGCTGCAACAGCTGAGCATGACCGGACCTCCAGCAATCCGCTCTTTC 857
 QY 784 CCTTCCCGCAAGCTGTTGGGCAATATGCTTCTTACTTACCAAGAGACCTGCGCT 843
 Db 858 TGTCTCCCGCAAGCTGTTGGGCAATATGCTTCTTACTTACCAAGAGACCTGCGCT 917
 QY 844 CGATGCGCGCTGGAATTTCTTATCATGCTACAGCACTGGAACCTTCTACCGGTAAATGTG 903
 Db 918 CGATGCGCGCTGGAATTTCTTATCATGCTACAGCACTGGAACCTTCTACCGGTAAATGTG 977
 QY 904 CATGCGCAGAGTAATTTCTTCTGCGGAGTCCGCTGTTCTTCTACAGGAGAGAGGT 963
 Db 978 CATGCGCAGAGTAATTTCTTCTGCGGAGTCCGCTGTTCTTCTACAGGAGAGAGGT 1037
 QY 964 GCGGAGCGGCTGTTGAGATGCGGCGGCTCGCAATCTGGGCTTGGTACCCGTGCT 1023
 Db 1038 GCGGAGCGGCTGTTGAGATGCGGCGGCTCGCAATCTGGGCTTGGTACCCGTGCT 1097
 QY 1024 GGTGCTTCCCTGCGAATTTGTGAGAGAGGTGCGGTTGTGCTTTTCACTTCACT 1083
 Db 1098 GGTGCTTCCCTGCGAATTTGTGAGAGAGGTGCGGTTGTGCTTTTCACTTCACT 1157
 QY 1084 CTGCGGATTCAGCAGCTCAATTTCTGCTGAACCACTTCTGTCGAGCTGTATTCG 1143
 Db 1158 CTGCGGATTCAGCAGCTCAATTTCTGCTGAACCACTTCTGTCGAGCTGTATTCG 1217
 QY 1144 GCGACCCAGAGGCAATGATGCTTTGAGAGAGAGAGGAGGAGCTGAGACCTGTTG 1203
 Db 1218 GCGACCCAGAGGCAATGATGCTTTGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 1277
 QY 1204 CTCTCTTGTGATGATTTGTTTCAAGTGGCTTGCAGTTCAGATTTAGCACCATCTGTT 1263
 Db 1278 CCTCTCTTGTGATGATTTGTTTCAAGTGGCTTGCAGTTCAGATTTAGCACCATCTGTT 1337
 QY 1264 TCCCGGCTTACTCGGTGCACTTTCGCAAGTTGCAACCGGCTGCGGACCTTTGCA 1323
 Db 1338 CCGCGGCTTACTCGGTGCACTTTCGCAAGTTGCAACCGGCTGCGGACCTTTGCA 1397
 QY 1324 GAGGATGGGCTCACTTATTTGCAAGCCCATTTGCGGCTGCAATTTGCTTAACATGAA 1383
 Db 1398 GAGGATGGGCTCACTTATTTGCAAGCCCATTTGCGGCTGCAATTTGCTTAACATGAA 1457
 QY 1384 GACACTAGAGGCTGCTGATTCAGAGCCAGAGCCGCTACA---AGTGTGTGCTCGAA 1440
 Db 1458 GACACTAGAGGCTGCTGATTCAGAGCCAGAGCCGCTACAAGGCGGCGGCTCGAA 1517
 QY 1441 GAATTTGATGAGAGGCTGTGAACACCATG---GATTAATGGAATGAATACG--- 1494
 Db 1518 GAATTTGATGAGAGGCTGTGAACACCATGATGAATGAATGAATGATGCTG 1577
 QY 1495 -GCTAATGCACTTCTGTG- TTCACTTGTGTGCTTCAATGATTTGTCTGATGC----- 1547
 Db 1578 AGGAGAGGCACTTCTGTGTTTCACTTGTGTGCTTCAATGATTTGTCTGATGCT 1637
 QY 1548 CTTTCAATTTTGA- GATATTGATCATTTCAACCTGCTGAGTCAAGTTGGAATTTTGG 1606
 Db 1638 ATCTCAATTTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTTGG 1697
 QY 1607 TGTGACAGGTGCTGTCTATCAAGTTGAGAGTTCAATTTCT- GATTGTTTC 1665
 Db 1698 TGTGACAGGTGCTGTCTATCAAGTTGAGAGTTCAATTTCT- GATTGTTTC 1757

Oy	1666	ACGGGAGTTCGTCT-----CCCATACCGGTACTCTATGATGATATCTGGT	1728
Db	1758	GTCGGCGTTCATATCTGTCTCCTCATATCATGTAAACGAT---ATCGTATCTTGTCT	1814
Oy	1719	TTAATTCATGAACACTGTTTCA	1741
Db	1815	CTAAGTCATGAGACCTCTGTTTAA	1837

RESULT 7

PCT-US03-07858-288
 Sequence 288, Application PC/TUS0307858
 GENERAL INFORMATION:
 APPLICANT: Monsanto Technology, LLC
 APPLICANT: Laurie, Cathy C
 TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 FILE REFERENCE: 38-77(52900)D
 CURRENT APPLICATION NUMBER: PCT/US03/07858
 CURRENT FILING DATE: 2003-03-14
 PRIOR APPLICATION NUMBER: US 60/365,301
 PRIOR FILING DATE: 2002-03-15
 PRIOR APPLICATION NUMBER: US 60/391,786
 PRIOR FILING DATE: 2002-06-25
 PRIOR APPLICATION NUMBER: US 60/392,018
 PRIOR FILING DATE: 2002-06-26
 NUMBER OF SEQ ID NOS: 2459
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 288
 LENGTH: 2054
 TYPE: DNA
 ORGANISM: Zea mays
 PCT-US03-07858-288

Query Match	75.6%	Score 1333.8	DB 2	Length 2054
Best Local Similarity	88.4%	Pred. No. 1.1e-238		
Matches 1558, Conservative	0	Mismatches 177	Indels 28	Gaps 9

Qy	4	GGAGTCCCTCTCTCTCCCAATCTCTCCCCGCTCCCCCTACCAATATAGACCAACCCA	63
Db	78	CGATTCTCTCTCTTCCCCCAATTCTCCCGCTCTCCCTCCGACCTCTCCCAATACGAC	137
Qy	64	GGCGATCCGAGCCACAGGCGCGGCATGCGCGCTCTGTGATGTGAATGCGGCGCCCG	123
Db	138	CACCATATAGGGGCCACGCGCGCGCAATGCGGCTTTGCGAGACGATGCGGCCCCCG	197
Qy	124	CGACGCGCGGGCGCGCGGCGAGTGGGCAATGATTCTCTCAAGAGACTCGCGCTTACG	183
Db	198	AGAGCGCGCGTGGCGCGGCGAGTGGGCTTGAATCTCTCCAGAGACTCCGAGGACCG	257
Qy	184	TTCCGCGGACGACTCTTGAGTTCATCTCCGCGCAGTGTAGAGAGTCACGCCCTGGCT	243
Db	258	GTCCGCGCGCGACTCTTGATTCATCTCGGCGCAGTGTAGAGAGTCAAGCCCTGGCT	317
Qy	244	CCCCACCAACCGGGCGGGGAGACTCCCGTTTCTCAACCTGGGGGGCAGAGCGCCACGA	303
Db	318	TCCCAACCAACCGGGCGGGAGACTCCCGTCAATCACTTGGCGGGCAGAGCGCCACGA	377
Qy	304	CGCCTTCGCGCTACACACCGGCGCTCGGCGGCGCGCTCTCCGCGGCTTTCGTTGG	363
Db	378	CGCCTTCGCGCTACACACCGGCGCTCGGCGGCGCGCTCTCTCCGCGGCTTTCGTTGG	437
Qy	364	CGGCTCTCTGACTACGCGCGTCTCCCGCGCTCGCGGACTACCGCGGCTCTTCGCGA	423
Db	438	CGGCTCTCTGACTACACCGTCTCCCGCGGCTCGCGGACTACCGCGGCTCTTCGCGA	497
Qy	424	GCTATCTTCGCGGCGCTTTCGAACGCGTGGCGCCACCCCAAGTTCAGCTGTCTT	483
Db	498	GCTCTCTTCGCGGCGCTTTCGAAGCGTGGCGCCACCCCAAGGATCAGTGTCTT	557
Qy	484	GATGGCCGTCCTCTTCTACGCGCGGCTGTACTCTGTCTTCGATGGGCGAGCGCTGGG	543
Db	558	GATGGCCGTCCTCTTCTACGCGCGGCTGTACTCTGTCTTCGATGGGCGAGCGCTGGG	617

OY	544	GCACCTCTCGCGGGGGGTCTCAATTGGCTTCGTGTGATCCAGTCCGGCTGGATGGGGCA	603
Db	618	GCAATAGCTCGCTGGGGGGCTCACCGGCTTCGTGTGATCCAGTCCGGCTGGATGGGGCA	677
OY	604	GCACTCGGGCCACCCAGCCGATCAACGGCCATCCGGTCTCGACCGCGTGTGACAGTGT	663
Db	678	CGACTCGGGGCCACCCGCAATCAACGGCCATCCGGTCTCGACCGCGTGTGACAGTGT	737
OY	664	CTCCGGGAATCTGCTCACCGGCTCTACAGTATGCTTGGTGGAAAGTGTAAACCAACACGCA	723
Db	738	CTCCGGAAACTGCTCACTGGCTCCAGACATCGCTGTGTGGAAAGTGTAAACCAACACGCA	797
OY	724	CCACATGCGCTCGGAACAGCCGTGACATGACCCGGACCTCCAGACATGCGGCTTTTGC	783
Db	798	CCACATGCGCTCGGAACAGCCGTGACATGACCCGGACCTCCAGACATGCGGCTTTTGC	857
OY	784	CGTCTCCCCCAAGCTGTTCGGCAACATATGGTCTTACTTCTCAACCAAGAACCTCGGCTT	843
Db	858	TGTCTCCCCCAAGCTGTTCGGCAACATATGGTCTTACTTCTCAACCAAGAACCTCGGCTT	917
OY	844	CGATGCGGCTCGAAATTTCTTCATCAGCTACACAGCACTGGAACCTTCTAACCCGGTAATGTG	903
Db	918	CGAGCGGCGCTCGAAATTTCTTCATCAGCTACACAGCACTGGAACCTTCTAACCCGGTAATGTG	977
OY	904	CATGCGCAAGATAATCTTCTCGCGGAGTCCGGCCCTTGTGTTCTCAACGGAAGAGAGGT	963
Db	978	CATGCGCAAGATAATCTTCTCGCGGAGTCCGGCCCTTGTGTTCTCAACGGAAGAGAGGT	1037
OY	964	GC CGCAGCGGTGCTTGAGATCCGCGGGGGTCCGACATTTCTGGGCTTGTAACCGGTGCT	1023
Db	1038	GC CGCAGCGGTGCTTGAGATCCGCGGGGGTCCGACATTTCTGGGCTTGTAACCGGTGCT	1097
OY	1024	GGTGGCTTCCCTGCGAATTGGTGGAGAGGGTTCGCTTTGTGCTTTTCAAGCTTCAACAT	1083
Db	1098	GGTGGCGGTGCTGCGAATTGGTGGAGAGGGTTCGCTTTGTGCTTTTCAAGCTTCAACAT	1157
OY	1084	CTGGGGGATTCAGACGTCCTCAATTTCTTCCTGTAACAATTCTTCGTCGACAGTGTATGTCCG	1143
Db	1158	CTGGGGGATTCAGACGTCCTCAATTTCTTCCTGTAACAATTCTTCGTCGACAGTGTATGTCCG	1217
OY	1144	GCCACCCCAAGGGCAATGACTGTGTTTGAAGAAGCAACGCGAGGCACTCGACATCTCTGTG	1203
Db	1218	GCCACCCCAAGGGCAACGACTGTGTTTGAAGAAGCAACGCGAGGCACTCGACATCTCTGTG	1277
OY	1204	CTCTCTTGGATGGATTGGTTTCAACGGTGGCTGACAGTTCCAGATTGAGCAACATCTGTT	1263
Db	1278	CCCTCTTGGATGGATTGGTTTCAACGGTGGCTGACAGTTCCAGATTGAGCAACATCTGTT	1337
OY	1264	TCCCCGCTTACTCTGGTGTCCACCTTTCGCAAGGTTGACACGGCCGTCCGCGACCTTTTGCA	1323
Db	1338	CCCCCGCTGCTCTGGTGTCCACCTTTCGCAAGGTTGACACGGCCGTCCGCGACCTTTTGCA	1397
OY	1324	GAAACATGGGGCTCACTTAATCTGCAAGCAATTCGAGGGTGCAAATGTGCTTACATGAGAA	1383
Db	1398	GAAACATGGGGCTCACTTAATCTGCAAGCAATTCGAGGGTGCAAATGTGCTTACATGAGAA	1457
OY	1384	GACACTCAGGGCTGCTCATTTGACAGCCAGGACCGGTACA--AGTGTGTGCTCCGAA	1440
Db	1458	GACACTCAGGGCTGCTCATTTGACAGCCAGGACCGGACCGGCGGGCGGCGGTCCGAA	1517
OY	1441	GAATTTGGTATGGAGGCTGTGAACACCCATG--GATTAATGGGATGAAGATACG--	1494
Db	1518	GAATTTGGTATGGAGGCTGTGAACACCCATGATGAATGAATGAACGAGGATATGTGCTG	1577
OY	1495	-GCTAATGGCACTTCTGGTG--TTCACTTGTGTGCCATGTGATGTCTGATGTC-----	1547
Db	1578	AGGGGAAGGCAACTTGTGTGTTCACCTTGTGTGCCACCGGATGTCTGTGTCTTCTA	1637
OY	1548	CTTTACAGTATTTTAGA--GATATGATCATTCACCTGCTGAGTCAAGTGTGAATTTTTCG	1606
Db	1638	ATCTCAGTGTGTTTGAATGTATGTGTATTTGATTAACCCGTCGAGTCCGGGCTGGAATTTTTCG	1697
OY	1607	TGTTGACAGTGTGCTGTCTATCCAGTGTGAGAGTTCAATGCTTCAATATGCTT--GGTGTTC	1665

D _b	1698	TGTTGACAGAGACCGCTATCCAGTTGAAGATTCAGCTTCAATTTGCTGGGTTGTC	1757
Q _y	1666	ACGGGATGTTCTGTTCT-----CCCTATCACGGTAACTATATGATGATGATCTTGCT	1718
D _b	1758	GTCGGCGTTCTATTCTGTTCTCTCTATATCATGTGTACGAT---ATCGTATCCTTGTCT	1814
Q _y	1719	TTAATTCATGAACACTGTTTCA	1741
D _b	1815	CTAAGTCATGACCTCTGTTTAA	1837

RESULT 8
PCT-US03-07858A-288
; Sequence 288, Application PC/TUS0307858A

```

? APPLICANT Monsanto Technology, LLC
? APPLICANT: Laurie, Cathy C
? TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
? FILE REFERENCE: 38-77(52900)D
? CURRENT APPLICATION NUMBER: PCT/US03/07858A
? CURRENT FILING DATE: 2003-05-09
? PRIOR APPLICATION NUMBER: US 60/365,301
? PRIOR FILING DATE: 2002-03-15
? PRIOR APPLICATION NUMBER: US 60/391,786
? PRIOR FILING DATE: 2002-06-25
? PRIOR APPLICATION NUMBER: US 60/392,018
? PRIOR FILING DATE: 2002-06-26
? NUMBER OF SEQ ID NOS: 2459
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 288
? LENGTH: 2054
? TYPE: DNA
? ORGANISM: Zea mays
? CCT-US03-07858A-288

```

Query Match	75.6%	Score 1333.8	DB 2	Length 2054
Best Local Similarity	88.4%	Pred. No. 1.1e-238		
Matches 1558	Conservative	0	Mismatches 177	Indels 28
				Gaps 9

QY	4	CGAGCTCCCTCTCTCTCCCAATCCTCCCGCTCCCTCCCAATAGACACCA	63
Db	78	CGATCCCTCTCTTCCCCTATTCCTCCCGCTCCCTCCCAATATGACAC	137
QY	64	GGCCGATCCGAGCCAGCGCGCGCATGCGGCTCTGTGATGCAATGCGCGCCCGG	123
Db	138	CACCCATAGGGGACAGCGCGCGCATGCGCGCTCTCGCGCAATGCGCGCCCGG	197
QY	124	CGAGCGCGCGCGCGCGCGAGCGTACGATGATCTCTCTCAAGAGCTCCGCGCTACGCG	183
Db	198	AGAGCGCGCGCGCGCGCGAGCGTTCGATCTCTCTCAAGAGCTCTCCGAGACGC	257
QY	184	TTCCGCGGACGACCTCTGGATCTCCATCTCGGCGAGTGTATCGACGTACGCGCTTGCT	243
Db	258	GTCCGCGCGCGACCTCTGATCTCCATCTCGGCGAGCGTGTACGATGACGCTTGCT	317
QY	244	CCCCACCAACCGCGCGCGCGAGCTCCCGCTTCTCAACCTGCGGCGGACAGAGCCACGA	303
Db	318	TCCCCACCAACCGCGCGCGAGCTCCCGCTATCACTTTGGCGGAGAGGCCACGA	377
QY	304	CGCCTTGCGCGCTTACCAACCGCGCGCTCGGCGCGCTCTCTCCCGCTTCTTGTTGG	363
Db	378	CGCCTTGCGCGCTTACCAACCGCGCGCTTGCGCGCGCTCTCTCTCTTGTTGG	437
QY	364	CCGCTCTCTTACTTACGCGCGTCTCCCGCGTCCGCGCATACGCGCGCTCTTCGCGCA	423
Db	438	CCGCTCTCTTACCACTACCGTCTCCCGCGCTCCGCGCATACCGCGCGCTCTTCGCGCA	497
QY	424	GCTATCTCTCGCGGCGCTCTTGAAAGCGGTGCGGCCCAACCCCAAGTCCAGCTGTCT	483
Db	498	GCTCTCTCTCGCGGCGCTCTTGAGAGCGGTGCGGCCCAACCCCAAGTCCAGCTGTCT	557
QY	484	GATGAGCGTCTCTTTCAGCGCGCGTGTACTGTCTGTGAGTACGCGCGCTTGAGC	543

Dp	558	GATGACCGTCTCTTTCTAAGCGGAGCTCTACCTGTCTCGCTGCGGACGCTTGGC	617
Qy	544	GCACCTCTCGCGGAGGGATCATTTGACCTTCGTGATCCAGTCCGGCTGATGGGCA	603
Dp	618	GCACATCTCGCTGGGGGGGCTCATCGGCTTGTCTGTGATCCAGTCCGGCTGGAGGCA	677
Qy	604	CGACTCGGGGACCAACCGCATCACCGGCATCCGGTCTCGACCGCGCTGTGCAAGTGTCT	663
Dp	678	CGACTCGGGGACCAACCGCATCACCGGCATCCGGTCTCGACCGCGCTGTGCAAGTGTCT	737
Qy	664	CTCCGGGAACTGCTCAACCGGCTCAGCATGCGCTGGGGAAGTGAACCAACACGCA	723
Dp	738	CTCCGGAAATGCTCTCACTGGCTCAGCATGCGCTGGGGAAGTGAACCAACACGCA	797
Qy	724	CCACATGCGCTGCAACAGCTGAGCAATGACCAGGACTCCAGACATGCGGCTTTG	783
Dp	798	CCACATGCGCTGCAACAGCTGAGCAATGACCAGGACTCCAGACATGCGGCTTTG	857
Qy	784	CGTCTCCCCCAAGTGTTCGGCAACATATGTCTCTACTTTCTAACCAAGGACCTTGCGTT	843
Dp	858	TGTCTCCCCCAAGTGTTCGGCAACATATGTCTCTACTTTCTAACCAAGGACCTTGCGTT	917
Qy	844	CGATGCGGCTCGAAATTTCTTCACTAGCTACAGCATGAGCCTTCTAACCGGTAATGTG	903
Dp	918	CGAGCGGCTCGAAATTTCTTCACTAGCTACAGCATGAGCCTTCTAACCGGTAATGTG	977
Qy	904	CATCGCAGGATTAATTTCTCGCGCAGTCCGCGCTGTCTTCTTCAAGAGAGAGGT	963
Dp	978	CATCGCAGGATTAATTTCTCGCGCAGTCCGCGCTGTCTTCTTCAAGAGAGAGGT	1037
Qy	964	GCCGACGCGTGTGATGATCGCGGGGCTGCAATTCGCGCTTGTAACCGGCTCT	1023
Dp	1038	GCCGACGCGTGTGATGATCGCGGGTGTGCGCGCTTGTGCGGCTTGTAACCGGCTCT	1097
Qy	1024	GGTGGCTTCCCTGCGCAATTTGTGGGAGAGGCTGCGCTTGTGCTTTCACTTCAACAT	1083
Dp	1098	GGTGGCTTCCCTGCGCAATTTGTGGGAGAGGCTGCGCTTGTGCTTCACTTCAACAT	1157
Qy	1084	CTGGGGGATTCAGACGTCGCAATTCGTCGTCGCAACCACTTCGTCGCAAGTATGTGCG	1143
Dp	1158	CTGGGGGATTCAGACGTCGCAATTCGTCGTCGCAACCACTTCGTCGCAAGTATGTGCG	1217
Qy	1144	GCCACCCAGGGCAATGACTGTGTGAAGACAGCGGACGCAAGCTCGACATCTGTG	1203
Dp	1218	GCCACCCAGGGCAATGACTGTGTGAAGACAGCGGACGCAAGCTCGACATCTGTG	1277
Qy	1204	CTCTCTTTGATGATTTGTGTTCCACGCTGCTGCAATTCGATTTGAGCAACATCTGT	1263
Dp	1278	CCCTCTTTGATGATTTGTGTTCCATGCGGCTGCAATTCGATTTGAGCAACATCTGT	1337
Qy	1264	TCCCGGCTACCTGGTGCCACTTTCGCAAGGTTGCAACCGGCGCTCCGCACTTTGCA	1322
Dp	1338	CCCGGCTACCTGGTGCCACTTTCGCAAGGTTGCAACCGGCGCTCCGCACTTTGCA	1397
Qy	1324	GAAACATGAGCTCATTTATTTCTGACGCAATTCGCGGTGCAATGTGCTTACATGGA	1383
Dp	1398	GAAACATGAGCTCATTTATTTCTGACGCAATTCGCGGTGCAATGTGCTTACATGGA	1457
Qy	1384	GACACTAGGGCTGTGATTTGACAGGCAAGGACCGCTACA---AGTGTGTGCTCCGA	1440
Dp	1458	GACACTAGGGCTGTGATTTGACAGGCAAGGACCGGCTCCGCA	1511
Qy	1441	GAAATTTGTAATGGAGGCTGGAACCCGATG---GATTAATGGGATGAAGATTCGG---	1499
Dp	1518	GAAATTTGTAATGGAGGCTGGAACCCGATGAAGTAAATGGGATGAAGATTCGGCTG	1577
Qy	1495	-GCTAATGGAACCTTGTGTG-ATCAGCTTGTCGCAATGATTTGTCTGATG-----	1547
Dp	1578	AGGGGAAGGCACTTCTGTGTGTTCACTTTGTGCGAAGGATTTGTCTGTTGCTTCTA	1637
Qy	1548	CTTTCACTTATTTGA-GATATTTGATTTTCACTGCTGAGTCAAGTTGGAATTTTCG	1606

TYPE: DNA
ORGANISM: Zea mays
US-09-857-524B-3

Query Match 66.6%; Score 1175; DB 30; Length 1448;
Best Local Similarity 98.3%; Pred. No. 4.5e-209;
Matches 1187; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY 541 GGGGCACTCTCGCGGGGGGCTCATTTGGCTTGTGATCCAGTCCGGCTGATGG 600
Db 38 GGGGCACTGCTCGCGGGGGGCTCATTCGGCTTGTGATCCAGTCCGGCTGATGG 97
QY 601 CCAGGATCTGGGGCCACACCGGATCCCGGCTCCGCTCCGCTCCGCTCCGCT 660
Db 98 CCAGGATCTGGGGCCACACCGGATCCCGGCTCCGCTCCGCTCCGCTCCGCT 157
QY 661 GCTCTCGGGAACTGGCTCAACCGGCTCAGCATGCTCGGGGAGTGAACCAACAC 720
Db 158 GCTCTCGGGAACTGGCTCAGCGGCTCAGCATGCTCGGGGAGTGAACCAACAC 217
QY 721 GCACCACTGCGCTGCAACAGCTGACCATGACCCGAGCTCCAGGACATGCGCT 780
Db 218 GCACCACTGCGCTGCAACAGCTGACCATGACCCGAGCTCCAGGACATGCGCT 277
QY 781 TGGCGTCTCCCGCAAGCTGTTGGCAACATATGCTCTTCTTCAACAGGACCT 840
Db 278 CGCTGCTCCCGCAAGCTGTTGGCAACATATGCTCTTCTTCAACAGGACCT 337
QY 841 GTTCGATCGCGCTCGAAATTTCTCATGCTACGATCCAGTCCCTTCAACCGG 900
Db 338 GTTCGATCGCGCTCGAAATTTCTCATGCTACGATCCAGTCCCTTCAACCGG 397
QY 901 GTTCGATCGCGGATTAATCTTCTCGCGAGTCCGCTGTTGTTCTCAGGAGAG 960
Db 398 GTTCGATCGCGGATTAATCTTCTCGCGAGTCCGCTGTTGTTCTCAGGAGAG 457
QY 961 GTTCGCGCAAGGTTGTTGATTCGGGGGTCGCGCACTTCGCGCTTGTATCC 1020
Db 458 GTTCGCGCAAGGTTGTTGATTCGGGGGTCGCGCACTTCGCGCTTGTATCC 517
QY 1021 GCTGATGCTTCCCTCGCAATTTGTTGGAGAGGTTGCTTGTGCTTTCAGCT 1080
Db 518 GCTGATGCTTCCCTCGCAATTTGTTGGAGAGGTTGCTTGTGCTTTCAGCT 577
QY 1081 CATTCGGGATTCAGGACGTTCAATTTCTGCAACCACTTCTCGCGAGCTGAT 1140
Db 578 CATTCGGGATTCAGGACGTTCAATTTCTGCAACCACTTCTCGCGAGCTGAT 637
QY 1141 CGGGCCACCCCAAGGCAATGCTGTTGGAAGAGAGCGGACGCTGCACTCT 1200
Db 638 CGGGCCACCCCAAGGCAATGCTGTTGGAAGAGAGCGGACGCTGCACTCT 697
QY 1201 GTGCTCTCTTGGATGATTTGTTTCAAGGTCGCTGCAAGTTCCAAATTTAG 1260
Db 698 GTGCTCTCTTGGATGATTTGTTTCAAGGTCGCTGCAAGTTCCAAATTTAG 757
QY 1261 GTTTCCTCGGCTTCTCGGTCACCTTCGCAAGTTGCAACGCGCTCCGCACT 1320
Db 758 GTTTCCTCGGCTTCTCGGTCACCTTCGCAAGTTGCAACGCGCTCCGCACT 817
QY 1321 CAGAGGATGAGGCTCATTTATTTCTGAGCCACATTTCTGGGTTGCAAT 1380
Db 818 CAGAGGATGAGGCTCATTTATTTCTGAGCCACATTTCTGGGTTGCAAT 877
QY 1381 GAAGCACTCAGGCTGCTGATTTGAGGACAGGACGCTACAAAGTGTGCT 1440
Db 878 GAAGCACTCAGGCTGCTGATTTGAGGACAGGACGCTACAAAGTGTGCT 937
QY 1441 GAATTTGATGAGAGCTGTGAACACCGATGATTAATGAGTGAAGATTA 1500
Db 938 GAATTTGATGAGAGCTGTGAACACCGATGATTAATGAGTGAAGATTA 997
QY 1501 GGCAACTTCTGGGTTGAGCTTGTGTCATGATTTCTGTGATGCTTTTAT 1560

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Db 998 GGCAACTTCTGGGTTGAGCTTGTGTCATGATTTCTGTGATGCTTTAT 1057
QY 1561 AGGATATGATTAATTAACCTCTGAGTCAAGTTGGAATTTCTGTTGACAG 1620
Db 1058 AGGATATGATTAATTAACCTCTGAGTCAAGTTGGAATTTCTGTTGACAG 1117
QY 1621 TGTCTATCCAGTTGAGAGTTCAATGCTCAATGCTGTTGTTCAAGGATG 1680
Db 1118 TGTCTATCCAGTTGAGAGTTCAATGCTCAATGCTGTTGTTCAAGGATG 1177
QY 1681 CTCCTATACCGGTAATTAATGATGATCTTCTTTAATTAATTAATTAAT 1740
Db 1178 CTCCTATACCGGTAATTAATGATGATCTTCTTTAATTAATTAATTAAT 1237
QY 1741 AAGATTA 1747
Db 1238 AAGATTA 1244

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RESULT 13

US-09-857-524B-3
Sequence 9, Application US/09857524B

GENERAL INFORMATION:
APPLICANT: Edgar B. Caboon
APPLICANT: Rebecca E. Caboon
APPLICANT: William D. Hitz
APPLICANT: Anthony J. Kinney
TITLE OF INVENTION: Membrane-Bound Desaturases
FILE REFERENCE: B1264
CURRENT APPLICATION NUMBER: US/09/857,524B
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,784
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
SEQ ID NO: 9
LENGTH: 1972
TYPE: DNA
ORGANISM: Trifolium aestivum
US-09-857-524B-3

Query Match 61.9%; Score 1091.4; DB 35; Length 1972;
Best Local Similarity 79.0%; Pred. No. 1.9e-193;
Matches 1355; Conservative 0; Mismatches 341; Indels 19; Gaps 4;

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QY 27 CCTCCCGCTTCCCTTACCAATGACACACCAAGCGGATCCAGCCGCG 86
Db 89 CCTCCCTCTCGCGCTCAGCTAATCCAGCCAGATGCGCGACGCGGAGC 148
QY 87 CAATCGCGCTCTGATGATGCAATGCGCGCGCGCGCGCGCGCGCGCGCG 146
Db 149 CAACGCGCGGAAACCGACGCAATGCGCGCGCGCGCGCGCGCGCGCG 202
QY 147 TCGGATGATCTCTTCAAGAGCTCCGCGCTCAAGTTTCGCGAGGACCT 206
Db 203 TCGGATGATCTCTTCAAGAGCTCCGCGCGCGCGCGCGCGCGCGCGCG 262
QY 207 CCATTCGCGCGAGTGTACAGCTGACGCGCTGCGCTCCCGACCAACCG 266
Db 263 CCATTCGCGCGAGTGTACAGCTGACGCGCTGCGCTCCCGACCAACCG 322
QY 267 TCGCGCTTCTACCTGCGCGGAGGAGAGCGCAACGAGCGCTTGC 326
Db 323 TCGCGCTTCTACCTGCGCGGAGGAGAGCGCAACGAGCGCTTGC 382
QY 327 CCTCGCGCGCGCGCTTCTCGCGCTTCTGTTGCGCGCTCTGATTAAC 386
Db 383 CCTCGCGCGCGCGCTTCTCGCGCTTCTGTTGCGCGCTCTGATTAAC 442
QY 387 CCGCGCGCTCGCGAGTACCGCGCGCTCTCGCGAGCTATCTCGCGGCG 446
Db 443 CCGCGCGCTCGCGAGTACCGCGCGCTCTCGCGAGCTATCTCGCGGCG 502

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Db 7843 TCCCTGGGGGGGCTGTTGAGCGGGGTGGGCCACCCCGAGATGCGAGTGGCCGGGAT 7784
QY 487 GGCCTGCTCTTCTTAAGCGCGGCTGTAAGCTGCTGCTGCAATGGCCAGCGCTGGGGCA 546
Db 7783 GCTGCTCTCTTCTTAAGCGCGGCTGTAAGCTGCTGCTGCAATGGCCAGCGCTGGGGCA 7724
QY 547 CTTCTGCGGGGGGCTGCAATGGCTGCTGCTGCAATGGCTGCTGCAATGGCTGCTGCA 606
Db 7723 CTTCTGCGGGGGGCTGCAATGGCTGCTGCTGCAATGGCTGCTGCAATGGCTGCTGCA 7664
QY 607 CTTGGGGCCACCAAGCATACCGGCTGCTGCTGCTGCAATGGCTGCTGCAATGGCTGCT 666
Db 7663 CTTGGGGCCACCAAGCATACCGGCTGCTGCTGCTGCAATGGCTGCTGCAATGGCTGCT 7604
QY 667 CCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
Db 7603 CCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7544
QY 727 CATGCTGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
Db 7543 CATGCTGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7484
QY 787 CTTCCCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
Db 7483 CTTCCCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7427
QY 847 TGGCGCTGCAATTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
Db 7426 TGGCGCTGCAATTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7367
QY 907 CCGCAGGATTAATCTTCTGCGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
Db 7366 CCGCAGGATTAATCTTCTGCGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7307
QY 967 GCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
Db 7306 GCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7247
QY 1027 GCGCTTCCCTGCGGATTTGGTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
Db 7246 GCGCTTCCCTGCGGATTTGGTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7187
QY 1087 CCGGATTTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
Db 7186 CCGGATTTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7127
QY 1147 ACCCAAGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
Db 7126 ACCCAAGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7067
QY 1207 TCCCTGGATGATTTGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266
Db 7066 TCCCTGGATGATTTGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7007
QY 1267 CCGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1326
Db 7006 CCGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6947
QY 1327 GCATGGGCTCACTTATTTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
Db 6946 GCATGGGCTCACTTATTTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6887
QY 1387 ACTGAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446
Db 6886 ACTGAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6827
QY 1447 GGTATGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
Db 6826 GGTATGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6778
QY 1507 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
Db 6777 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6730

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QY 1567 ATTGATCATTTCAACTT-----GCTGAGTCAAGTTGAATTTTCTGTTGACAGTGGC 1620
Db 6729 ATTGATCATTTTAACTTTAACCGCTTGGAGTTGGATGCAATTTTCTGTTGACAGTGGC 6670
QY 1621 -TGTCTATCAAGTTGAGA-----GTTCAATGCTTCAATAGTCTGCTGTTTCAACGGGATGTT 1675
Db 6669 TTGCTTTGCACTGMAAGAGTGGGTTTATGCTTCAATGCTTCACTGTTCTTCATGTATTT 6610
QY 1676 CTTTCTCCCTTATC 1689
Db 6609 AGATTGCTCGATTTC 6596

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Search completed: January 1, 2004, 04:20:52
Job time : 3937.96 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 16:17:02 ; Search time 445.364 Seconds
(without cleanup)

9535.036 Million cell updates/sec

Title: US-09-857-524B-3

Sequence: 1 gcacgagctccctctctc.....ttaaaaaaaaaa

Scoring table: IDENTITY_NUC

Searched: 4483691 seqs, 1203673480 residues

Total number of hits satisfying chosen parameters: 8967382

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending Patents NA, New: *

1:	/csgn2_6/pdatocal1/pna/	PCT	NEW	COMB.	seq. *
2:	/csgn2_6/pdatocal1/pna/US06	NEW	COMB.	seq. *	
3:	/csgn2_6/pdatocal1/pna/US07	NEW	COMB.	seq. *	
4:	/csgn2_6/pdatocal1/pna/US08	NEW	COMB.	seq. *	
5:	/csgn2_6/pdatocal1/pna/US10	NEW	COMB.	seq. *	
6:	/csgn2_6/pdatocal1/pna/US10	NEW	COMB.	seq. *	
7:	/csgn2_6/pdatocal1/pna/US10	NEW	COMB.	seq.2:	
8:	/csgn2_6/pdatocal1/pna/US06	NEW	COMB.	seq. *	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	1349	76.5	151.1	7	US-10-425-1144-14218	Sequence 14218, A
2	891.4	50.5	146.0	7	US-10-425-1144-17460	Sequence 17460, A
3	609.6	34.1	196.7	7	US-10-425-1144-14991	Sequence 14991, A
4	602	34.1	120.7	7	US-10-425-1144-28231	Sequence 28231, A
5	491.2	27.8	170.2	7	US-10-702-777-26	Sequence 26, App1
6	486.2	27.6	183.8	7	US-10-425-1144-14869	Sequence 14869, A
7	459	26.0	195.1	8	US-60-496-751-1	Sequence 1, App11
8	453.8	25.7	138.9	8	US-60-496-751-3	Sequence 3, App11
9	452.8	25.6	134.1	8	US-60-496-751-2	Sequence 2, App11
10	439.2	24.9	214.4	7	US-10-425-1144-15122	Sequence 15122, A
11	385.2	21.8	171.9	7	US-10-425-1144-10327	Sequence 10327, A
12	365.4	20.7	168.5	7	US-10-702-777-4	Sequence 4, App11
13	337.6	19.1	96.6	7	US-10-425-1144-65172	Sequence 6172, App
14	273.8	15.5	107.1	7	US-10-425-1144-10518	Sequence 10518, A
15	213.6	12.1	66.3	7	US-10-425-1144-14800	Sequence 14800, A
16	194	11.0	6.6	7	US-10-425-1144-10881	Sequence 10881, A
17	103	5.8	26.2	7	US-10-680-765-14762	Sequence 14762, A
18	100.4	5.7	34.0	7	US-10-680-765-11214	Sequence 11214, A
19	89	5.0	145.5	7	US-10-425-1144-5594	Sequence 5694, App
20	83.6	4.7	12.5	5	US-09-897-5164-4197	Sequence 4197, App
21	80.2	4.5	85692	1	PCT-US03-198787-1	Sequence 1, App11
22	80.2	4.5	85692	1	PCT-US03-19069-1	Sequence 1, App11
23	79.4	4.5	61.6	7	US-10-425-1144-55327	Sequence 5327, App
24	76.8	4.4	138.0	7	US-10-417-7104-138	Sequence 138, App1
25	76.4	4.3	36.0	7	US-10-425-1144-13841	Sequence 13841, App

26	76.4	4.3	630	7	US-10-425-114A-28252	Sequence 28252, Appl
27	76.4	4.3	1574	7	US-10-324-316-11	Sequence 11, Appl
28	76.4	4.3	1574	7	US-10-324-316-11	Sequence 11, Appl
29	75.6	4.3	2253	8	US-60-494-566-34	Sequence 34, Appl
30	75.6	4.3	164051	8	US-60-494-566-16	Sequence 16, Appl
31	75	4.3	86941	1	PCR-US03-18787-2	Sequence 2, Appl1
32	75	4.3	86941	1	PCR-US03-18787-2	Sequence 2, Appl1
33	74.4	4.2	37707	8	US-60-500-315-11904	Sequence 11904, A
34	72.8	4.1	2151	7	US-10-389-647-153	Sequence 123, Appl
35	72.6	4.1	1848	7	US-10-425-114A-23176	Sequence 23176, A
36	72	4.1	986	7	US-10-425-114A-17564	Sequence 17564, A
37	72	4.1	1041	7	US-10-425-114A-16902	Sequence 16902, A
38	71.8	4.1	1450	1	US-10-425-114A-15517	Sequence 15517, A
39	70	4.0	1705	1	PCR-US03-27533-523	Sequence 523, Appl
40	70	4.0	1772	7	US-10-296-115-562	Sequence 562, Appl
41	69.8	4.0	2200	7	US-10-425-114A-35258	Sequence 35258, A
42	69.6	3.9	2336	7	US-10-679-063-119	Sequence 119, Appl
43	69.6	3.9	2336	7	US-10-679-063-393	Sequence 393, Appl
44	68.6	3.9	8705	1	PCR-US03-33131-16	Sequence 16, Appl
45	68.6	3.9	10330	7	US-10-656-265-24	Sequence 24, Appl

ALIGNMENTS

```

RESULT 1
US-10-425-114A-14218
Sequence 14218, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingtong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21153131B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 14218
LENGTH: 1541
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB148-051-G4_FLI
US-10-425-114A-14218

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Query Match	76.5%	Score 1349	DB 7	Length 1541
Best Local Similarity	100.0%	Prod. No. 0		
Matches 1349	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	399	CGACATACCGCGCGCTCTCTCGCGGCGCATCTCCGCGGGCTCTTGAAAGCGTCGACC		458
Db	1	CGACATACCGCGCGCTCTCTCGCGGCGCATCTCCGCGGGCTCTTGAAAGCGTCGACC		60
Qy	459	CCACCCCCAAGGTCAGCTCGTCTGATGGCGCTCTTTTACGCGCGCTGTACTCG		518
Db	61	CCACCCCCAAGGTCAGCTCGTCTGATGGCGCTCTTTTACGCGCGCTGTACTCG		120
Qy	519	TCCTGCGATGCGCGACGCGCTGGGCGCATCTCTCGCGGGGGTCTATTGGCTTCGT		578
Db	121	TCCTGCGATGCGCGACGCGCTGGGCGCATCTCTCGCGGGGGTCTATTGGCTTCGT		180
Qy	579	GGATTCAGTCCGGCTGATGGGCCACACGACTGGGGCCACACCGGATCAACGGGCATATCCGG		638
Db	181	GGATTCAGTCCGGCTGATGGGCCACACGACTGGGGCCACACCGGATCAACGGGCATATCCGG		240
Qy	639	TCCTGACACGCGTCGCGAGGTCCTCCGCGAACTGCTCAACGGGCTCAGCATTCGCT		698
Db	241	TCCTGACACGCGTCGCGAGGTCCTCCGCGAACTGCTCAACGGGCTCAGCATTCGCT		300

OY	699	GATGGAATGTAAACACAAACAGCACACATCGCTGCAACAGCGCTGGACCATGACCGG	758
Db	301	GGTGGAAGTGAACCAACAACAGCACACATGCTTGCAACAGCTGGACCATGACCGG	360
OY	759	ACTCTGACGACATGCGCTCTTTGCGCTCTCCCGCAAGCTGTTGGCAACATATGTCCT	818
Db	361	ACCTTCACGACATGCGCTCTTTGCGCTCTCCCGCAAGCTGTTGGCAACATATGTCCT	420
OY	819	ACTTCACGACGAGCCCTGGCGCTTCGATGCGCGCTCGAATAATCTTCATGACATCAGC	878
Db	421	ACTTCACGACGAGCCCTGGCGCTTCGATGCGCGCTCGAATAATCTTCATGACATCAGC	480
OY	879	ACTGGAACCTTCTACCCCGGTAAATGTGATCGACGAGATAAATCTTCCGCGAGTCCGCC	938
Db	481	ACTGGAACCTTCTACCCCGGTAAATGTGATCGACGAGATAAATCTTCCGCGAGTCCGCC	540
OY	939	TGTTGCTTCTCACGGAGAAAGAGGTGCGCGACGCGTGTCTTGAGATCGCGGGGCTCGCA	998
Db	541	TGTTGCTTCTCACGGAGAAAGAGGTGCGCGACGCGTGTCTTGAGATCGCGGGGCTCGCA	600
OY	999	CATTCTGGGCTTGGTAACCGTGTGCTGTGTGCGCTTCCCTGCGCAATGTGTGGAGAGGTCG	1058
Db	601	CATTCTGGGCTTGGTAACCGTGTGCTGTGTGCGCTTCCCTGCGCAATGTGTGGAGAGGTCG	660
OY	1059	CGTTTGTCTTTTACGCTTCAACCATCTGCGGATTCAGACGTCGCAATTTCTGCTGAAC	1118
Db	661	CGTTTGTCTTTTACGCTTCAACCATCTGCGGATTCAGACGTCGCAATTTCTGCTGAAC	720
OY	1119	ACTCTCGCTCGGAGGTGATGTGCGGGCCACCCAAAGGGGAATGACTGTGTTGAGAAAGCA	1178
Db	721	ACTCTCGCTCGGAGGTGATGTGCGGGCCACCCAAAGGGGAATGACTGTGTTGAGAAAGCA	780
OY	1179	CGGACGAGCAGCTCGACATCTCTGTGCTCTCTTTGATGGAATTTGTTTCCACGGTGGCTGC	1238
Db	781	CGGACGAGCAGCTCGACATCTCTGTGCTCTCTTTGATGGAATTTGTTTCCACGGTGGCTGC	840
OY	1239	AGTTCCAAATTGAGACCAATCTGTTTCCCGCTACCTCGGTGCACTTTCGCAAGTTTG	1298
Db	841	AGTTCCAAATTGAGACCAATCTGTTTCCCGCTACCTCGGTGCACTTTCGCAAGTTTG	900
OY	1299	CACCGGCGCTCGCGACCTTTGCAAGAGATGGGCTCACTTAATCTGACGCCACATCT	1358
Db	901	CACCGGCGCTCGCGACCTTTGCAAGAGATGGGCTCACTTAATCTGACGCCACATCT	960
OY	1359	GGGGTGCAATATGTGCTTACATGGAAGACCTCAGGGCTGTGTCATTTGCAAGGCCAGAGCG	1418
Db	961	GGGGTGCAATATGTGCTTACATGGAAGACCTCAGGGCTGTGTCATTTGCAAGGCCAGAGCG	1020
OY	1419	CTACAAGGTGTGTGCTCGAAGATTTGTATGGAAGGCTGTGAACCAACCATGGAATAA	1478
Db	1021	CTACAAGGTGTGTGCTCGAAGATTTGTATGGAAGGCTGTGAACCAACCATGGAATAA	1080
OY	1479	TGGATGAGAATACGGGCTAAATGGCACTTCTGTGTTCAAGTTGTGTCGCATGTGATTG	1538
Db	1081	TGGATGAGAATACGGGCTAAATGGCACTTCTGTGTTCAAGTTGTGTCGCATGTGATTG	1140
OY	1539	TCTGATGACCTTTCAGTTATTTAGAGATTTGATTAATCAACTGCTCCGAGTCAAGTTGG	1598
Db	1141	TCTGATGACCTTTCAGTTATTTAGAGATTTGATTAATCAACTGCTCCGAGTCAAGTTGG	1200
OY	1599	AATTTTCGTGTGACAAAGTGGCTGTCTATCCAGTTGGAGAGTTCATGCTTCAATATGTCTG	1658
Db	1201	AATTTTCGTGTGACAAAGTGGCTGTCTATCCAGTTGGAGAGTTCATGCTTCAATATGTCTG	1260
OY	1659	GTTGTTCACGGGATGTTCTGTTCTCCCTATCACGGTAACATATGATGATGATCTTCTCT	1718
Db	1261	GTTGTTCACGGGATGTTCTGTTCTCCCTATCACGGTAACATATGATGATGATCTTCTCT	1320
OY	1719	TTAATTCATGAACACTGTTTCAAAATTA 1747	
Db	1321	TTAATTCATGAACACTGTTTCAAAATTA 1349	

RESULT 2
US-10-425-114A-17460
; Sequence 17460, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 17460
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3069-031-B5_FLI
US-10-425-114A-17460

Query Match 50.5%; Score 891.4; DB 7; Length 1408;
Best Local Similarity 88.0%; Pred. No. 2.1e-225;
Matches 1082; Conservative 0; Mismatches 116; Indels 31; Gaps 9;

541 GCGCGACCTCCTCGCGGGGGTCTCATTTGCTTCGTGATCCAGTCCGCGTGGATGGG 600
3 GGGCGACATGCTCGCTGGGGGGCTCATCGGCTTCGTGGATCCAGTCCGCGTGGATGGG 62
601 CCAAGACTCGGACCAACACCGCATCACCGGCATCCGGTCTCTGACCCGCGTGTGAGGT 660
63 CCAGACTCGGGCCACCAACCGCATCACCGGCATCCGGTCTCTGACCCGCGTGTGAGGT 122
661 GCTCTCGGGGAATGCGCCATCCGCGCTGAGATGCGCTGAGGAGTGAATGACCAACAG 720
123 GCTCTCGGGGAATGCGCCATCCGCGCTGAGATGCGCTGAGGAGTGAATGACCAACAG 182
721 GCACCAATCGCTGACCAACAGCTGAGATGCGCTGAGGAGTGAATGACCAACAG 780
183 GCACCAATCGCTGACCAACAGCTGAGATGCGCTGAGGAGTGAATGACCAACAG 242
781 TGCGCTCTCCCAAGCTGTTGCGCAATATGTTCTTATCTTCAACCAAGCAACCTGGC 840
243 CGCTGCTCTCCCAAGCTGTTGCGCAATATGTTCTTATCTTCAACCAAGCAACCTGGC 302
841 GTTGATGATCGCTCGAATCTTTCATGATGATGATGATGATGATGATGATGATGATGAT 900
303 CTGACACCGCTCGAATCTTTCATGATGATGATGATGATGATGATGATGATGATGAT 362
901 GTGATCGCCAGATTAATCTTCTCGCGACGTCGCTGTTGTTCTTCAACGAGAGAG 960
363 GTGATCGCCAGATTAATCTTCTCGCGACGTCGCTGTTGTTCTTCAACGAGAGAG 422
961 GTGCGCGAGCGGTTGCTTGAAGATGCGGAGGATGCGCAATCTGAGGCTTGTATCCGTT 1020
423 GGTGCGCGAGCGGTTGCTTGAAGATGCGGAGGATGCGCAATCTGAGGCTTGTATCCGTT 482
1021 GGTGCGCGCTTCCGCGCGAATTTGGTGGGAGAGGTTCCGTTGTTGCTTTCAGCTTAC 1080
483 GGTGCGCGCTTCCGCGCGAATTTGGTGGGAGAGGTTCCGTTGTTGCTTTCAGCTTAC 542
1081 CATGCGCGGATTCAGACGTCATATTTGCTGTAACCATCTTCTGTCGACGATGATGT 1140
543 CATGCGCGGATTCAGACGTCATATTTGCTGTAACCATCTTCTGTCGACGATGATGT 602
1141 CCGGCGACCAAGGGCAATGATGCTTTGAGAGAGAGACGCGAGGCAAGCTGACATCTT 1200
603 CCGGCGACCAAGGGCAATGATGCTTTGAGAGAGAGACGCGAGGCAAGCTGACATCTT 662
1201 GTGCTCTCTTGATGATTTGGTTCCAGGATGCGCTGCAATTTCCAGATTTGAGCAATCT 1260

Db 1219 AGGAGATGCGCTTGTGTTAAGGATCTTTCAGAGAAACATAGTCTTCTTAATATGT 1278
Qy 1349 GCCACATTCCTGGGATGCAATATGCTTACATGAGACACATCAGGGCTGCTGATGAG 1408
Db 1279 GTGTCTGTTCTGAGAGGCAATGCTCTACATTCAGACCTTGAGAAATGCTGCTTGCAG 1338
Qy 1409 GCCAGACCGCTACAGTGTGTGCTCCAGAAATTTGATGAGAGGCTGTGACACC 1468
Db 1339 GCCAGAGACGGTTCCA---ATCCGGTTCCAAGAAATTTGTTGGAGGCTGTAAACACT 1395
Qy 1469 CATGATTAATGGG 1482
Db 1396 CATGATTAATGGG 1409

RESULT 4
US-10-425-114A-28231
Sequence 28231, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yinhua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28231
LENGTH: 1207
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4748-018-D3_FLI
US-10-425-114A-28231

Query Match 34.1%; Score 602; DB 7; Length 1207;
Best Local Similarity 89.6%; Pred. No. 7.9e-149;
Matches 658; Conservative 0; Mismatches 75; Indels 1; Gaps 1;
Qy 4 CGAGCTCCTCTCTCTCCCAATCTCCCGCTCCCTCCCAACCA-AATCAGACACACCA 62
Db 13 CGAATTTCCCACTTCCCAATTTCTCCCGCTCCCTCCCAACCAACCA 72
Qy 63 AGGCGATCCGAGCGAGCGCGCGCAATGCGCCCTCTGTGATGCAATGCGGCGCCG 122
Db 73 CACCCATAGGGGCGACGCGCGCGCAATGCGCCCTCTGTGAGCAATGCGGCGCCG 132
Qy 123 GCGACGCGCGGCGCGCGCGCGAGCTGTGCGCATGATCTCTCCAGAGACTCGGCTAGC 182
Db 133 GAGACGCGCGGTGTGCGCGCGAGCTGTGCTTGAATCTCTCCAGAGACTCGGCGAGC 192
Qy 183 CTTCGCGCGAGCACTGTGATCTCCATCTCCGCGAGCGTGAAGAGTCAAGCGCCGCGC 242
Db 193 GCTTCGCGCGAGCACTGTGATCTCCATCTCCGCGAGCGTGAAGAGTCAAGCGCCGCGC 252
Qy 243 TCCCGCACACCGCGCGCGCGAGCTCCCGCTTCTCACCTTGCGCGGCGAGAGCGCACCG 302
Db 253 TTCCCGCACACCGCGCGCGCGAGCTCCCGCTTCTCACCTTGCGCGGCGAGAGCGCACCG 312
Qy 303 ACGGCTTCGCGCGCTTACACACCGCGCTTCGCGCGCGCGCTTCGCGCTTCTTGTG 362
Db 313 ACGGCTTCGCGCGCTTACACACCGCGCTTCGCGCGCGCGCTTCGCGCTTCTTGTG 372
Qy 363 GCGGCTTCGAGTACGCGCTTCGCGCGCGCGCGTTCGCGCGCGCGCTTCGCGCGC 422
Db 373 GCGGCTTCGAGTACGCGCTTCGCGCGCGCGCGTTCGCGCGCGCGCTTCGCGCGC 432
Qy 423 AGCTATCTCGCGCGCGCTTTCGAAAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGC 482

Db 433 AGCTCTCTCCGCGGCTCTTTCAGAGCGGCTGAGCCCAACCCCAAGGTAACAGCTGCC 492
Qy 483 TGATGCGCGCTCTCTTCTTACGCGCGCTGTAACCTGCTCTGATGCGCGCGCTGAG 542
Db 493 TGATGCGCGCTCTCTTCTTACGCGCGCTTACCTGCTCTGATGCGCGCGCTGAG 552
Qy 543 CGGACCTCTCGCGGCGGCTTCTATTCATTCGCTGATTCAGTCCGCGCTGATGAGCC 602
Db 553 CGGACATGCTCGTGGGCGGCTTCTGATTCAGTCCGCGCTGATGAGCC 612
Qy 603 ACGACTCGGCGCACACCGCATTCACCGCGCTTCTGACCGCGCTGATGAGTGC 662
Db 613 ACGACTCGGCGCACACCGCATTCACCGCGCTTCTGACCGCGCTGATGAGTGC 672
Qy 663 TCTCGGGAACGCTTCTACCGCGCTGAGTGCCTGATGAGTGAAGTGAACACACACCG 722
Db 673 TCTCGGGAACGCTTCTTCTTCTGAGTGCCTGAGTGCCTGATGAGTGAAGTGAACACACACCG 732
Qy 723 ACCACATCCGCTGC 736
Db 733 TCGACATCCGCTGC 746

RESULT 5
US-10-702-777-26
Sequence 26, Application US/10702777
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/702,777
FILING DATE: 06-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE: 19-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-702-777-26

Query Match 27.8%; Score 491.2; DB 7; Length 1702;
 Best Local Similarity 62.0%; Pred. No. 2e-119;
 Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

155 ATCTCTCCAGAGAGTCCGCGCTCACGCTCCGCGAGAGACTGTGATCTTCATCTCC 214
 DB ATTCACGCGGAGAGACTCCGCGCGCACAAAGTCCGCGATCTGTGATCTTCATCTCCAG 131
 215 GCGGAGGTGACAGAGTCAAGCCCTGCTCCCGCACACCCCGGCGGCGAGACTCCCGCTT 274
 DB GCGAAGGTCTACAGCTCTCTCGGTGGCGCGGAGACACCCCGGCGGCGAGAGTCCGCTC 191
 132 GCGAAGGTCTACAGCTCTCTCGGTGGCGCGGAGACACCCCGGCGGCGAGAGTCCGCTC 191
 275 CTCACCTCTGCGGCGGAGAGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 334
 DB CTCACCTCTGCGGCGGAGAGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 251
 192 CTCACCTCTGCGGCGGAGAGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 251
 335 GCGCGGCTCTCTCGGCGGCT 388
 DB TGGCGGCT 311
 252 TGGCGGCT 311
 389 CCGCGGCT 448
 DB CCGCGGCT 371
 312 GAGATCTCTCAAGAGTCAAGGAGCTTTTGAACGAGATGTGCGGATCTCGGAGATCTTCGAG 371
 449 CCGGCT 508
 DB AAGAGAGGCTCAACACATCATGTGAGAGTCTCTGCGGCTCTCTCTCTCTCTCTCTCTCT 431
 372 AAGAGAGGCTCAACACATCATGTGAGAGTCTCTGCGGCTCTCTCTCTCTCTCTCTCTCT 431
 509 CTGTACT 568
 DB GTCTACGCGGTGCGGCT 491
 432 GTCTACGCGGTGCGGCT 491
 569 GCGTCT 628
 DB GCGTCT 551
 492 GCGTCT 551
 629 GCGATCT 688
 DB CCAAGCT 611
 552 CCAAGCT 611
 689 AGCATCT 748
 DB AGCATCT 671
 612 AGCATCT 671
 749 CATGACCCGAGCT 808
 DB TACGACCCGAGCT 731
 672 TACGACCCGAGCT 731
 809 ATATGCT 868
 DB ATATGCT 791
 732 ATATGCT 791
 869 AGCTACACAGCT 928
 DB AGCTACACAGCT 851
 792 AGCTACACAGCT 851
 929 CAGTCCGCT 988
 DB CAGTCCGCT 911
 852 CAGTCCGCT 911
 989 GGGGCT 1048
 DB GGGGCT 971
 912 GGGGCT 971
 1049 GAGAGGCT 1108
 DB GAGAGGCT 1031
 972 GAGAGGCT 1031
 1109 TGGCTCAACCACT 1168
 DB TGGCTCAACCACT 1091
 1032 AGCTCAACCACT 1091

QY 1169 GAGAGACAGACCGGAGGAGAGCTGACATCTGTGCTCTCTCTGATGATGATGATGATGAT 1228
 DB 1092 GAGAGACAGACCGGAGGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1151
 QY 1229 GGTGGCTCTGAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1288
 DB 1152 GGTGGCTCTGAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1211
 QY 1289 CCGAAGTTCAGACCGGCGGCTGCGGAGCTTTCAGAGACATGAGGCTGATTCATTCGCA 1348
 DB 1212 AGAGAGATTCGCGCTCTGCGGAGCTTTCAGAGACATGAGGCTGATTCATTCGCA 1271
 QY 1349 GCCAATTCCTG---GTCGAAATGTCTTACATGAGAGACACTAGGCTGCTGATTCG 1405
 DB 1272 TTGGGTTTGGGAGAGAGCTATGTCAGAGACATTCGAGCGTGAAGGATGCGCGTT 1331
 QY 1406 CAGGCGGAGAGCGCTTCAAGATGAGTGTGCTCTCGAGATTCGAT---GGAGGCTG 1462
 DB 1332 CAGGCGGAGAGCGCTTCAAGATGAGTGTGCTCTCGAGATTCGAT---GGAGGCTG 1391
 QY 1463 AACACCATGATTAATGAGAT 1484
 DB 1392 AACACCATGATTAATGAGAT 1413

RESULT 6 US-10-425-114A-14869

Sequence 14869, Application US/10425114A
 GENERAL INFORMATION:
 APPLICANT: Liu, Jindong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425, 114A
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 14869
 LENGTH: 1828
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3030-005-A3_FLI
 US-10-425-114A-14869

Query Match 27.6%; Score 486.2; DB 7; Length 1828;
 Best Local Similarity 61.2%; Pred. No. 4.5e-118;
 Matches 820; Conservative 0; Mismatches 513; Indels 6; Gaps 2;

155 ATCTCTCCAGAGAGTCCGCGCTCACGCTCCGCGAGAGACTGTGATCTTCATCTCC 214
 DB 172 ATCTCTCCAGAGAGTCCGCGCTCACGCTCCGCGAGAGACTGTGATCTTCATCTCC 211
 QY 215 GCGAGGTGACAGAGTCAAGCCCTGCTCCCGCACACCCCGGCGGCGAGACTCCCGCTT 274
 DB 232 GCGAGGTGACAGAGTCAAGCCCTGCTCCCGCACACCCCGGCGGCGAGACTCCCGCTT 291
 QY 275 CTCACCTCTGCGGCGGAGAGCGGCGGAGAGCGGCTTTCGCGCTTACACCCCGCTTGGG 334
 DB 292 TCMAACCTTCTGCGGCGGAGAGTCAAGTATTCATTCATTCATTCATTCATTCATTC 351
 QY 335 CCGCGGCT 391
 DB 352 TGGTCAACCACT 411
 QY 392 GCGTCTGAGTACCGGCGGCT 451
 DB 412 GGTCTCAACCACT 471

QY 452 GTGCGCCCAACCCCAAGTCCAGCTGCTGATGAGCGCTCTTCTAAGCCGCGCTG 511
 DB 472 AAGGCGCATGTGACTTCTTGACACCTTGACATCTGTTGCTGTATGTTCCATTTGATG 531
 QY 512 TACCTGCTCTCGCATGCGCCAGCGCTGGGCGACCTCTCCGCGGGGGTCTCATTTGCG 571
 DB 532 TATGCTGTGTGAGTGACACTAGTGTGTGCGCTCATTTGGGCTCAGGATGATTAAGG 591
 QY 572 TTGCTGTGATCCAGTCCGCTGATGAGGCGACAGACTCGGCGCCACACCGCATCACCGG 631
 DB 592 TTGCTGTGATCCAGTCCGCTGATGAGGCGACAGACTCGGCGCCACACCGCATCACCGG 651
 QY 632 CATCCGCTCTCGACCGCGCTGTCAGAGTCTCTCCGCGAATGCTCATCCGCGCTCAG 691
 DB 652 AGCAATGTTTCAACAAGTTGACAGATCTCTCTGGAATGCTTGAATGGATTAAGC 711
 QY 692 ATGCGCTGTGTAAGTGTACCAACACGACCAACATGCGCTGCAACAGCTGGAACAT 751
 DB 712 ATTTGCTGTGTAAGTGTACCAACATGCTCACCACATGCTGCAACAGCTTGAATCAT 771
 QY 752 GACCCGAGCTCCAGACATGCGCTTGTGCGCTCTCCCGCAAGCTGTTGGCAACATA 811
 DB 772 GACCTGATCTGAGACATGCGCTTGTGCGCTCTCCGCTTCTGCGGTTCTTCAATTCGATA 831
 QY 812 TGGTCTACTTCTACCAAGGACCTGCGCTGATGCGCTGCAAAATCTTCATCAGC 871
 DB 832 ACTTCTCATTTCTATGAGGAGAGTTGAGATTGATTTCAATTGCAAGTTCTTGATCTGC 891
 QY 872 TACCAAGCTGACCTTCTTACCCGCTGATGTCATGCGAGATTAATCTTTCGCGCAG 931
 DB 892 TACCAAGCTGACCTTCTTACCCGCTGATGTCATGTCGAGGATTAATCTTTCGCGCAG 951
 QY 932 TCCGCGCTGTGCTTCTACGAGAGAGAGGAGGCGCGCTGCTGAGATCGCGGCG 991
 DB 952 ACCATTTCTCTATTTGTTGAGGCGCTTAAGTCAAGATTAAGCTTGAACATTAATGAGG 1011
 QY 992 GTGCGCACATTTCTGAGCTTGTATCCCGTGTCTGTGCTGCTTCCGCGAATGTTGAGG 1051
 DB 1012 ATCTGTTGTGTTGAGCTTGTGCTTCTTGTGCTTGTGCTTCTTGTGCTTGTGCTGAG 1071
 QY 1052 AAGGTCGCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1111
 DB 1072 AAGGTCGCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1131
 QY 1112 CTGAACCACTTCTGCTGCGACGCTGATGTCGCGGCGACCGAGGCGATGATGCTTGA 1171
 DB 1132 TTGAATCACTTGTGCTGCAATGATGTTGAGGCTACCGAGTGGAGATGATGCTTGA 1191
 QY 1172 AAGCAGACGCGAGCGCTGACATCTGTGCTCTGCTTGTGATGATGATGCTTGA 1231
 DB 1192 AAGCAGACGCGAGCGCTGACATCTGTGCTCTGCTTGTGATGATGATGCTTGA 1251
 QY 1232 GGCCTGACGTTCTGATGAGCAACATCTGTTTCCCGCTTACCTGCTGCGACCTTGC 1291
 DB 1252 GGCCTGACGTTCTGATGAGCAACATCTGTTTCCAAAGGCTACCTGCTGCGACCTTGA 1311
 QY 1292 AAGGTCGACCGCGCTCCGCGACCTTGTGCAAGAGAGGCTCACTTATTTGAGCG 1351
 DB 1312 AACATTTTCCCTTGTGAGTGAACCTTGTGCAAGAGAGGCTCACTTATTTGAGCG 1371
 QY 1352 ACATTTCTGGGCTGCAATGCTTATGATGAGAGACACTCAGGCTGCTGATGAGCGC 1411
 DB 1372 TCAATTTTGGAGGCGCAATGATGAGACATTAAGACCTCAGGCTGCTGATGAGCGC 1431
 QY 1412 AAGACGCTACAGTGTGTGCTGCAAGATTTGTATGAGGAGCTGTAACACCAT 1471
 DB 1432 AAGGACTTGAACA--ACCTGCGCTTAAGAAATTTGTGTGAGGAGCTGTATATACCAT 1488
 QY 1472 GGAATAATGAGATGAAGAT 1490
 DB 1488 GAGTGTGATTTTGGAGTT 1507

RESULT 7
 US-60-496-751-1
 ; Sequence 1 Application US/60496751
 ; GENERAL INFORMATION:
 ; APPLICANT: Ustin, Virginia
 ; APPLICANT: Roman, Byron
 ; APPLICANT: Gonzalez, Jennifer
 ; TITLE OF INVENTION: Fatty Acid Desaturases from *Primula*
 ; FILE REFERENCE: MONS:044USP1
 ; CURRENT APPLICATION NUMBER: US/60/496, 751
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1953
 ; TYPE: DNA
 ; ORGANISM: *Primula juliae*
 ; US-60-496-751-1

Query Match 26.0%; Score 459; DB 8; Length 1953;
 Best Local Similarity 60.3%; Pred. No. 7, 4e-111;
 Matches 794; Conservative 1; Mismatches 516; Indels 6; Gaps 2;

QY 189 CCGACGACCTTGTGATCTCCATCTCCGCGACGCTGTACGACGTACGCGCTGCTCCCG 248
 DB 187 CAGTGACCTATGAT 246
 QY 249 ACCACCGCGCGCGACCTTCCGCTTCTACCTCTGCGCGCGCGCGCGCGCGCGCGCG 308
 DB 247 TTCAACCG 306
 QY 309 TCGCGCGCTTACCAACCG 368
 DB 307 TCTGCGCTTACCAACCG 366
 QY 369 TCTCTG---ACTAGCGCTCTCCCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 425
 DB 367 TCTTAAATAAATAATGCTGCTGCGAGACCTTTCGATGATGCAAACTTCTTACAGAG 426
 QY 426 TATCTCCGCGCGCGCTTCTGAAAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 485
 DB 427 TATATAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
 QY 486 TGGCGCTCTCTTCTTACGCGCGCGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCT 545
 DB 487 TGAATCTTATGTTGTTCTCTGATGCTGAGGCTGCTTGTGATGATGATGATGATGAT 546
 QY 546 ACTTCTCGCGCGCGCTCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
 DB 547 ATTGCTTTGTGAGGCGCAATGAGGCTTGTGCTGATGCTGATGCTGATGCTGATGCT 606
 QY 606 ACTGCGCGCAACCGCGATCACCGCGATCCGCTCTGCAACCGCGCTGCTGCTGCTGCT 665
 DB 607 ATTCCGCGACATTAACCGATTAATGATGATGATGATGATGATGATGATGATGATGAT 666
 QY 666 CCGGGAATGCTCTCAACCGGCTCAGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725
 DB 667 GCTCAATGCTCTCAACCGGCTTATGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 QY 726 ACATGCTCTGCAACAGCTGACCATGACCCGAGCTTCCAGACATGCTGCTTGTGCG 785
 DB 727 ACATGCTCTGCAATGCTGAGTACGACCTGACCTGACATGATGATGATGATGATGAT 786
 QY 786 TCTTCCCAAGCTTGTGCGCAACATGATGCTTCTTCTTCAACGAGACCTGCGCTTGC 845
 DB 787 TGTCCCGGAAGTTCTTATCTCCCTCACTTCTGCTTCTTCAACGAGGCTGATGATG 846
 QY 846 ATGCGCTCTGCAATCTTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 905
 DB 847 ACGGTGTGTGAGGTTTGTGTTCAATACAGACATGCTGCTTCTTCAACGAGGCTGCT 906
 QY 906 TCGCCAGATTAATCTTCTGCGAGTCCGCTGCTGCTTCTTCAACGAGGAGGCTGCT 965

Qy	369	TCCTCTG---ACTAAGCCGCTCTCCCGCGCGCTCCGCGACATCAACGGCGCTCTCCGCGAGC	425
Db	281	TTCTAGAAAAACATCTCCGTCTCGAAGACCTTTTCCGACTATCCGAACCTTTCTAAGACGCT	340
Qy	426	TATCTTCCGCGGGCTTTTGAAACGCGTCGAGCCCAACCCCAAGTCCAGCTCGTCTGA	485
Db	341	TTCATTAAGATGGGAGATGTTTCGTGCGAGAGGCCACATGCGCTACGGCAGCTTGTCAATTA	400
Qy	486	TGCGCGTCTCTTTCTAAGCGCGCGCTGTACTCGTCTCTCGATGCGCAGCGCGCTTGGGCGC	545
Db	401	TGATACTTAATGTGGTTCCTCTGTGTGACTGGGGGCTTTGCAATGGAATTCGGTGGTGTC	460
Qy	546	ACCTCCTCGCGGGGGGCTCATTTAGGCTTCCCTGTGATCCCAAGTCGCGCTGATATGGGCGACG	605
Db	461	ATTGTGTTTGTGTGAGCGCGCAATGGGGTTTCCCTGTGATCCAGTGGGATAGATAGTCAATG	520
Qy	606	ACTCGGGCCACCAACCGCATCACGGGCCATCCGGTCTCTGACCGCGCTGTGACGGTCTCT	665
Db	521	ATTCCGGACATTAACCGGATTAATGACTGTACAGAAATGGAACCGGGTGTCTAGATCTCTGA	580
Qy	666	CCGGGAATCTCCCTACCGGCGCTCAGCATTCGCTGTGGGAAGTGTAAACACAAACGCAAC	725
Db	581	GCTCAAACTCTCTCCAAAGGATTAAGCATTCGGGTGTGGGAAGTGAACACACACGCGAAC	640
Qy	726	ACATCGCCTGCAACAGCGCTGACCATATACCGGACCTCCAGACATGCTCGCTTTTCCCG	785
Db	641	ACATTGGCTGCATAATGCTGTGGAATGACACCTCTACCTCCAGTACATTTCCCTGTTGGATTG	700
Qy	786	TCTTCCCCAAAGCTGTTCCGCAACATATGTGTCTACTTTCAACCAAGGACCTGGCGTTGC	845
Db	701	TGTCCTCCGAAGTCTTTAATCTCCCTCACTTCTCGTTTCTTACGACAAAGATGTAACATTCG	760
Qy	846	ATGCGCGCTGGAATCTTCATCAGTACAGTACAGACATCGAATCTTACCCGGTAATGTGA	905
Db	761	ACGGTGTGTGAGGATTTTGTGTTCAATACCAAGCATGTGTGCTTTTATCCGGTCAATGTGTG	820

Qy	189	CCGACGACCTTGGATCTCCATCTCCGGACGAGTACGACGTCAAGCCCTGGCTCCCC	248
Db	101	CAGGAGACTTGGATTCATTCATTCACGGTCAAGTTTCAACGTTTCTTCTGGGTGGGC	160
Qy	249	ACCAACCGGGGGGCGACCTCCCGCTTTCACCTCTGGCGGGGAGGACGCACCGACGCT	308
Db	161	TTCAACCGGGGGGCACTCGCTCCCTCTCTGCGCTTGCAGACATATGTGACCGACGCTT	220
Qy	309	TGCGCGCTTACCAACCGCCCTTGAGGCGCGCGCTCTCTCGCGCTTCTTGTTGGCGGC	368
Db	221	TCTGTGCTTACCATCCCTCTTCACACTCCCGGCTCTCTCCCTCTCTTCACCAACCTAC	280

QY	369	TCCTCTG---ACTAAGCCGCTCTCCCGCGCGTCCGCGACATACCGCGCGCTCTCGCGAGC	425
Dp	281	TTCTAGAAAAACATCTCCGTGTCGAGACCTCTTTCGACTATCGCAACCTTTACACAGCT	340
QY	426	TATCTTCGCGGGGCTCTTCGAAAGCCTCCGAGCCCAACCCCAAGATCAGCTCGCTCGA	485
Dp	341	TTTCATAGATGGGGAATGTTTCGTGCGAGAGGCCACATGCGTAACGGACCTTTGTATTA	400
QY	486	TGCGCGTCTCTCTTCACGCGCGCTGTACTCGTCTCTGCATGCGCAGCGCTTGCGGC	545
Dp	401	TGATACTATGTTGGTGTCTCTCTGTGACTGCGGGGTCTTTCAGTGAAGAAATCCGTGGGTGC	460
QY	546	ACCTCCCTCGGGGGGGGTCTATGGCGTCTGTCGATCCAGTCCGCGTGAATGGGGCAAG	605
Dp	461	ATTGGTGTGTGAGCGCGCAATGGGGTGTTCCTGAGATCCAGTGGGATGATAGTCATG	520
QY	606	ACTCGGGCCACCAACCGCATCACGGCCATCCGGGTCCGACCGCGGTGTCAGGTGCTCT	665
Dp	521	ATTTCGGACATTAACCGGATTAATGACTGACAGAAATAGAAACCGGTTCGTCAGATCCTGA	580
QY	666	CCGGGAACTGCTTCACCGGCGCTGAGCATGCGCTGTGGAAAGTGTAAACACACACGCAAC	725
Dp	581	GTCTCAACCTGCTCTCCAAAGGAGATTAGCATCGGGGTGTGGAAGTGGAACACACACGCAAC	640
QY	726	ACATCGCTCTGACACAGCTTGACCATATACCCGGAACCTCCAGCACATGCGCTCTTGGCG	785
Dp	641	ACATGTGCTCTCAATAGCTGTGAGATACACCTTCGACCTCCAGTACATTCCTGTGTGGTGG	700
QY	786	TTCTCCCCAAGCGTGTGGGCAACATATGCTCTACTCTTACCTCAACAGCAACCGTCGCTTG	845
Dp	701	TGTCGCCGAAAGTCTTTTAATCTCCTCACTTCTGCTTTCTACGACAGAAAGTGAACCTTCG	760
QY	846	ATGCGCGCTCGAAATCTTTCATGACTGACGACGACGACGACCTTCTACCCGGTAATGTGCA	905
Dp	761	ACGGTGTGTGAGGTTTGTGTTCAATACGAGCACTGTGTGTTTATCCGGTCAATGTGTG	820
QY	906	TGCGCAGAGTAATCTTCTGCGCGAGTCCGCGCTGTCTGTTCTCACGAGAGAGGGTGC	965
Dp	821	TTGTGTAGCTGAAATGCTGCTTGCAGAGTGGTTTATCTGCTTTTTCAGAGGAGGAGGTGG	880
QY	966	CGCAGCGGTGCTTGAAGTGGCGGGGTGGCCACATTCGCGGCTTGATACCGGTGCTGG	1025
Dp	881	CGAACAGGGTGCAGAGAAATCTTGACTACGAGTCTTGTGCTTGTTCGCTCTCGC	940
QY	1026	TGCGTTCCTCCGCGAAATGGTGGGAGAGGGTCCGGTGTGTGCTTTTACGCTTCAACATCT	1085
Dp	941	TTTCTTCCCTTCTCTAATGGGGGTGAGAGATTAATGTTTTTGTCTCGACGCTACCTCGTTA	1000
QY	1086	GCGGAGTTACAGACGTGCCAATTCGCTGTAACCATTTCTGTCGACGCTGTATGTGGGC	1145
Dp	1001	CGGGGATATCAACAGTGCAGTTCAGCTTGAACCATTTCTCATCTGAAGTTTACGTGGGCC	1060
QY	1146	CATCCCAAGGCAATGACTGTGTTGAGAGAGAGACGAGGCAAGCTGTGAATCTGTGCT	1205
Dp	1061	CACCCGTAAAGGTAAAGATGTGTTTAAAGAAACAGACTGAGAGGACATCAACATATCGTGC	1120
QY	1206	CTCCCTTGAATGGAATGGTGTCCACGSGTGGCTCGACGTTCCAGATTGAGACCAATCTGTTC	1265
Dp	1121	CGGCGTGAATGGAATGGTTCATAGCGGGGTTCGACGTTTCAGGTCGACACCATTTGTTC	1180
QY	1266	CCGCGCTAAGCTCGGTGCACTTTCGCAAGGTGACCCGCGCTCCGCACTTGTGCAGA	1325
Dp	1181	CGGGAATGCTTAAGGGGTCAAGTTTCGAAAGATTTCTCTTTTGTGAGGGAATTTGTGTAA	1240
QY	1326	AGCATGGGCTCACTTAATCTTCGACGCCACATTTCTGGGGTGCAAATGTGCTTACATGAGA	1385
Dp	1241	AACACATTTGAATCTTCAATATTTGCGCTTTTACTAAAGCAAAATGTGTGACGCTTGAGA	1300
QY	1386	CATCAAGGGGTGCTGATTCAGAGGCCAGACCGGTACAGGTGGGTGTGCTCCGAAGATTT	1445
Dp	1301	CCCTTGAAAAACAGCCCATTTAGAGGCTCGGACCTCTC---TAATCCGATCCCAAGATTA	1357

QY 1446 TGGTATGAGAGGCTGTGAACA 1466
 Db 1358 TGGTGTGGAGGCTGTAAAAA 1378

RESULT 9
 US-60-496-751-2
 ; Sequence 2, Application US/60496751

GENERAL INFORMATION:
 APPLICANT: Urbain, Virginia
 APPLICANT: Froman, Byron
 APPLICANT: Gonzalez, Jennifer
 TITLE OF INVENTION: Fatty Acid Desaturases from *Primula*
 FILE REFERENCE: MONS:044USP1
 CURRENT APPLICATION NUMBER: US/60/496,751
 CURRENT FILING DATE: 2003-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 1341
 TYPE: DNA
 ORGANISM: *Primula juliae*
 US-60-496-751-2

Query Match 25.6%; Score 452.2; DB 8; Length 1341;
 Best Local Similarity 60.7%; Pred. No. 3,8e-109;
 Matches 777; Conservative 0; Mismatches 498; Indels 6; Gaps 2;

QY 189 CCGAGCAGCTTGTGATCTCCATCTCCGGCAGCTGTACAGAGTACAGCCCTGCTCCCC 248
 Db 53 CAGGTACCTATGATATCAATTCACGGTCAAGTTTACAGCTTCTTCTGGGCTGGCG 112
 QY 249 AACACCCGGGGCGGCACTCCCGCTTCTACCTTGGCGGGGAGAGCCACCGAGGCT 308
 Db 113 TTCAACCCGGGGGCACTCCCGCTTCTTGGAGAGCAATGTGACCGAGCTT 172
 QY 309 TCGCCGCTACACACCGGCTTCCGGCGGCGGCTTCTTCTTCTTCTTCTTCTTCTTCT 368
 Db 173 TCTCGCTTACATCCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 232
 QY 369 TCTCTG--ACTAGCGGCTCTCCCGGCTCCGCGCATACCGGCGGCTTCTTCTTCTTCT 425
 Db 233 TTCTAGAAAAACATTCGCTGTCGAGACCTTCTCCGGCTATCGAAATCTTACAGAGCT 292
 QY 426 TATCTCCCGGCGGCTTCTTGAACCGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCG 485
 Db 293 TTCAATAGATGGGATGTTTGTGTCAGAGGGGCGACATGCTTACGAGACCTTGTATTA 352
 QY 486 TGGCGCTCTCTTCTTACGCGCGGCTGTACTCTGCTTCTGATCGGCGGCGGCGGCGGCG 545
 Db 353 TGAATCTTATGTTGTTTCTCTGTGATCGGGGTGCTTGTGATGAGATCCGTGGGTGC 412
 QY 546 ACCTCTCGCGGGGCTTCTATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 605
 Db 413 ATTGTTTGTGAGCGGCAATGGGGTTTCTGATTCGATCGGATGATGATGATGATGATG 472
 QY 606 ACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 665
 Db 473 ATTCCGGAATTAACCGGATTAATGATGACGAGAAATGAAACCGGTTCTGCTCAATCTGA 532
 QY 666 CCGGGAATGCTCTCAACCGGCTCAGCATGCTGTGAGAAATGTAACCAACACGAGACC 725
 Db 533 GCTCAAACTGCTCTCAAGGATTAAGCATCGGGTGTGAGAGTGAACCAACACGAGACC 592
 QY 726 ACATGCTGTGCAACAGCTTGAACCATGACCCGAGACCTCGAGCATGCGGCTTTGGCG 785
 Db 593 ACATGCTGTGCAATGCTGAGATGAGACCTGACCTCGAGCATATTTCTTGTGGTTG 652
 QY 786 TCTCCCGCAAGCTGTTTGGGCAATATGTTCTTACTTCTTACCAAGGAGCCCTGGCTTG 845
 Db 653 TGTCCCGCAAGTCTTAACTCTTCACTTCTGTTTCTTACGACAGAGAGCTCAAGCTTGC 712
 QY 846 ATGCCGCTCGAAATTTCTTCATGAGTACAGACATGAGACCTTCTACCGGATATGTGCA 905

Db 713 AGGTTGTGAGAGTTTGTGTTCAATACAGAGCTGTGTTTATCCGGTATGTGTG 772
 QY 906 TGGCCAGATTAATCTTCTCGGCACTCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 965
 Db 773 TTGCTAGGCTGAAACATGCTTGGCGAGCTCTTATATCTGCTTTTGTGAGAGGAGGTG 832
 QY 966 CGCAGCGTTGTGATGATCGCGGGGTGGCCCATTTCTGAGGCTTGTATCCGTTGCTG 1025
 Db 833 CGAACGGGTGCAAGGATTTCTTGACTAGCGGTTTGTGCTTGTGCTTGTGCTTGTG 892
 QY 1026 TGGCTTCCCTGCGAATTTGTGAGAGGCTGCGGTTTGTGCTTGTGCTTGTGCTTGTG 1085
 Db 893 TTTCTTCCCTCTTAATTTGGGGTGAAGATATATGTTTGTGCTGCGAGCTACTCCGTTA 952
 QY 1086 GCGGATTTAGACAGCTTCAATTTGCTGTAACCACTTCTGCTCCAGCTGTATGTGGGC 1145
 Db 953 CGGGATTAACAACGTCAGTTTCAAGTTTCAATTTCTATCTGATGAGTTTGTGAGGCGC 1012
 QY 1146 CACCCAGGCAATGACTGTTTGAAGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1205
 Db 1013 CACCGTAGATGATGATTTGTTTAAAGAAACAGCTGAGGAGACATCAATATCTGTC 1072
 QY 1206 CTCTTGTGATGATTTGTTTCAAGGCTGCTGAGTTTCAAGTTGAGCAATCTGTTTC 1265
 Db 1073 CGGCGTGTGATGATTTGTTTCAATGCGGGTTGAGTTTCAAGTTGAGCAATCTGTTTC 1132
 QY 1266 CCGGCTTACTCGGTGCACTTTCGCAAGTTGACCGGCGGCGGCGGCGGCGGCGGCGG 1325
 Db 1133 CGGGAATGCTTGTGAGGCTGAGTTTCTGGAATTTCTTGTGAGGAGATTTGTGTAGA 1192
 QY 1326 AGCATGGGCTACTTATTTGTGAGGCAATTTGCGGGGTCAATGTGCTTATATGAGA 1385
 Db 1193 AACCAATTTGATTAATTAATTTGCTTTTCTTAAAGCAATGTTGAGCTTGAAG 1252
 QY 1386 CACTCAGGCTGCTGATTTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1445
 Db 1253 CCTGAGAAACACAGCATTTAGGCGTGGGAGCTCTC--TATCGATCCCAAAATTA 1309
 QY 1446 TGGTATGAGAGGCTGTGAACA 1466
 Db 1310 TGGTGTGGAGGCTGTAAAAA 1330

RESULT 10
 US-10-425-114A-15122

GENERAL INFORMATION:
 APPLICANT: Liu, Jindong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53313)B
 CURRENT APPLICATION NUMBER: US/10/425,114A
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 15122
 LENGTH: 2144
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3051-045-B9_F11
 US-10-425-114A-15122

Query Match 24.9%; Score 439.2; DB 7; Length 2144;
 Best Local Similarity 59.0%; Pred. No. 1.4e-105;
 Matches 791; Conservative 0; Mismatches 543; Indels 6; Gaps 2;
 QY 155 ATCTCTCAAGAGCTCCGCGCTCAAGCTTCCGCGGAGAGACCTGTGATCTCATCTCC 214


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Db      100 ATCAATCTGAGAGCTGAAGAGCACAATAAGCCAGGGATTGTGATTTCAATCCAA 159
Qy      215 GGGAGAGTATGACATCAAGCCCTGGCTCCCAACACCCGGGCGGCACTCCGGCTT 274
Db      160 GGAAGATTACATATTTTCAATTTGGGCAAGAACACCCCTGAGAGAAAGTTTCCCTTG 219
Qy      275 CTCACCTTGGGCGGAGAGACGCGACGACGCTTGGCGGCTTACCAACCGCCCTGGG 334
Db      220 TTGAACCTTGGAGCCAGATGTGACTGATTTGTAGCATACATCAAGCTCAGCA 279
Qy      335 CGCCGCTCTCCGCGCTTCTTGTGG---CGCCCTCTGATACACCGCTCTCCGCC 391
Db      280 TGAAGTATCTGATCTCTTCTTCAAGGATACCTTAAGATTTCAAGGCTCAGAG 339
Qy      392 GGTCCGCGGACATACCGCGCCCTCTCCGCGACATCTCCGCGGCGCTTTCAGACG 451
Db      340 GTGTCAAAAGATTACGAAGCTTGTGTGATTTGTCAAAATGGGCTTTTGTGAAG 399
Qy      452 GTGCGCCCAACCCCAAGGTCAGTCTGTCTGATGGCGGCTCTTCAACGCGCGCTG 511
Db      400 AAAGAGCATGTAATCTTTTACACATCTCTCTGTCTGTCTATGTTTCAATTTGTT 459
Qy      512 TACCTGTCTCGCATGCGCAGCGCTGGCGCACCTCTCGCGGGGCTCTCATTTGCG 571
Db      460 TATGATGATAGGGTGAAGTGTGTGGGCTCATCTTGTGTGCTGCCCTTTTGTGGG 519
Qy      572 TTGCTGTGATCCAGTCCGGCTGTGATGGGCGACAGATCGGGGCGACCAACCGCATCCGG 631
Db      520 TTGCTTTGATCGAAAGCACTTACGTTGGTGTATGATCTGGGCGACATGAGTTATGTCT 579
Qy      632 CATCCGCTCTGACCGCGCTGCGAGTCTCTCGGGAACTGCTCAACCGCGCTCAG 691
Db      580 AGCCCTGCTTACAACAATTGGACAAATCTTTTGGCAATTTGCAATGATGGGATTAAC 639
Qy      692 ATCGCTGTGAGAGTGTAAACAACAACAACGACATCGCTCGCAACAGCTTGACAT 751
Db      640 ATTGATGTGTGAAGTGAAGTCAATGCTCAACATCTCATGATGATGTGTGAT 699
Qy      752 GACCGGAGCTTCCAGACATGCGGCTTTTGGCTTCCCGCAAGCTTGTGGCAATTA 811
Db      700 GATCTGATCTCAGACATACCTGTGTGCGCTGTCAACGCTTCTTCAATTCATTC 759
Qy      812 TGGTCTTACTTACCAAGGACCCGCGGCTGTGATGCGCGCTCGAAATTTCTACATCAG 871
Db      760 AATCTTGTCTTATGAGAAATTTGTTGATTTATCAAGTTTCTCATCACAC 819
Qy      872 TACAGACATGACCTTTTACCGGTAATGTGATGCGCAGAGTAATCTTCTCGCGAG 931
Db      820 TACAGACATTTCAATTTACCAAGTTTGTGCTTGTGCAAGGTCATTTGTAACCTCCAG 879
Qy      932 TCCGCTCTTGTGTTCACGAGAAAGAGGTGCGCAGCGGTTCTTGATTCGCGGG 991
Db      880 ACTTTGTCTGTGTCTTCTAGAGAAAGGTGCCAGATAGAGCTTTTAACTAATGGGG 939
Qy      992 GTGCGCAATTTGGGCTGTGTAACCGTGTGTGTGCTTCCCTGTGCGAATTTGTGGAG 1051
Db      940 ATCTTGTGTGTGTGTGTGTCTCTGTGTGTCTTCACTTCAAAATTTGGGAGAA 999
Qy      1052 AAGGTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1111
Db      1000 AAGGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1059
Qy      1112 CTGAACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1171
Db      1060 TTGAACATTTCTTCAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1119
Qy      1172 AAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1231
Db      1120 AAGCAAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1179
Qy      1232 GGCCTGACCTTCCAGATTGAGCAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1291

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Db      1180 GGCCTGCAATTCAGCTTGTGAGCACCATTGTGTCCCAAGGCTTCCAAGGCAATTTGAG 1239
Qy      1292 AAGCTTGAACCGCGCGCTCCGACCTTTGCAAGAGCATGGGCTCAATATTCAGAGC 1351
Db      1240 AAAATCTCACCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1299
Qy      1352 ACATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1411
Db      1300 ACATTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1359
Qy      1412 AGAAGGCTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1471
Db      1360 AGGA---ATCTGATGAACCTTCTTCCAGAAATTTGTGTGTGTGTGTGTGTGTGT 1416
Qy      1472 GGATTAATGGAATGAAGATA 1491
Db      1417 GGATGATTTTGTGTGAAGA 1436

RESULT 11
US-10-425-114A-10327
; Sequence 10327, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 10327
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700904851_FLI
US-10-425-114A-10327

Query Match      21.8%; Score 385.2; DB 7; Length 1719;
Best Local Similarity 62.1%; Pred. No. 2,4e-91;
Matches 625; Conservative 0; Mismatches 378; Indels 3; Gaps 1;

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Db	369	ATTATATATCAAGGTTTCTCATACAGCTACAGACCTTACAACTTACACCAAGTTTGTGCT	428
Qy	906	TCGCCAGGATTAATCTTCTCGCGCAGTCCGCCCTGTGTGTTCTACGGAGAAAGGGTGC	965
Db	429	TTGCAGGGGTCAATTTGTACTCTCCAGACTTTGTGTCTGTGTTCTCTGAGAGAAAGGTC	488
Qy	966	CGCAGCGGTTCTTGAGATTCGGGGGGGTGCGACAATTCTGGGCTGTGTAACCGTGTGCG	1022
Db	489	CAGATTAGCCTTTTACATTAATGGGGATCTTGTGTGTTGGTGTGTTCCCTCTGTTGA	548
Qy	1026	TGCGTTCCCTGCGCAGATTTGTGTGAGAGAGGGTGCAGCTTTGTGCTTTACAGTTCAACATCT	1085
Db	549	TCTCTTACCTACCAATTTGGGGAGAAAGGTCATGTTGTGTGTGCGCAGTTTGTCTGTT	608
Qy	1086	GGGGGATTACAGCAGCTCCAATTTCTGCTGAACCACTTCTCGTCCGAGCTGTATGTGCGGC	1145
Db	609	GTTCAATTCACAGCACCCTTCAATTTGTTTGAACCAATTTCTCAGCAGATGTGTATGAGGGCC	668
Qy	1146	CACCAAGGGGCAATGACTGTGTTGAGAGCAGAGGGCAGGGCAGCGTGCACATCCGTGCT	1200
Db	669	CACCAATTTGGCAATGACTGTGTTGAGAGCAAACTGTGTGGCACAATTGACATTTCTTCTCT	728
Qy	1206	CTCTCTGGATGATTTGTTTCCACGGGTGGCTCTGAGTTCCAGATTGAGACCACTCTGTTTC	1265
Db	729	CCTCATGGATGATTTGTTTCTTTGGTGGCTTGTCAATTCAGCTTGAGACCAATTTGTTCC	788
Qy	1266	CCCGCTTACCTCGGTGCCACTTGGCAAGTTGACCGGGCGCTCCGCACTTTGCAAGA	1322
Db	789	CMAGGCTTCCMAAGGGCACAATTTGAGGAAATCTCACTTTGGTGAATTGATCTTTGCAAGA	848
Qy	1326	AGCATGGGCTCACTTATTTCTGAGCCACTTCTGGGGTGCAAAATGTCCTTACATGGAAGA	1385
Db	849	AGCACAATTTCCCTTACAGAGATTGACATTTGTTGAGGCCCAATCTTTGAGATCTTAAAGA	908
Qy	1386	CACTCAGGGCTGTGTCATTTGAGGCGCAGGACCGCTCAAGTGTGTGCTCTCGAAGATT	1445
Db	909	CCCTCAGAGACTGTGCTTCTTCAAGCCAGGA---ATCTCAGTACACCTTCTTCCAGAAAT	965
Qy	1446	TGTTATGGAGCGCTGTGAACCCCATGGATTAATGGATGAAGATA	1491
Db	966	TGTTGTGGAGCTTTTAACTCATGATGATTTTGTGAAGA	1011
RESULT 12			
US-10-702-777-4			
: Sequence 4, Application US/10702777			
: GENERAL INFORMATION:			
: APPLICANT: Thomas, Terry L.			
: TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A			
: NUMBER OF SEQUENCES: 27			
: CORRESPONDENCE ADDRESS:			
: STREET: 400 Garden City Plaza			
: CITY: Garden City			
: STATE: New York			
: COUNTRY: United States			
: ZIP: 11530			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patentin Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/10702,777			
: FILING DATE: 06-Nov-2003			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US/08/934,254			
: FILING DATE: 19-SEP-1997			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Presser, Leopold			
: REGISTRATION NUMBER: 19,827			

:	REFERENCE/DOCKET NUMBER:	8383ZTXWVU
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE:	(516) 742-4343
:	TELEFAX:	(516) 742-4366
:	TELEX:	230 901 SANS UR
:	INFORMATION FOR SEQ ID NO: 4:	
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	1685 base pairs
:	TYPE:	nucleic acid
:	STRANDEDNESS:	both
:	TOPOLOGY:	linear
:	MOLECULE TYPE:	DNA (genomic)
:	SEQUENCE DESCRIPTION:	SEQ ID NO: 4:
:	US-10-702-777-4	
Query Match	20.7%; Score 365.4; DB 7; Length 1685;	
Best Local Similarity	55.8%; Pred. No. 4.1e-86;	
Matches 740; Conservative	0; Mismatches 581; Indels 6; Gaps 2	
Qy	155 ATCTCTTCCAAGAGAGCTCCGGCGTCACGCTTCGCCGCAAGACTCTTGATCTCCATCTCC	214
Db	68 ATTACCTCAGAATGAACCTCAGAACCCAGATTAATGATCTCGATTCAA	127
Qy	215 GGCAACGTATGACAGTCACGCSCCGTCCGCCACAACCAGGAGGAGCATCTCCCGCTT	274
Db	128 GGGAAAGCTTAGATGTTTCGATTTGGGTGAAGAACATCCAGGTGGAGCTTCTCTTG	187
Qy	275 CTCACCTGCGGAGGACAGACGCAACGACGCTTCGCGGCTTACCAACCGGCTCGGCG	334
Db	188 AAGAGTCTGTGCTGACAAAGAGTAATCATATTGTTGCAATTCATCTGCTCTACA	247
Qy	335 CGCCGCTCTCGCCGCGCTTTTGTTG--CCGCTCTGACTAGCCGCTCTCCCC	391
Db	248 TGAAGATCTTGAATGTTTTTCACTGGGTATTATCTTAAAGATTACTCTGTTTCTAG	307
Qy	392 GCGTCCGCGCACTACCGCGCTCTCGCGAGCATCTCGGAGGCGCTCTGSAAGC	451
Db	308 GTTCTTAAAGTTTATGAGAGCTGTGTGTTGAGTTTCTAAAATGGGTTTGTATGACAA	367
Qy	452 GTCCGCCCAACCCCAAGTCCAGCTGCTCCCTGATGCGCTCTTCTACGCGCGCTG	511
Db	368 AAAGTCAATATTATGTTTGAACATTGTGCTTTAAGAAATGCTGTTGATAGTGTT	427
Qy	512 TACTCTGCTCGATGCGCACGCGCTGGGCGACCTCTCGGGGGGCTCTATTGGC	571
Db	428 TATGGGTTTGTGTTGTGAGGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	487
Qy	572 TTGCTCTGAATCCAGTCCGCTGATATGGGACAGATCGGGCAACACCGATACCGGC	631
Db	488 TTTCTTTGATTCAGAGTGTGATGGAATGGAATGTTGGGCAATTAATAGTAAGTCT	547
Qy	632 CATCCGATCTCGACGCGCTGATGAGGTGCTCCGGGAATGCTCACCGGCTCTAGC	691
Db	548 GATTCAAGGCTTAATAAGTTTATGGATATTTTGTCTGAATTTGCTTCAAGATAAGT	607
Qy	692 ATGCGCTGTGGAAGTGTAAACAACAACAACAATCGCTGACACAGCTTGACCAT	751
Db	608 ATTGTGTGTGGAATGGAACCAATTAAGCATCATCATGCTGTAAATAGCCTTGAATAT	667
Qy	752 GACCGGACCTCCAGCAATGCGGCTCTTGGCGCTTCCCGCAAGCTGTGGGAATTA	811
Db	668 GACCTTAATTAATTAATTAATCAATTCCTGTTGTGTCTTCAAGTTTGTGTTCACTC	727
Qy	812 TGCTCTACTTCTTCAACAGGACCTCGGCTTGCATGCGGCTCGAATTTCTTCAACG	871
Db	728 ACCTCTCATTTCTATGAAAGATGATCTTTGATCTTTATCAAGATTTCTTTGTAGT	787
Qy	872 TACAGACATGAGACTTCTACCGGTAATGTGATCGCAGAGTAATCTTCTCGCGAG	931
Db	788 TATCAACATTTGACATTTTACCTTAATATGTTGTCTGTAGGCTCAATATATATGTAACA	847
Qy	932 TCAGCCTGTTCTTCTCAAGGAAGAAGGTGCGCAGCGGTTGTTGAATCGCGGG	991

Db 848 TCTCTCATATGTTGTTGACCAAGAGAAATGTCCTCATGAGCTCAGGAACTCTTGGGA 907
 Qy 992 GTGCGACCATCTGAGGCTGTGTACCGCTGTGTGTGCTTCCCTGCGAATGTGGAG 1051
 Db 908 TGGCTAGTGTCTTCGATTTGGTACCCGTTGTTTCTTGTGCTTAATGGGGTGA 967
 Qy 1052 AAGGTCGCTTTGTGCTTTTCACTTCAACATCTGCGGATTCAGACGCTCCAAATCTGC 1111
 Db 968 AGAATATATGTTGTATGTCAGATTTATCAGTGAATGCAACAATCTCAGTTCTCC 1027
 Qy 1112 CTGAACCACTTCTCGTCCGACGTATGTCGGGCAACCAAGGCAATGATGTTGAG 1171
 Db 1028 TTGAACCACTTCTCTCAAGTGTATGTTGAAAGCTTAAAGGGAATATGTTGAG 1087
 Qy 1172 AAGCAGAGGCAAGGCAAGCTCGATCTGCTCTCTGATGATGATGTTTCCAGGT 1231
 Db 1088 AACAACAGATGAGGCACTGATCTTCTGCTCTCTGATGATGATGTTTCCAGGT 1147
 Qy 1232 GGCCTGAGTTCAGATTTGAGCAACATCTGTTTCCCGCTACCTGCTGCACTTCCG 1291
 Db 1148 GGAATTCATTTCCAAATTTAGATCTATTTGTTCCCAAGATGCTGATGCACTTACG 1207
 Qy 1292 AAGTTCGACCGGCGCTCGGCACTTTGCAAGAGCATGGGCTCATTTATCTGAGCC 1351
 Db 1208 AAAATCTCCGCTCAGTGTATGATGATGCAAGAAATATTTGCTTACATTTATGCA 1267
 Qy 1352 AATTTCTGGGGTGCATATGCTTATATGAGAGACATCAGGCTGCTCTGATGAGGCC 1411
 Db 1268 TCTTTCTCAAGGCAATGAAATGACATCAGAAATTTAGAGAACACACATTTGAGGCT 1327
 Qy 1412 AGACCGCTACAAAGTGTGTGCTCCGAGAAATTTGTATGGAGGCTGTGAGAACCCAT 1471
 Db 1328 AGG---GATATACCAAGCGCGCTCCGAAATTTGTATGGAGGCTCTTCACTCAT 1384
 Qy 1472 GGATAAA 1478
 Db 1385 GGTTAAA 1391

RESULT 13
 US-10-425-114A-6172
 ; Sequence 6172, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114A
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 6172
 ; LENGTH: 966
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700556019_FLI
 US-10-425-114A-6172

Query Match 19.1%; Score 337.6; DB 7; Length 966;
 Best Local Similarity 66.2%; Pred. No. 6.9e-79;
 Matches 503; Conservative 0; Mismatches 254; Indels 3; Gaps 1;
 Qy 731 GCGTGAAGAGCTTGACCATGACCCGACCTTCACACATGCGCTCTTGGCGCTGCC 790
 Db 2 GCGTGAAGAGCTTGATATGATGACCTGATGACACATGCGGCTCTTGGCGCTGCC 61
 Qy 791 CCGAAGCTGTCGGAACATATGCTCTTACCAAGGAGCCCTGGCGTTGATGCC 850

Db 62 TCGCGCTTCTTCATTCGATTAATCTTCTATTTCTATGAGAGAGTGGAGTTGATTTCC 121
 Qy 851 GCGTGAATCTTCATGACGTACAGACCTTCTTACCGGTATGTCATGCC 910
 Db 122 ATTGCAAGGTTCTTATCTGCTACGACATTCATTTTATCCGATATGTTGCTGCC 181
 Qy 911 AGAATAAATCTTCTGCGCAGTCCCGCTGTCTCTTCTACGAGAGAGGCTGCCAG 970
 Db 182 AGGTCACCTTGTATCTGACAGACATTCGCTATTTGTTTGGAGCGTAAATGACGAT 241
 Qy 971 CGGTTGCTTGAATGCGGGGCTGCCACATTTCTGGGCTGTGTATCCGTTGCTGCT 1030
 Db 242 AGAGCTTGAACATATATGAGGATCTTGTGTTGAGTGTGCTCTTCTTGTGCTCT 301
 Qy 1031 TCCGCGCAATTTGTTGAGAGAGGCTGCGTTGTGCTTTCAGTTCACATCTGCGGG 1090
 Db 302 TTCTGCAAAATTTGCTGAGAGGCTGTATGTTGTGCTTGTGCTGCTGCTGCTTCTCC 361
 Qy 1091 ATTGACAGTTCATTCCTGCTGACACATTCCTGCTGCAAGTATGTCGGGCAACC 1150
 Db 362 ATCCAGCATTCATTCCTGCTGATATCATTTGCTGCAAAATGTATGTTGGCTACCG 421
 Qy 1151 AAGGCAATGACTGTGTTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1210
 Db 422 AGTGGAAATGACTGTGTTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 481
 Qy 1211 TGGATGATGTTGTTCCAGGCTGCTGAGTTCAGATTTGAGACATCTGTTCCCGC 1270
 Db 482 TCGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 541
 Qy 1271 CTACCTGCTGACCTTTCGCAAGGTTGACCGGCTGCGGACCTTTGCAAGAGAT 1330
 Db 542 CTACCTGCTGACCTTTCGCAAGGTTGACCGGCTGCGGACCTTTGCAAGAGAT 601
 Qy 1331 GGGCTCACTTATTCGACGCAATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1390
 Db 602 AATTTGCTTATGAGAGGCTGTGCTTATTTGGAGGCAATGAGGACATTTAGACCTTC 661
 Qy 1391 AGGCTGCTGCTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1450
 Db 662 AGGCTGCTGCTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 718
 Qy 1451 TGGAGGCTGTAACACCCATGATTAATGGATGAAGAT 1490
 Db 719 TGGAGGCTGTTAATCCATGCTGAGGTATTTGAGTT 758

RESULT 14
 US-10-425-114A-10518
 ; Sequence 10518, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114A
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 10518
 ; LENGTH: 1071
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700942135_FLI
 US-10-425-114A-10518

Query Match 15.5%; Score 273.8; DB 7; Length 1071;
 Best Local Similarity 68.6%; Pred. No. 5.6e-62;

Matches 393; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

QY 912 GGAATAATCTTCGCGCAGTCCGCCCTGTTGCTTCACGAGAGAGGGTCCCGAGC 971

Db 1 GGAATTAATCTTGTGACAGCTCTTTTCTTGTATATGTTAAAGAGAGGTGAGACA 60

QY 972 GGTGCTTGAGATCGCGGGGTGCGCAATTCGTGGGCTTGTAACCGTTGCTGGTCTT 1031

Db 61 GATGAGATGAGCTTTTGGGGCTGCTGCGTTCGGGTTGTGACCTTTGTGGTTTCC 120

QY 1032 CCTTCCGAATTTGTGAGAGAGGTGCGCTTTGTGCTTTACAGTTTCAACATCTGGGGA 1091

Db 121 TCTTGGCCAAATGTTGGAGAGGGTGTGTTGTTTGTGAGCTTTTCTGTTAACGGGT 180

QY 1092 TTCAGACGCGCAATTCGTGCTGACACATTCCTGCGAGGTGATGTCGGGCCACCA 1151

Db 181 TTCAGACGCGCAATTCGTGCTGACACATTCCTGCGAGGTGATGTCGGGCCACCA 240

QY 1152 AGGCGAATGACTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211

Db 241 GCGGGCGCATTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 1212 GGTGATGATGTTTCCACGCTGCTGAGTTTCAAGATTGACACATCTGTTTCCCGCC 1271

Db 301 GGTGATGATGTTTCCACGCTGCTGAGTTTCAAGATTGACACATCTGTTTCCCGCC 360

QY 1272 TACCTGGGTGCGCACTTTCGCAAGGTGTCACCGGCGCTGCGCACTTTCGCAAGAGATG 1331

Db 361 TGCACAGGTGCGCACTTTCGCAAGGTGTCACCGGCGCTGCGCACTTTCGCAAGAGATG 420

QY 1332 GGTCTCACTTATTCGAGCGCAATTCGTGGGCTGCAATGCTTAACTGAGAGACATCA 1391

Db 421 ATCTCTTATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480

QY 1392 GGGCTCTGCTGATTCGAGCGCGCAATTCGTGGGCTGCAATGCTTAACTGAGAGATG 1451

Db 481 GGAATGCTGCTTTCGAGCGCGCAATTCGTGGGCTGCAATGCTTAACTGAGAGATG 537

QY 1452 GGGAGGCTGTAACACCACTGATTAATGAGAT 1484

Db 538 GGGAGGCTGTAACACCACTGATTAATGAGATG 570

RESULT 15

US-10-425-114A-14800

Sequence 14800, Application US/10425114A

GENERAL INFORMATION:

APPLICANT: Liu, Jindong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114A

NUMBER OF SEQ ID NOS: 2003-04-28

SEQ ID NO 14800

LENGTH: 663

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: LIB3028-013-H6_FLI

US-10-425-114A-14800

Query Match 12.1%; Score 213.6; DB 7; Length 663;

Best Local Similarity 66.5%; Pred. No. 3.7e-46;

Matches 322; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

QY 1001 TTCTGGCTTGTGACCGTTGCTGCTGCTTCCCTCGAATTCGAGAGAGAGAGAGAG 1060

Db 2 TTTTGATTTGTTCCCTATATGATCTCATCCCTGCCAAATTTGGGAGAGAGAGATG 61

QY 1061 TTTTGCTTTTACGTTTCAATCTGCGGATTCAGACGTCATTCATTTGCTGTAACAC 1120

Db 62 TTTTGTGTTGCGCATTTTGTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121

QY 1121 TTTCTGCGACGCTGATGTCGCGGCGCACCAAGGCAATGACTGTTTGAAGAGAGAG 1180

Db 122 TTGCGAGAGATGATGATGAGGCGCCACCAATGCAATGACTGTTTGAAGAGAGAG 181

QY 1181 GCAAGCAGCTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240

Db 182 GGTGCGACATGAGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241

QY 1241 TTCAGATTGAGACATCTGTTTCCCGCTTACCTCGGTCACCTTGGCAAGTTGCA 1300

Db 242 TTCAGATTGAGACATCTGTTTCCCGCTTACCTCGGTCACCTTGGCAAGTTGCA 301

QY 1301 CCGGCGCTCGCGACCTTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1360

Db 302 CTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361

QY 1361 GGTGCAATGCTGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1420

Db 362 GAGGCCAATCTTGGACTCTTAAAGACCTTAAAGACTGCTCTCCAGGCGCAGGA---AT 418

QY 1421 ACAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1480

Db 419 CTCAGTAACCTTCTTCCAGAAATTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 478

QY 1481 GGAT 1484

Db 479 GGAT 482

Search completed: January 1, 2004, 04:50:00

Job time : 449.364 secs

useful for screening cDNA expression libraries -
 Claim 10; Page 42-43; 57pp; English.

The present sequence is a sphingolipid desaturase
 from clone cdelc.p0001.08; it is isolated from corn developing
 embryo cDNA library, cdelc. The present sequence is useful for producing
 transgenic plants having altered levels of sphingolipid desaturase which
 in turn would alter the fatty acid composition. The enzyme is also useful
 for producing polyclonal or monoclonal antibodies. The polynucleotide
 is useful as primer or probe for screening cDNA libraries to
 isolate desired full-length cDNA clones.

Sequence 462 AA;

Query Match 100.0%; Score 2521; DB 21; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1.4e-251;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPSPVDMPAPGADAGDVYRMISSEKELRAHASADDLWISGVDYDTPMLPHHGGDL 60
 1 MPSPVDMPAPGADAGDVYRMISSEKELRAHASADDLWISGVDYDTPMLPHHGGDL 60
 61 PLITLAGQDATDAFAAYHPPSARPLRRFVGRSDYAVSPASADYRLLAQSSAGLFE 120
 61 PLITLAGQDATDAFAAYHPPSARPLRRFVGRSDYAVSPASADYRLLAQSSAGLFE 120
 121 RVGPTRVQVLMAVLYFAALYLVLACASAMHLLAGLIGFWITQSGMGGHDSGHRIT 180
 121 RVGPTRVQVLMAVLYFAALYLVLACASAMHLLAGLIGFWITQSGMGGHDSGHRIT 180
 181 GHPLVDVVOVLVSGNCLTGLSIAMWKCNNHTNTHACNSLDHDPDLOHMLPAVSPKLEGN 240
 181 GHPLVDVVOVLVSGNCLTGLSIAMWKCNNHTNTHACNSLDHDPDLOHMLPAVSPKLEGN 240
 241 IWSYFQRTLAFDAASKFISYQHTFYPWCIARINLLAQSLFVLEKRVQRLLEIA 300
 241 IWSYFQRTLAFDAASKFISYQHTFYPWCIARINLLAQSLFVLEKRVQRLLEIA 300
 301 GVATFMAVYPLVLAASLPPMMERVAFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 360
 301 GVATFMAVYPLVLAASLPPMMERVAFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 360
 361 EKQTAGTLDILCSPPMDFHGGLOFOLEHNLFPRLPRCHLRKVAFAVADLCKKGLTYS 420
 361 EKQTAGTLDILCSPPMDFHGGLOFOLEHNLFPRLPRCHLRKVAFAVADLCKKGLTYS 420
 421 ATFWGANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 462
 421 ATFWGANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 462

RESULT 2

AAV71555 standard; Protein; 469 AA.

AAV71555;
 12-OCT-2000 (first entry)
 Wheat sphingolipid desaturase #1.
 Wheat sphingolipid desaturase; membrane-bound desaturase;
 transgenic plant; fatty acid.
 Triticum aestivum.
 W0200032790-A2.
 08-JUN-2000.
 02-DEC-1999; 99MO-US28589.

03-DEC-1998; 98US-0110784.

(DUPO) DU PONT DE NEMOURS & CO E. I.

Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

WPI; 2000-412336/35.

N-PSDB; AAD01353.

polynucleotide encoding delta-6 desaturase enzyme useful for producing
 transgenic plants and for producing antibodies specific to which is
 useful for screening cDNA expression libraries -

Example 4; Page 49-50; 57pp; English.

The present sequence is a sphingolipid desaturase
 from clone wrel.p0004.c7; it is isolated from wheat etiolated
 seedling root cDNA library, wrel.

The present sequence is useful for producing
 transgenic plants having altered levels of sphingolipid desaturase which
 in turn would alter the fatty acid composition. The enzyme is also useful
 for producing polyclonal or monoclonal antibodies. The polynucleotide
 is useful as primer or probe for screening cDNA libraries to
 isolate desired full-length cDNA clones.

Sequence 469 AA;

Query Match 81.9%; Score 2064; DB 21; Length 469;
 Best Local Similarity 80.9%; Pred. No. 2.6e-204;
 Matches 372; Conservative 35; Mismatches 51; Indels 2; Gaps 1;

3 PSVDAMPAPGADAGDVYRMISSEKELRAHASADDLWISGVDYDTPMLPHHGGDLPL 62
 12 PEADAMPAA--SKDADVMISTKELQAAADDLWISGVDYDTPMLRHHPGSEVL 69
 63 LTLAGQDATDAFAAYHPPSARPLRRFVGRSDYAVSPASADYRLLAQSSAGLFEV 122
 70 ITLAGQDATDAFAAYHPPSARPLRRFVGRSDYAVSPASADYRLLAQSSAGLFEV 129
 123 GTPPKQLVLAVALYFAALYLVLACASAMHLLAGLIGFWITQSGMGGHDSGHRITGH 182
 130 GHTPKELVLAAMSVLFCIALYCVLACSSGAHMFAGLIGFWITQSGMGGHDSGHRITGH 189
 183 PVLDRVVOVLVSGNCLTGLSIAMWKCNNHTNTHACNSLDHDPDLOHMLPAVSPKLEGN 242
 190 PALNRLLQVSSGCLTGLSIAMWKCNNHTNTHACNSLDHDPDLOHMLPAVSPKLEGN 249
 243 SYFYQRTLAFDAASKFISYQHTFYPWCIARINLLAQSLFVLEKRVQRLLEIA 302
 250 SYCYERTLAFDAASKFISYQHTFYPWCIARINLLAQSLFVLEKRVQRLLEIA 309
 303 ATFWANVPLVLAASLPPMMERVAFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 362
 310 AAFWVWYPLVLAASLPPMMERVAFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 369
 363 QTAGTLDILCSPPMDFHGGLOFOLEHNLFPRLPRCHLRKVAFAVADLCKKGLTYS 422
 370 QTAGTLDILCSPPMDFHGGLOFOLEHNLFPRLPRCHLRKVAFAVADLCKKGLTYS 429
 423 FVGANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 462
 430 FVEANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 469

RESULT 3

AAV71554 standard; Protein; 450 AA.

AAV71554;
 12-OCT-2000 (first entry)
 Soybean sphingolipid desaturase #2.

XX	Soybean; sphingolipid desaturase; membrane-bound desaturase;
KM	transgenic plant; fatty acid.
XX	Glycine max.
OS	WO200032790-A2.
PN	
XX	08-JUN-2000.
PD	
XX	
PF	02-DEC-1999; 99WO-US26589.
XX	
PR	03-DEC-1998; 98US-0110784.
XX	(DUPO) DU PONT DE NEMOURS & CO E I.
PA	
PI	Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
DR	WPI: 2000-412336/35.
XX	N-PSSB; AAD01352.
PT	Polynucleotide encoding delta-6 desaturase enzyme useful for producing
CC	transgenic plants and for producing antibodies specific to which is
PS	useful for screening cDNA expression libraries -
XX	Claim 10; Page 47-48; 57pp; English.
XX	
CC	The present sequence is a sphingolipid desaturase
CC	from clone asl.p0017.b4:fis isolated from soybean seedling cDNA
CC	library, ssl. The present sequence is useful for producing
CC	transgenic plants having altered levels of sphingolipid desaturase which
CC	in turn would alter the fatty acid composition. The enzyme is also useful
CC	for producing polyclonal or monoclonal antibodies. The polynucleotide
CC	is useful as primer or probe for screening cDNA libraries to
CC	isolate desired full-length cDNA clones.
SO	Sequence 450 AA:
Query Match	58.9%; Score 1484; DB 21; Length 450;
Best Local Similarity	60.0%; Pred. No. 2,3e-144;
Matches 266; Conservative 62; Mismatches 113; Indels 2; Gaps 2	
QY	21 RMISKEKRAASADDLMISIGDYDVTPLPHNPGDLRLTLTAGDATDAFAAYHP 80
DB	9 KYITSEELKGNGKSGDLMISIOGKYVNSDWKEHGGDVPISNLAGODVDTDAFIAYHPG 68
QY	81 SARPLRRFPVG-RLSDDVAVPASADYRRLLAQSASSGLFERVGTTPKVQLVMVLRYA 139
DB	69 TAWSHLEKFEGYHLSDPKVEVSADVKLASEFKLGIPDKGHVTSCTLASAVMWLI 128
QY	140 ALYLVLACASAMHLIAGLIGFVVIQSGMGHDGHRITGHPVLDRVVQVLSGNCLTG 199
DB	129 VLIVGLRSTSWAHHGSGMLIGLIMQSAVYGHDGHIYVMTTNGFNKVAQILSNCILTG 188
QY	200 LSIAMWKCNHTTHIACSLLDHDPDLQMPLEPASPCLKGINWSFYORTIAFDAASKFF 259
DB	189 ISIAMWKTNHAHHIACSLLDHDPLQAMPVFVASRFENSTITSHFYGRKLEFDIARFL 248
QY	260 ISYQHMFPPYPMICARITLQAQSLAFVLTREKVRPRLLEIAGVATFMAAPLYLVASLRPW 319
DB	249 ICYOHFFTFPWCARVALYIOTILLRSRRVOORAININGILVFWFWPFLVSLRNW 308
QY	320 WERYAVLVESFTICGIQHVQFCLNHFSSDYYVGPCKGNDWEFEKOTAGTLDILCSPPMDMF 379
DB	309 PERMVFLVASAVCSIQIHIOFCNLNFAANYVGPSSGNDWEFEKQTSGLIDISCASMDF 368
QY	380 HGGLQFOIEHHLFPLLPRCHLRKVAHAVRDLCKRHGLTYSAATFGANVLTWKTIRAAAL 439
DB	369 FGGLOFOLEHHLFPLLPRCQRKISPLVSDLCCKGNLPYRSHPWEABNQMTIRLTRAL 428
QY	440 QARTATSGCARKNLVMEAVNTHG 462
DB	429 QARDULTN-PARKNLLMEAVNTHG 450

RESULT 4
AAG29290
ID AAG29290 standard; Protein; 449 AA.
AC AAG29290;
DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 34824.
XX Protein identification; signal transduction pathway; metabolic pathway; XX hybridisation assay; genetic mapping; gene expression control; promoter XX termination sequence.
OS Arabidopsis thaliana.
PN EPI033405-A2.
PD 06-FEB-2000.
PX 25-FEB-2000; 2000EP-0301439.
PF 25-FEB-1999; 99US-0121825. PR 05-MAR-1999; 99US-0123180. PR 09-MAR-1999; 99US-0123548. PR 23-MAR-1999; 99US-0125788. PR 25-MAR-1999; 99US-0126264. PR 29-MAR-1999; 99US-0126785. PR 01-APR-1999; 99US-0127462. PR 06-APR-1999; 99US-0128234. PR 08-APR-1999; 99US-0128714. PR 16-APR-1999; 99US-0129845. PR 19-APR-1999; 99US-0130077. PR 21-APR-1999; 99US-0130449. PR 23-APR-1999; 99US-0130510. PR 23-APR-1999; 99US-0130891. PR 28-APR-1999; 99US-0131449. PR 30-APR-1999; 99US-0132048. PR 04-MAY-1999; 99US-0132407. PR 04-MAY-1999; 99US-0132484. PR 05-MAY-1999; 99US-0132485. PR 06-MAY-1999; 99US-0132486. PR 06-MAY-1999; 99US-0132487. PR 07-MAY-1999; 99US-0132863. PR 11-MAY-1999; 99US-0134256. PR 14-MAY-1999; 99US-0134218. PR 14-MAY-1999; 99US-0134219. PR 14-MAY-1999; 99US-0134321. PR 14-MAY-1999; 99US-0134370. PR 18-MAY-1999; 99US-0134768. PR 19-MAY-1999; 99US-0134941. PR 20-MAY-1999; 99US-0135124. PR 21-MAY-1999; 99US-0135533. PR 24-MAY-1999; 99US-0135629. PR 25-MAY-1999; 99US-0136021. PR 27-MAY-1999; 99US-0136392. PR 28-MAY-1999; 99US-0136782. PR 01-JUN-1999; 99US-0137222. PR 03-JUN-1999; 99US-0137528. PR 04-JUN-1999; 99US-0137502. PR 07-JUN-1999; 99US-0137724. PR 08-JUN-1999; 99US-0138094. PR 10-JUN-1999; 99US-0138540. PR 10-JUN-1999; 99US-0138847. PR 14-JUN-1999; 99US-0139119. PR 16-JUN-1999; 99US-0139452. PR 16-JUN-1999; 99US-0139453. PR 17-JUN-1999; 99US-0139492. PR 18-JUN-1999; 99US-0139454. PR 18-JUN-1999; 99US-0139455. PR 18-JUN-1999; 99US-0139456.


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Db      128 VLXGLACTSIWAHLISAVLLGLMLTQSAVVGDSGHYTVSTKPCNKLIQLLSGNCLTG 187
Qy      200 LSIAMWKCNHNTHTIACNSLDHDPDLOHMPFPAVSPKLFQNIWSYFYORTLAFDASKFE 259
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      188 ISIAMWKTHNAHNIACNSLDHDPDLOHLPFAVSTKPFNSMTSRFGKLTDPDLARFL 247
Qy      260 ISYQHTFYPVNCIARINLLAQSALFVLTKEKVPORLLEIAGVATFWAMVPLLVASLPNW 319
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      248 ISYQHTFYPVNCVGINLFIQTFELLFSKRHPDRLALNAGILVWTFMPLVSLPWN 307
Qy      320 WERVAVFLSFITCGIQHVFCLNHFSSDYYVGPFGNDWFEKQTGTIDILCSPMWDMF 379
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      308 QSEFIFVFPVSFAVTALQHVQFCINHPAADVYTGPPGNDWFEKQTGTIDILCSFMDWF 367
Qy      380 HGGLOFQIEHHLFPRLPCHLRKAPAVRDLCKKHGLTYSATFWGANVLTWTKTLRAAL 439
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      368 FGGLOFQIEHHLFPRLPCHLRKAPAVRDLCKKHGLTYSATFWGANVLTWTKTLRAAL 427
Qy      440 QARTATSGAPKNLVMEAVNTHG 462
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      428 QARDATN-PVLKRLMEAVNTHG 449

RESULT 5
AAVS1333
ID      AAVS1333 standard; Protein; 449 AA.
XX
XX      AAVS1333;
XX
XX      27-APR-2000 (first entry)
XX
XX      B. napus sld1 protein.
XX
XX      Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;
XX      transgenic plant; crop plant; delta-8-unsaturated long-chain base;
XX      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
XX      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
XX      pharmaceutical; food; chemical raw material.
XX
XX      Brassica napus.
XX
XX      DE19828850-A1.
XX
XX      30-DEC-1999.
XX
XX      27-JUN-1998; 98DE-1028850.
XX
XX      27-JUN-1998; 98DE-1028850.
XX
XX      (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
XX      Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
XX      MPI; 2000-127549/12.
XX
XX      N-PDSB; AA244832.
XX
XX      New sphingolipid desaturase that selectively introduces double bond
XX      into sphingolipide and capnoids -
XX
XX      Claim 8; Fig 2; 62pp; German.
XX
XX      This invention describes a novel sphingolipid desaturase that selectively
XX      introduces a double bond into the sphingobase of the ceramide residue of
XX      sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
XX      desaturase, or a vector containing the DNA sequence, can be used to
XX      produce transgenic plants, especially crop plants, with an increased or
XX      decreased delta-8-unsaturated long-chain base content or an altered
XX      delta-8-unsaturated long-chain base cis/trans ratio, especially to
XX      compensate for a delta-8-unsaturated long-chain base deficiency, to
XX      exclude production of delta-8-unsaturated bases, to increase tolerance
XX      or resistance to soil salinity, ion stress or toxicity, drought, wet
XX      conditions, cold or frost and/or phytopathogenic microorganisms, or to
XX      alter size growth and flowering time. Cells, transgenic organisms or

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CC      CC plants containing the DNA sequence can be used to produce sphingolipids
CC      and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC      can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC      materials. This sequence represents the Brassica napus sphingolipid
CC      desaturase sld1 protein described in the method of the invention.
XX
SQ      Sequence 449 AA;
Query Match 56 7%; Score 1429; DB 21; Length 449;
Best Local Similarity 57.3%; Pred. No. 1,1e-138;
Matches 254; Conservative 66; Mismatches 121; Indels 2; Gaps 2;
21 RMISSEKELRAHASADDLWISISGDVYVTPWLPHPGGLPLITLLAGODATPAFAAYHP 80
8 RITTSDDLKKNQPGELWISIGKYDVDSHWKSHHGSAALINLAGOVTDFAIYHNG 67
81 SARPLIRRFVVG-RUSDVAVSPASADYRRLAQLSAGLPERVGPPTPKVQLVMAVLPYA 139
68 TAWRHLENLHNGVYHVVDHVSVDVSRDRLAEPFSGKGLFDKKGHVTLTYLTICVAAMLA 127
140 ALYVLVACASAMAHLLAGLIGFWTQSGMCHDSGHHITGHPVLDRVVOVLSGNCLTG 199
128 VYGVVACTSIWAHLISAVLLGLMLTQSAVVGDSGHYTVSTKPCNKLVQLLSGNCLTG 187
200 LSIAMWKCNHNTHTIACNSLDHDPDLOHMPFPAVSPKLFQNIWSYFYORTLAFDASKFE 259
188 ISIAMWKTHNAHNIACNSLDHDPDLOHLPFAVSTKPFNSMTSRFGKLTDPDLARFL 247
260 ISYQHTFYPVNCIARINLLAQSALFVLTKEKVPORLLEIAGVATFWAMVPLLVASLPNW 319
248 ISYQHTFYPVNCVGINLFIQTFELLFSKRHPDRLALNAGILVWTFMPLVSLPWN 307
320 WERVAVFLSFITCGIQHVFCLNHFSSDYYVGPFGNDWFEKQTGTIDILCSPMWDMF 379
308 QSEFIFVFPVSFAVTALQHVQFCINHPAADVYTGPPGNDWFEKQTGTIDILCSFMDWF 367
380 HGGLOFQIEHHLFPRLPCHLRKAPAVRDLCKKHGLTYSATFWGANVLTWTKTLRAAL 439
368 FGGLOFQIEHHLFPRLPCHLRKAPAVRDLCKKHGLTYSATFWGANVLTWTKTLRAAL 427
440 QARTATSGAPKNLVMEAVNTHG 462
428 QARDVTN-PVLENLMEALNTHG 449

RESULT 6
AAVS1348
ID      AAVS1348 standard; Protein; 458 AA.
XX
XX      AAVS1348;
XX
XX      27-APR-2000 (first entry)
XX
XX      Sphingolipid desaturase protein.
XX
XX      Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;
XX      transgenic plant; crop plant; delta-8-unsaturated long-chain base;
XX      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
XX      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
XX      pharmaceutical; food; chemical raw material.
XX
XX      Unidentified.
XX
XX      DE19828850-A1.
XX
XX      30-DEC-1999.
XX
XX      27-JUN-1998; 98DE-1028850.
XX
XX      27-JUN-1998; 98DE-1028850.
XX
XX      (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX

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PI Heinz E, Zaehring U, Schmidt H, Sperling P;
 XX MPI: 2000-127549/12.
 DR N-PSDB; AA244851.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 XX into sphingolipids and capnoids -
 XX
 PS Disclosure; Fig 15; 62pp; German.
 XX
 CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a sphingolipid desaturase protein
 CC described in the method of the invention.
 CC
 XX
 SQ Sequence 458 AA;
 Query Match 56.6%; Score 1427.5; DB 21; Length 458;
 Best Local Similarity 55.1%; Pred. No. 1.7e-138;
 Matches 254; Conservative 77; Mismatches 123; Indels 7; Gaps 3;
 QY 3 PSYDAMPAPDPAAGADGDMISSEKELPAHASADLMISIGDYDYDTWLPNHPGGDLPL 62
 DB 4 PSIEVINSIADGK-----KYTSKEKLNPNPDLWISIKGYVNTWNAKEHKGADPL 58
 QY 63 LTLAAGDADTAPAAHYPPSARPLRRPFVG-RISDVAVSPASADYRLLAQLSAGLPER 121
 DB 59 INLAGODVDAFAHFGHTAMKLDLFGYHLKDQVSDISRDYKLASEPAKAGMFEK 118
 QY 122 VGPFPYQVLAVALFYAALYLVLAACSAWAHLAAGLIGFWIIOGSMGHDGHHRTG 181
 DB 119 KKGIVYSLCFVSLLSACVGYLVGSGFWIHLSAIIIGLAWQIAVLGHDGHTQMA 178
 QY 182 HVALDRVQVLSGNCUTGLSIAMWKNHNTHTIACNSLDHDPDLOHMPLEFVSPKLGNT 241
 DB 179 TEGMNKFAGIFIGNCTGISIAMWKNHNTHTIACNSLDYDPDLOHMPLEAVSSKLFNSI 238
 QY 242 WGFYQRTLAFLDASKFEFISYOHMTFEPVWCIRINILNOSALFVLTEKVPORLEIAG 301
 DB 239 TSFVYRQQLTFDLARFVSYOHLYLVYIMCVARVNLVYQTLILLISKRKIPRGNIILG 298
 QY 302 VAFMAWYPLVLVSLNMMERVAFLVFSFTICIOHQVFCIANHSSDYYVGPCKGDMFE 361
 DB 299 TLIFMWFPVLVRLNMMERVAFLVFSFVTSIOHIFLNFSGDYYVGPCKGDMFE 358
 QY 362 KQTAGTLDLILCSFWMDFHFGLOFOIEHLFPLPRCHLKVAPAVADLCCKHGLTYSAA 421
 DB 359 KQTRGIDIASCSMMWDFHFGLOFOIEHLFPLPRCHLKVAPAVADLCCKHGLTYSAA 418
 QY 422 TFMGAVLVTKTLRAALQARTSGAPKULVWEAVNTTG 462
 DB 419 SFYDANVTTLKTLRTALQARDLTN-PAPONLAMEAENTTG 458

DT 15-SEP-1996 (first entry)
 XX
 DE Borage delta-6-desaturase.
 XX
 XX Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 XX polyunsaturated fatty acid; octadecatetraenoic acid;
 XX chilling resistance; oilseed.
 XX
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT Region 156..163
 FT /label= Lipid_box
 FT 196..200
 FT /label= Metal_box-1
 FT Region 372..377
 FT /label= Metal_box-2
 XX
 XX MO9621022-A2.
 XX
 PD 11-JUL-1996.
 XX
 XX 28-DEC-1995; 95MO-IB01167.
 XX
 XX 30-DEC-1994; 94US-0366779.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Freyassinet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 XX WPI; 1996-333997/33.
 DR N-PSDB; AAT30395.
 XX
 PT Transgenic plants comprising the borage delta-6-desaturase gene -
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 XX
 PS Claim 3; Page 52-53; 75pp; English.
 CC Borage delta-6-desaturase (AAR98455) catalyses the conversion of
 CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
 CC deduced from that of the delta-6-desaturase gene (AAT30395) isolated
 CC from a borage membrane-bound polyosomal library. The sequence is
 CC distinct from that of Synchocystis delta-6-desaturase (AAR98456).
 CC Expression of the desaturase in transgenic plants, esp. sunflower,
 CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
 CC increased GLA prodn. Alteration of the plant membrane lipids as a
 CC result of expression of the desaturase may also result in increased
 CC resistance to chilling.
 CC
 XX
 SQ Sequence 448 AA;
 Query Match 55.3%; Score 1393; DB 17; Length 448;
 Best Local Similarity 55.8%; Pred. No. 5.9e-135;
 Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;
 QY 21 RMISSEKELPAHASADLMISIGDYDYDTWLPNHPGGDLPLTLAAGDADTAPAAHYPP 80
 DB 7 KITSDLNHKKPGDLWISIGKAVDWDKDHGSGFPLKSLAGQETDAFVAHRA 66
 QY 81 SARPLRRPFVG-RISDVAVSPASADYRLLAQLSAGLIGFWIIOGSMGHDGHHRTG 139
 DB 67 STWKNDKFTGTGTYLKDYSVEVSKDYRLVFEFSKMGYDKKHGMFATLCTIAMLFM 126
 QY 140 ALTVLACASAWAHLAAGLIGFWIIOGSMGHDGHHRTGHPVLDREVQVLSGNCUTG 199
 DB 127 SVYGVLFCEGVLYHLFSGCLMGFLWIOGWIIGHDAGYMWVSDSRNKKFGIIPAANCLSG 186
 QY 200 LSIAMWKNHNTHTIACNSLDHDPDLOHMPLEFVSPKLGNTSYGYOQLTADAAKFP 259
 DB 187 ISIGWKNHNTHTIACNSLDYDPDLOHMPLEFVSPKLGNTSYGYOQLTADAAKFP 246
 QY 260 ISYQHWTFPVMCIARINILNOSALFVLTEKVPORLEIAGVATGMWVPLVLVSLPNW 319

XX Nucleic acid containing oleosin 5'-regulatory region - useful for
PT modulating fatty acid synthesis and lipid metabolism in plants,
PT particularly to increase content of gamma-linolenic acid

XX Example 2; Page 61; 101pp; English.

XX The present sequence is borage delta-6 desaturase, an enzyme that
CC catalyzes the conversion of linoleic acid to gamma-linolenic acid
CC (GLA). Delta-6 desaturase cDNA (see AX24917) was isolated from a
CC borage membrane-bound polysomal cDNA library using a partial clone,
CC obtained from an EST database search, as probe. The borage delta-6
CC desaturase nucleic acid can be operably linked to the seed-specific
CC 5' regulatory region (see AX24916) of the *Arabidopsis thaliana*
CC oleosin At5g1 gene in claimed expression cassettes of the invention.
CC Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton,
CC peanut, oilseed rape or *Arabidopsis* are obtained that show increased
CC levels of GLA or octadecatrienoic acid. The levels of desirable
CC fatty acids in oilseed crops can be manipulated to provide seed
CC oils of use in human health and industrial applications.

XX Sequence 448 AA;

Query Match 55.3%; Score 1393; DB 20; Length 448;
Best Local Similarity 55.8%; Pred. No. 5.9e-135;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

QY 21 RMISSELRNHAASADLWISISGVDYDVTWMLPHHFGDLPILTLGQDADTAFAAYHPP 80
DB 7 KYTSELKNDKPGDLMISIQKAYDVSDVNDHFGSPFLKSLAQEVTDAFVAFHFA 66
QY 81 SARPLRRFFVG-RLSDYAVSPASADYRRLAQLSAGLPERVGPPTKVQVLMVAFYA 139
DB 67 STWKNDKFFFTGYLLDYSVEVSKYRKLVEFSSKMGLYDKKHIMFATLCTIAMLFPAM 126
QY 140 ALTYLACASAMHLLAGLIGFWIQSGMGHDSGHHRTTGHPRVLDRAVQVLSGCLTG 199
DB 127 SVYGVLFCEGVLVHLSFGCLMGFLMIQSGWIGHDAGHYVWVSDRLKFGIGFPAANCLSG 186
QY 200 LSTAMKKNHNTHTIACNSLDHDPDLOHMPFAVSPFLFGNITSYFQRTLADDAASKFF 259
DB 187 ISIGMKNMNNHAIHICNSLSDYDLPDLOYPFLVSSKFFSLSHFEKRLTSDLSRFF 246
QY 260 ISYQHTFYPVWCIAINLTAQSALFVLTAKRVPRQLLEAGVATPAMVPLVASTLPM 319
DB 247 VSQHTFTFYMCAALNMYVQSILMLTKRNVSYRAQELGCLVPSIMPLVSCLPNM 306
QY 320 WERVAFLFSFTTCGIGHVQFCINHFSSDYYVGPCKGDMFEKQTAGTLDILCSPMMDWF 379
DB 307 GERIMFVIASLSTGMQVQFSLNHFSSVYVGKPKGNMFEKQTAGTLDILCSPMMDWF 366
QY 380 HGLGLOIIEHNLPRRLPRCHLRYAPRVRLCKKHGTLTSAATFGWANVLTWTLRAAL 439
DB 367 HGLGLOIIEHNLPRKPRCMRLKISPVVIELCKKHNLRYVASFSSKANEMTLTTLRTAL 426
QY 440 QARTATSGAPKULWEAVNTHG 462
DB 427 QARDITK-PLPKULWEALHTHG 448

RESULT 10

AAVS1349 standard; Protein: 448 AA.

AAVS1349;

27-APR-2000 (first entry)

Sunflower HADES protein.

XX sphingolipid desaturase; sldi; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;

KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KM pharmaceutical; food; chemical raw material.

XX *Helianthus annuus*.

XX DE19828850-A1.

XX 30-DEC-1999.

XX 27-JUN-1998; 98DE-1028850.

XX 27-JUN-1998; 98DE-1028850.

XX (GVSE-) GVS GES ERWERB & VERM LANDWIRTSCHAFTLICH.

PI Heinz E, Zehringer U, Schmidt H, Sperling P;

DR WPI; 2000-127549/12.

PT New sphingolipid desaturase that selectively introduces double bond
PT into sphingolipids and capnoids -

XX Disclosure; Page 33-34; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a desaturase protein, HADES, isolated
CC from *Helianthus annuus* (sunflower) which is used in the method of the
XX invention.

XX Sequence 448 AA;

Query Match 55.2%; Score 1391; DB 21; Length 448;
Best Local Similarity 55.8%; Pred. No. 9.6e-135;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

QY 21 RMISSELRNHAASADLWISISGVDYDVTWMLPHHFGDLPILTLGQDADTAFAAYHPP 80
DB 7 KYTSELKNDKPGDLMISIQKAYDVSDVNDHFGSPFLKSLAQEVTDAFVAFHFA 66
QY 81 SARPLRRFFVG-RLSDYAVSPASADYRRLAQLSAGLPERVGPPTKVQVLMVAFYA 139
DB 67 STWKNDKFFFTGYLLDYSVEVSKYRKLVEFSSKMGLYDKKHIMFATLCTIAMLFPAM 126
QY 140 ALTYLACASAMHLLAGLIGFWIQSGMGHDSGHHRTTGHPRVLDRAVQVLSGCLTG 199
DB 127 SVYGVLFCEGVLVHLSFGCLMGFLMIQSGWIGHDAGHYVWVSDRLKFGIGFPAANCLSG 186
QY 200 LSTAMKKNHNTHTIACNSLDHDPDLOHMPFAVSPFLFGNITSYFQRTLADDAASKFF 259
DB 187 ISIGMKNMNNHAIHICNSLSDYDLPDLOYPFLVSSKFFSLSHFEKRLTSDLSRFF 246
QY 260 ISYQHTFYPVWCIAINLTAQSALFVLTAKRVPRQLLEAGVATPAMVPLVASTLPM 319
DB 247 VSQHTFTFYMCAALNMYVQSILMLTKRNVSYRAQELGCLVPSIMPLVSCLPNM 306
QY 320 WERVAFLFSFTTCGIGHVQFCINHFSSDYYVGPCKGDMFEKQTAGTLDILCSPMMDWF 379
DB 307 GERIMFVIASLSTGMQVQFSLNHFSSVYVGKPKGNMFEKQTAGTLDILCSPMMDWF 366

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QY 380 HGGLOFOIEHHLFPRPCRLKRVAPAVRDLCCKHGLTYSATFGANVLTWKTLPAAAL 439
DB 367 HGGLOFOIEHHLFPRPCRLKRVAPAVRDLCCKHGLTYSATFGANVLTWKTLPAAAL 426
QY 440 QARTATSGGAPKRLVMEAVNTHG 462
DB 427 QARDITK-PLPKNLVMEALHTHG 448

RESULT 11
AAU79830
ID AAU79830 standard; Protein; 448 AA.
XX
AC AAU79830;
XX
DT 15-JUL-2002 (first entry)
XX
DE Borage officinalis delta6-desaturase.
XX
KW delta6-desaturase; sunflower; soybean; maize; tobacco;
KM peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
XX chilling tolerance; borage.
XX
OS Borage officinalis.
XX
FH Key
FT Location/Qualifiers
FT 156..163
FT /label= Lipid_box
FT 196..200
FT /label= Metal_box_1
FT 372..377
FT /label= Metal_box_2
FT Region
FT 372..377
FT /label= Metal_box_2
XX
PN US635861-B1.
XX
PD 12-MAR-2002.
XX
PF 19-SEP-1997; 97US-0934254.
XX
PR 13-OCT-1992; 92US-0959952.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
PA (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX Thomas TL;
XX
DR WPI; 2002-380944/11.
DR N-PSDB; ABK49502.
XX
PT Novel nucleic acid encoding evening primrose delta6-desaturase which
PT converts linoleic acid to gamma linolenic acid useful for producing
PT gamma linolenic acid in transgenic plant or bacteria
XX
PS Example 9; Column 31-34; 53pp; English.
XX
CC The invention describes an isolated nucleic acid encoding an evening
CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
CC nucleic acid are useful for producing a plant such as sunflower, soybean,
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC gamma linolenic acid (GLA) content, and also for inducing or increasing
CC production of GLA in a bacteria or plant deficient, lacking in or
CC producing low levels of GLA. The nucleic acid is also useful for inducing
CC chilling tolerance in plants. This is the amino acid sequence of the
CC borage delta6 desaturase involved in the production of gamma linolenic
CC acid.
XX
SQ Sequence 448 AA;
XX
Query Match 55.0%; Score 1387; DB 23; Length 448;
Best Local Similarity 55.5%; Pred. No. 2.5e-134;
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Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;
QY 21 RMISKELEAAHASADDLWISISGDYDVTWMLPHHGGDLPLTLTLAGODATDAFAAYHP 80
DB 7 KIITDELKNHDKPGDLMISTIOGKAYDVSDWKDHPGSGFLKSLAGQVTLFAFAFHA 66
QY 81 SARPLLRPFVVG-RLSDYAVSPASADYRRLAQLSSAGLFERVGGTPKQVLVMAVLYA 139
DB 67 STMKQLDKRFETGYLKDYSVEVSKDYRLVPEFSKMGLYDKKHIMFATLCFIAMLFAM 126
QY 140 ALIYVLACASAMAHLAGGLIFWVITQSGMCHDGHRIITHPVLDRVQVLSGNCITLG 199
DB 127 SVYGVLPCEGYLVHLSFGCLMGFLWISQGWIGHDGHVYVSDSLNKKMGIFANCLISG 186
QY 200 LSIAMWKCHNTHHIAACNSLDHDPDLQHMPLFAVSPKLFGNITWSYFQRTLAFDAASKFE 259
DB 187 ISIGMKNNHNAHIAACNSLEIDPDQYIPLFVSSKSPFGSLTSHFERGLTFDSLSRFF 246
QY 260 ISYQHTFYPVNCIARINILAQSALEFVITERKVPQRLLEIAGVATFWAWYPLLVASLPNW 319
DB 247 VSYQHTFYPVNCIARINILAQSALEFVITERKVPQRLLEIAGVATFWAWYPLLVASLPNW 306
QY 320 WERVAPVLFSPITIGIOWVQCLNHFSSDYVGPCKNDMEFKQTAGTIDLCSPMDWF 379
DB 307 GERIMEVIALSLVTMOQVQFSLNHFSSVYGVKSGKNNWFEKQYDGTDLDISCPMDWF 366
QY 380 HGGLOFOIEHHLFPRPCRLKRVAPAVRDLCCKHGLTYSATFGANVLTWKTLPAAAL 439
DB 367 HGGLOFOIEHHLFPRPCRLKRVAPAVRDLCCKHGLTYSATFGANVLTWKTLPAAAL 426
QY 440 QARTATSGGAPKRLVMEAVNTHG 462
DB 427 QARDITK-PLPKNLVMEALHTHG 448

RESULT 12
ABG73095
ID ABG73095 standard; Protein; 448 AA.
XX
AC ABG73095;
XX
DT 17-APR-2003 (first entry)
XX
DE Borage delta-6-desaturase #1.
XX
KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KW octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
XX borage.
XX
OS Borage officinalis.
XX
FH Key
FT Location/Qualifiers
FT Misc-difference 370
FT /note= "Encoded by TTG"
XX
PN US2002108147-A1.
XX
PD 08-AUG-2002.
XX
PF 21-DEC-2001; 2001US-0029756.
XX
PR 13-OCT-1992; 92US-0959952.
PR 19-SEP-1997; 97US-0934254.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
PA (THOM/) THOMAS T L.
XX
XX Thomas TL;
XX
PI
```

DR MPI; 2003-06659/06.
DR N-PSDB; ABX15366.
XX
PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
PT for producing plant with increased gamma linolenic acid content, and
XX for inducing octadecatrienoic acid production in plant
XX
PS Example 9; Fig 5B; 55pp; English.
XX
XX The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GUA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GUA content from the plant
CC cell, for inducing or increasing production of GUA in an organism lacking
CC in or producing low levels of GUA and for inducing production of
CC octadecatrienoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecatrienoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GUA substrate. This sequence represents
CC a borage delta-6-desaturase polypeptide.
XX
SQ Sequence 448 AA;

Query Match 55.0%; Score 1387; DB 24; Length 448;
Best Local Similarity 55.5%; Pred. No. 2.5e-134;
Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;

QY 21 RMISSELRRAHSAADLMISGDDVYDVTWMLPHHPCGDLPLTLTGODATFAFAHNP 80
DB 7 KYTSDBLKXNDPRGDMISIGKADYSDWVKDHPGSGPLSLAGQETDAFAVHFA 66
QY 81 SAPPRLRRFVVG-RLSDYAVSPASADYRLLAQLSSAGLFERYVPTPKQVLVMAVLEYA 139
DB 67 STWKNDLKFPTGYLLKDYSEVSKDYRKLVEFSKGLYDKKHIMFATLCFIAMLFAM 126
QY 140 ALVLVLAASAMHLLAGLIGFWITQSGMGHDSGHNRTGHPVDLDRVQVLSGNLTG 139
DB 127 SVGVLFCEGVLVHLFSGGLMGFLMIQSGWIGHDAGHYVWVSDSLKKEFGIIPAACLSG 186
QY 200 LSIAMWKNHNTNHHIACNSLDHDPDLOHMPDLFAVSPFLFGNINSYFYORTLAFDAASKPF 259
DB 187 ISIGWKKMKNHNAHIIACNSLEYPDLOIYIFLVVSSKFFSLSHFBEKLTDSLSRF 246
QY 260 ISYQHTFYPVNCIARIINLLAQSALFVLTREKVPQRLLEIAGVATFWAWYPLLVASLPNV 319
DB 247 VSYQHTFYPVNCIARIINLLAQSALFVLTREKVPQRLLEIAGVATFWAWYPLLVASLPNV 306
QY 320 WERVAFVLPFTICGIGHOFCINHFSSDYVGPVKNDWPEKOTAGTLDILCSPMWDF 379
DB 307 GERIMFVIALSVYGMQOVFSINHFSSVYVGPKNNMPEKOTDITDIDSCPMWDF 366
QY 380 HGLLOFQIEHNLFPRLPRCHLRKAVAPARDLCKKGGITVAAATFWGANVLTWTLRAAL 439
DB 367 HGSQOQIEHNLFPKRCRCLRKISPYVIELCKKHLPIYASFSKANEVTLTLRTAL 426
QY 440 QARTATSGAPKXULWEEAVNTHG 462
DB 427 QARDITK-PLPKXULWEEALHTHG 448

RESULT 13
AAG53861
ID AAG53861 standard; Protein; 449 AA.
XX
AC AAG53861;
XX
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68613.
XX

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
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XX 08-APR-1999; 99US-0128714.
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XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 23-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
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XX 01-JUN-1999; 99US-0137222.
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XX 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
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XX 18-JUN-1999; 99US-0139459.
XX 18-JUN-1999; 99US-0139460.
XX 18-JUN-1999; 99US-0139461.
XX 18-JUN-1999; 99US-0139462.
XX 18-JUN-1999; 99US-0139463.
XX 18-JUN-1999; 99US-0139750.
XX 18-JUN-1999; 99US-0139753.
XX 21-JUN-1999; 99US-0139817.
XX 22-JUN-1999; 99US-0139899.
XX 23-JUN-1999; 99US-0140353.

PR	24-JUN-1999;	99US-01406354;
PR	24-JUN-1999;	99US-01406359;
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PR	30-JUN-1999;	99US-01412871;
PR	01-JUL-1999;	99US-01418847;
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PR	02-JUL-1999;	99US-01420055;
PR	06-JUL-1999;	99US-01428390;
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PR	02-AUG-1999;	99US-01463888;
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PR	03-AUG-1999;	99US-01470308;
PR	04-AUG-1999;	99US-01473022;
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PR	17-AUG-1999;	99US-01493366;
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PR	20-AUG-1999;	99US-01497222;
PR	20-AUG-1999;	99US-01497232;
PR	20-AUG-1999;	99US-01499293;
PR	23-AUG-1999;	99US-01499602;
PR	23-AUG-1999;	99US-01499930;
PR	25-AUG-1999;	99US-01505064;
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PR	27-AUG-1999;	99US-01510800;
PR	30-AUG-1999;	99US-01513003;
PR	31-AUG-1999;	99US-01515438;

PR	01-SEP-1999;	99US-0151930;
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
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PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
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PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
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PR	21-OCT-1999;	99US-0160770.
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PR	21-OCT-1999;	99US-0160815.
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PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match	55.0%	Score 1387	DB 21	Length 449
Best Local Similarity	55.8%	Pred. No. 2.5e-134		
Match 247	Conservative	69	Mismatches 125	Indels 2
Gap 2				
QY	21	RMISSEKLRAHASADDLWISISGDVYDTPWLPHHPGGDLRLTLGAGDATDAFAAYHP	80	
DB	8	KYINTEDLKKGNKSGDLMWIAIQKVVNSDWIKTHPGGDVYLNLVGQDVDAFAIAPHG	67	
QY	81	SARPLRRFPFG-RUSDVAVSPASADYRRLLAQSSACLPERVGTTPKQVLYMAVLYTA	139	
DB	68	TAMHLDHLTFGYHIRPQVSEVSBDYKRMMAEFKKGLFENKGHVTLTYTLAFAVAMPLG	127	
QY	140	ALYVLACASAMAILAGGLIGFWIIOGSMGCHDSGHHRTGHPALDRVVOQLSGNCTLTG	199	
DB	128	VLQGVLAQTSFPAIQIAAALLGLMLIGQAYIGHDSGHVYVMSNKSYNPFAQLSSNCILTS	187	
QY	200	LSIAMWKNNTHTTHIACNSLDHPDLOHMLPVAVSPKLFGNWISFYORTLAFDAASKFF	259	
DB	188	ISIAMWKTTHNAHHLACNSLDYDDLOHIIPVAFASTKFFSSLTSRFYORKLTFDVAARFL	247	
QY	260	ISYOHMFYPMWCJARITULAQSLFLVTEKRVORRLLEIGVATFPMAYPLVLVASLPMW	319	
DB	248	VSIOHFTIYPMCKGRINLFIQTLLPSSKKEVEDRALNPGLILVFWIMFPLVASCLEMW	307	
QY	320	WERVAFLVFSFTICGIOHQVQCLNHFSSDVAVGPBKDMFEKQTAGTLDILCSBMDWF	379	

DB 308 PERFFVFTSFVTALQHIQFTLNHPADYVGPPTGSDWFEKQAAGTIDISCRSYDMWF 367
 QY 380 HGLGQFQIEHNLPRRLPRCHLRKAPAVRDLCKHGLTYSAAFTWGANVLTWTLRAAL 439
 DB 368 FGLGQFQIEHNLPRRLPRCHLRKAPAVRDLCKHGLTYSAAFTWGANVLTWTLRAAL 427
 QY 440 QARTATSGGAPKNLWEAVNTHG 462
 DB 428 QARD-VANPVKNLWEALNTHG 449

RESULT 14
 AA51334
 ID AA51334 standard; Protein: 449 AA.
 AC AA51334;
 AC 27-APR-2000 (first entry)
 DE A. thaliana sld1 protein.
 XX Shingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material.
 OS Arabidopsis thaliana.
 XX DE19828850-A1.
 PN 30-DEC-1999.
 XX 27-JUN-1998; 98DE-1028850.
 XX 27-JUN-1998; 98DE-1028850.
 PR 27-JUN-1998; 98DE-1028850.
 XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 PA Heinz E, Zaehring U, Schmidt H, Sperling P;
 PI WPI; 2000-127549/12.
 DR N-PSDB; AA244833.
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 XX Claim 8; Fig 4; 62pp; German.
 PS This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents the Arabidopsis thaliana sphingolipid
 CC desaturase sld1 protein described in the method of the invention.
 SO Sequence 449 AA;

Query Match 55.0%; Score 1387; DB 21; Length 449;
 Best Local Similarity 55.8%; Pred. No. 2.5e-134;
 Matches 247; Conservative 69; Mismatches 125; Indels 2; Gaps 2;

QY 21 RMISSEKELRAHASADDLWISIGDYYVTPMLPHRGGDLPLTLGADATDAFAAYHPP 80
 DB 8 KYTNEDDLKHNKSGDLWIAIGKVVNVSDWIKTHRGDVTILNLVGQDVTDAFIAFHFG 67
 QY 81 SARPLLRRFPVG-RSDYVSPASADYRRLAQLSSAGLPERVGPTRKQVLMAVLFPA 139
 DB 68 TAWHHDHLFTGYHIDRFQVSEVSRYRMAAEFRRLGFEKNGHTLYTLAFVAMFPG 127
 QY 140 ALYVLVACASAMHLLAGLIGFWITGSGMMGDSGHHITGHPVLDVRYVLSGNCITG 129
 DB 128 VLYGVLAFTSVFPAALGLLWISAVIGHDSGYVIMSKSYNRFRAQLISGCLTG 187
 QY 200 LSIAMWKCNHNTTHIACNSLDHDPDLQHNPLFAVSPKLGNTWYFQRTLAFDAASKPE 259
 DB 188 ISIAMWKTNHMAHNLACNSLDYDPDLQHPVFAVSTKFPSSLRSRYDKLTFDPVAFRL 247
 QY 260 ISYQHWTFYPVNCIARINILAQALFVLETKRYPORLEIAGVATWANYPLVLASLPW 319
 DB 248 VSYQHTFYYPVWCFGRINLFIQTFLLFSKREVPDRLNFAGITLVWTFPLVSLPWN 307
 QY 320 MERVAVLFSFTICGLOHVFCLNHFSSDYVGPBKNDMPKOTAGTLDIICSPWMDWF 379
 DB 308 PERFFVFTSFVTALQHIQFTLNHPADYVGPPTGSDWFEKQAAGTIDISCRSYDMWF 367
 QY 380 HGLGQFQIEHNLPRRLPRCHLRKAPAVRDLCKHGLTYSAAFTWGANVLTWTLRAAL 439
 DB 368 FGLGQFQIEHNLPRRLPRCHLRKAPAVRDLCKHGLTYSAAFTWGANVLTWTLRAAL 427
 QY 440 QARTATSGGAPKNLWEAVNTHG 462
 DB 428 QARD-VANPVKNLWEALNTHG 449

RESULT 15
 AAG07392
 ID AAG07392 standard; Protein: 449 AA.
 AC AAG07392;
 AC 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 4528.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 XX 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139482.
PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142380.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 13-JUL-1999; 99US-0143542.
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PR 19-JUL-1999; 99US-0144325.
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PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147933.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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PR 16-AUG-1999; 99US-0149368.
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PR 18-AUG-1999; 99US-0149426.
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PR 20-AUG-1999; 99US-0149723.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.

A;Gene: sld1
A;Map position: 3
A;Note: F2A19.180
C;Function:
A;Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated, MUID:59003197]
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthes

Query Match	55.0%;	Score 1387;	DB 2;	Length 449;
Best Local Similarity	55.8%;	Pred. No. 3.4e-112;		
Matches 247;	Conservative 69;	Mismatches 125;	Indels 2;	Gaps 2

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QY      21 RMISSELELRARASADDLMISISDDVDVDTFWLPHNRGGDLPLTLTAGQDATDAFAAYHPP   80
       :|:::| | :|||: ||:| | :| | | :| | | | | | | | | | | | | | | | |
Db      8 KYITNEDLKKNKSGDLPWIAIGKVNVNSDWIKTHRPGDVTILNLVGQDVTDFAFAPHNG   67
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QY 81 SARPLRRFFVG-RLSDYAVSPASADYRRLLAQSSAGLEFRVETPKQVLMAVLFYA 13
: | | | | : | | | | : | | | | : | |
DQ 68 TAMHHLDHLFTGYHIRDFQVSEVSRDYRRMAAEFRKLGLENKGHTLTYTLAFVAAAMFLG 122

Dy 140 ALVLTACASMAHLGLGSLGEVWISQSGMGGHSHRRTGHPRVDRYVQLSNCITG 19
||| ||| : : : : : : : : : : : : : : : :
Dd 128 VLGYLACTSVFAHQIAAALLGLIMTIGSAIYIGHDSGHYYIVMSNKSYNRPQLLSNCITG 18

Db 188 ISIAWKKWTHNAHHLACNSLDYDPDLQHPVFAVSTKFPSSLTSRFDYRKLTDFDPVARFL 24

Db 248 VSYQHFTYYYPWMCFGRINLFIQIFLLFSKREVEDRALNAGILVFTWTFLLVSLPNW 300

Db 308 PERFFVFTSTVTALQHIQFLTNHFADVYVGPTGDMFEKQAAGTIDISCRSYDMF 366

Db 368 FGGIQFQLEHHLPRLPRCHLRKRSPPVQELCKGNLPYRSMSEANVLITLTKTAY 422

428 QARD-VANPVVKLWWEALNTHG 449

RESULT 5
JC7556
linoleoyl-CoA desaturase (EC 1.14.19.3) - *Mucor rouxii*

C:Species: *Mucor rouxii*
C:Date: 30-Jun-2001 #sequence 30-Jun-2001 #text_change 03-Jun-2002
C:Accession: JC7556

Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A1>Title: Delta6-desaturase of *Mucor rouxii* with high similarity to plant delta6-desaturase
A1,Reference number: JC7556; MUID: 20563795; PMID:11112411

A: Molecule type: DNA
A: Residues: 1-523 <LAO>
A: Cross-references: GB:AF290983

C;Comment: This enzyme, a membrane-bound key enzyme, is responsible for the C;keywords: oxidoreductase; transformation

1 MBPBMADPAGDAAAGACAGDVTWTSKRTDHY-AG-----AGADNNTWTSKGVNIV 48
Best Local Similarity 31.2%; Pred. No. 1.2e-55;
Matches 163; Conservative 77; Mismatches 177; Indels 106; Gaps 1

DB I MPRT-----AAD-RLSTSTSSNITEEKQELIKGDSVP-I-YEQKVRV 477

QY 49 TPWLPHHGGDLPRLTLAQDATDAFAAYHPRA-RPLRRFFVGRLSDYAVSPASAD-- 100

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Db      48  NNFWAKHFGGEALRSALGRDVTDEIRTMHPQVYEKLINLYCIGDYMPPDIVIRPASMKQ 107
Oy      106  -----Y 106

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107 RLLAQSSAGLFE-----RVCPTKQQLVLMVLFYALYVLVLCASAMAHLLAGL 159

160 IGFVWIGSGMGHDSGHRITGHPYLDRAVYQVLSGNCLETGI¹SAWVKCNHNTTHIACNSL 219

220 DHDBDLQHMPPLFAVSPKLFNGINWSYFYQRTLAFDAASKFPISYQHWTFYPVNCIARINLL 279

280 AQSALFVLTEKRVPRLLLEIAGVATFWAMVPLVLASLPNNMWRVAFVLFSPTICGIHQVQ 339

Qy 340 FCLNHSSDVYVGPCKND--WFEKQTACTLDILCSPPMMDHFGIOFOIEHHLLFPRILPR 397

398 CHLRKVPVRDLCRKHGLTYSATFWGANVLTWKTLRAALQ 440

RESULT 6

linoleoyl-CoA desaturase (EC 1.14.19.3) W0802.4 - *Caenorhabditis elegans*
N/Alternate names: Delta6 fatty acid desaturase
C:Species: *Caenorhabditis elegans*

C:Accession: T26280; T37238
R:Swindurne, J.; Ainscough, R.
submitted to the EMBL Data Library, March 1996

A:Accession: T26280
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Accession: J1473 -MTF-

A, Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2.4
A, Experimental source: clone W08D2
R, Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 320 611-614 1998

A;Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase
A;Reference number: Z21637; MUID:98149727; PMID:9480865
A;Accession: T37238
A;Source: translated from CB/EMBL/DDAT
A;Structure: evolutionary; translated from CB/EMBL/DDAT

A: Molecule type: mRNA
A: Residues: 1-38, 69-430, 'V', 432-473 <NAP>
A: Cross-references: EMBL:AF031477; NID:g3088519; PIDN:AAC15586.1; PID:g3088520
C: Gene name:

A, Map position: 4
A, Introns: 13/3; 39/2; 234/3; 277/3; 370/1; 413/3
C, Superfamily: Ctenorhabbitis elegans Delta6 fatty acid desaturase
A, Gene: CESP:W00B2.4

Query Match	Score	DB 1	Length
Best Local Similarity	28.1%	Pred. No. 2e-31	
	18.0%		473

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04      35 DDLWISISGDVYDVTWMLPHHPCG-----DLP-----LITLAG----- 67
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68 --QDATDAFAAHHPPSAR-----PLLRFF-----FYGR-----LSDYAVSPAS 103
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Db RNSDATHIFHAFHEGSSQAYKQDLKKGHEHDEPLEKOLEKRLDKVDINVASDVSAQ 128
 QY 104 -----ADYRRLAQLQSAG-----LPERVGPPKQVLVMAVLF---YAAIYVLA 146
 Db 129 EKQVESPEKLRQKLDHDDGMKANETVFLPKAIS-----TLSTMAKFAVLYQYLGWITTS 183
 QY 147 CASAMWHLLAGGLIGFWIISGMWGHDSGHRITGHEVLDKRVVQVLSGNCITGLSIAMWK 206
 Db 184 C-----LLALAQPGFWLTHFPCQOPTRKPLADTSLPFGNLTQGSFSDRMWK 232
 QY 207 CNNTHTIACNSLDHDDLOHMPFLFAVSPLYFGNISYFYORTLAPDASKPISTQOHT 266
 Db 233 DKNTHTAATNTVLDHGDIDLAPLFAFIP---GDLCKY---KASFEKALIKTIVPQOHT 285
 QY 267 FYVVMCIARTNLAAQSALFVLTEKRVQRLL-----ELAGVATFPAWYLLVASLPMW 320
 Db 286 FTALMPLEPFSWTSQVQWPKENQMKYQORNAFWEQATVGHMAWVYQFLPLTPW 345
 QY 321 ERVAFVLFSTICG--IOHVQCLNHPSSDVYVGPVK--NDWFEKQTAGTLDILCSPM 375
 Db 346 LRAVAFISQMGGLIAHY-VTFNHSVUKY--PANSRLNNPALQILITRMTPSPF 402
 QY 376 MDVFGGLQFOIBHLLPRLPRCHLRKVAVDLCKKGLTYSAATFWGANVLTWKTLL 435
 Db 403 IDWLMGGLANYQIBHLLPPTPRCNLACMKYKCKENNLPLYVDYFDGYAMNLQOLK 462
 QY 436 --AAALQART 444
 Db 463 NMAEHIOAKKA 473

RESULT 7

110155
 110155 l1noeoyl-COA desaturase (EC 1.14.19.3) [validated] - human
 N:Alternate names: Delta6 fatty acid desaturase; protein DKFZps56C201.1
 C:Species: Homo sapiens (man)
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
 C:Accession: T13155; T08765
 R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
 J. Biol. Chem. 274, 471-477, 1999
 A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
 A:Reference number: Z17612; MUID:99085046; PMID:9867867
 A:Accession: T13155
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-444 <CHO>
 A:Cross-references: EMBL:AF126799; NID:94406527; PID:94406528; PIDN:AAD20018.1
 R:Mambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z16471
 A:Accession: T08765
 A:Molecule type: mRNA
 A:Residues: 'RTG', '138-428', 'D', '430', 'W', '432-444' <MAN>
 A:Residues: 'RTG', '138-428', 'D', '430', 'W', '432-444' <MAN>
 A:Cross-references: EMBL:AL050118
 A:Experimental source: adult uterus; clone DKFZps56C201
 C:Genetics:
 A:Gene: GDB:FADS6
 A:Cross-references: GDB:9956652
 A>Note: DKFZps56C201.1
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: cytochrome; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty
 F:18-94/Domain: cytochrome b5 core homology <CBS>
 F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 16.2%; Score 408; DB 2; Length 444;
 Best Local Similarity 26.7%; Pred. No. 1.9e-27;

Matches 122; Conservative 63; Mismatches 172; Indels 100; Gaps 19;

QY 12 GDAAAGADVMM--ISSKELRAHSAADLMISISGDVYDTPWLPNHPGDLPLTLTAGOD 69
 Db 8 GEGAABEVSVPFWSMEIOKHLRTDRMLVIDRKVYNITKWSIOHFGGQGVIGHVAGED 67
 QY 70 ATAPAPAYNH-----PSAPPLRRFPVGRLS-----DYAV-SPASADYRRLAQLSSA 116

Db 68 ATDAFRAHPRDLEFVGKFLKPLL-----IGELAPBPSQDHGKSKITEDFALRKTAEWM 123
 QY 117 GLPERVGPVKQVLVMAVLFPA-----ALYVLACASAM-AHLLAGGLIGFWIISGMW 171
 Db 124 NLFK-----TNHVFLLLAHIALLESIAWTFYFPGNGMIFLITLTAFTQAQAGWQ 179
 QY 172 HDSGHRITGHPVLDKRVVQVLSGNCITGLSIAMWKCNHTHTIACNSLDHDDLOHMPFL 211
 Db 180 HDYGLSTVYRKPRKMLYHKFVYGLKASAMWNRHROHAKPIIFHKDPPVNMHLHF 239
 QY 232 AVSPKLFGNISYFYORTLAPDASKPISTQOHTFYPVWCIAIRINLAQSALFVLTEKR 291
 Db 240 VLGE-----W-----QPIEYGGKKLKYLPYNH-----QHEYFPLIG-- 270
 QY 292 VPORLELGVATFPAWYLLVASL--PW---WVAVFVLFSTP-----ICG-----I 335
 Db 271 -PRLIPM-----YFOYQIMTMIVKKNWVDLAWVSYYIRFYIYIFPYGLALLPL 323
 QY 336 OHVQCLNHP-----SSDVYVGPVKGNDFEKEKOTAGTLDILCSPMQWPHG 381
 Db 324 NFRFLSHFWVWVQMHIVWEIDQAY-----RDMSSQLTATCNVQSFNDWFGS 377
 QY 382 GLQFOIEHLLPRLPRCHLRKVAVDLCKKGLTY 418
 Db 378 HNFQIEHLLPPTPRCNLACMKYKCKENNLPLYVDYFDGYAMNLQOLK 462

RESULT 8

JG0180
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
 C:Accession: JG0180
 R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.;
 Biochem. Biophys. Res. Commun. 255, 575-579, 1999
 A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desaturase
 A:Reference number: JG0180; MUID:99160394; PMID:10049752
 A:Accession: JG0180
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-444 <AKI>
 A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BA75496.1; PID:94514722
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthesis
 F:18-94/Domain: cytochrome b5 core homology <CBS>
 F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 15.9%; Score 400; DB 2; Length 444;
 Best Local Similarity 26.4%; Pred. No. 9.6e-27;

Matches 115; Conservative 68; Mismatches 166; Indels 86; Gaps 15;

QY 26 KELRAHASADLMISISGDVYDTPWLPNHPGDLPLTLTAGODATDAFAAYH-----P 79
 Db 24 BEIQKNTLRDRLVIDRKVYNITKWSQGRHGVIGHYSGEDATDAFRLDLPVG 83
 QY 80 PSAPPLRRFPVGRLSY-----AVSPASADYRRLAQLSSAGLFEKVGPPKQVLV 132
 Db 84 KFLKPLL-----IGELAPBPSQDHGKSKITEDFALRKTAEWMNLFK-----T 128
 QY 133 MAVLFPAAL-YVLACASAMWHLLAGGLIGFWI-----OSGMWGHDSGHN 177
 Db 129 NHLPFLLSHIIWESIMFPL--SYGNGHIFPVITAFVLTASQAGWQIYGHYGH 185
 QY 178 RITGHVLDKRVVQVLSGNCITGLSIAMWKCNHTHTIACNSLDHDDLOHMPFLFAVSPK 237
 Db 186 SVYKSIWNIHVKFVYGLKASAMWNRHROHAKENIFPKDDIKSLHVFVGE-- 243
 QY 238 FGNISYFYORTLAPDASKPISTY--QHTFYPVWCIAIRINLAQSALFVLTEKVPQR 295
 Db 244 ---W-----QPIEYGGKKLKYLPYNHQHEYFPLIGPPLIPYFOYQIMTMIR-- 292
 QY 296 LLEIAGVATFPAWYLLVASLPMWVAVFVLSFT-----ICGIQHV--QFCIN 343

Db 293 WVDLAIASVYARF--FTYIIPYGLIGALVFLNFRLESHFWVAVVQMNHIVMEIDD 350
 QY 344 HFSDDVYVPRKNDMEFEKQTAGTLIDILCSPMWMDHGGLOQFOIEHNLPRRLPRCHLRKY 403
 Db 351 HY-----RDWFSSQLATCNVEOSFFNDWFSGLNFQIEHNLPTPRRHNLHKI 399
 QY 404 APAPRDCKKGLTY 418
 Db 400 APLVKSLSCKHGLE 414

RESULT 9
 T4319
 Deltas fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
 C:Accession: T4319; T24875
 R:Michaelsen, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
 FEBS Lett. 439, 215-218, 1998
 A:Title: Functional identification of a fatty acid deltas desaturase gene from *Caenorhab*
 A:Reference number: Z22422; MUID:99059458; PMID:9845325
 A:Accession: T4319
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-447 <MIG>
 A:Cross-references: EMBL:AF078796; NID:94003522; PIDN:AC95143.1; PID:94003523
 R:Swindurne, J.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19947
 A:Accession: T24875
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-197; VSHIFNN', 198-447 <WIL>
 A:Cross-references: EMBL:281122; PIDN:CA03352.1; GSPDB:GN00022; CESP:T13F2.1
 A:Experimental source: clone T13F2
 C:Genetics:
 A:Gene: CESP:T13F2.1; des-5
 A:Map position: 4
 A:Insertions: 48/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
 C:Superfamily: *Caenorhabditis elegans* Delta6 fatty acid desaturase
 C:Keyword: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match: 14.7%; Score 370.5; DB 1; Length 447;
 Best Local Similarity 26.2%; Pred. No. 3.5e-24;
 Matches 117; Conservative 61; Mismatches 177; Indels 91; Gaps 17;

QY 35 DDLWISISGDVYDVTWMLPHHPGDLPLITLAGODATDAFAAYHP----- 79
 Db 16 DGMKQCIDDAV-----LRSHPGS-AITTYKMDATVYFHTHGSKEAYOMTELKKE 68
 QY 80 -PSARP-----LRRFPVGRISDVAVSPASADYR-RLAQ--LSSAGLP 119
 Db 69 CPTQBEIPDKIDDPKIGIDVNMGTGFNISSEKSAQINISFTDLRRVRABEGMDGSPLE 128
 QY 120 ERVGFPKQVLMAVLF-----YALYLVLACASAMAHLLAGLIGFWIWSGMMGHS 174
 Db 129 Y-----IRKLEITFTILFAFYLYQHTYVLPAL-----LMGVAMQOLGMLIHIF 173
 QY 175 GHHRTGHPVLDVVVQVLSGNCLTGLSIAMWKCNHNTTHIACNSLDHDPDLQHPPLFAYS 234
 Db 174 AHHQLFKRRYNDLASYPVGNFLQVSHIFNNFSSGGMKEQHNHAAATNVVGRDGDLDLVPYAYV 233
 QY 235 PKLGNIMSYFYQRTLAFDAASKFISYQHTFYPVMCIARINLAQSLFVLTEKRVQ 294
 Db 234 AEHLNYSQDSVMTL-----FRQGVHMTF--MLPFLRLSWLLQSIIFV---SQMPT 281
 QY 295 R-----LLEIAGVATFMAVPLVLSLPMWMEVAVLFESFTICG--IOHVOFCIN 343
 Db 282 HYYDYRNATAIYQVGLSLHMASLQVLFPLPDMSTRIMFVLVSHVVGGLLSHV--VTFN 340
 QY 344 HFSDDVY-VGPRKNDMEFEKQTAGTLIDILCSPMWMDHGGLOQFOIEHNLPRRLPRCHLRK 402

Db 341 HYSVEKFAISSNINSNYACLOIMTTRNMRPGRFIDMLWGLNGLYQIEHNLPTPRHNLNT 400
 QY 403 VAPAVRDCKKGLTYSA-----ATFM 424
 Db 401 VMLPVEFAAANGLPYMDYFTGFW 426

RESULT 10
 H88791
 protein T13F2.1 [imported] - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2016, 1998
 A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: H88791
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-454 <STO>
 A:Cross-references: GB:chr_IV; PIDN:CA03352.1; PID:93879828; GSPDB:GN00022; CESP:T13F2.1
 C:Genetics:
 A:Gene: T13F2.1
 A:Map position: 4
 C:Superfamily: *Caenorhabditis elegans* Delta6 fatty acid desaturase

Query Match: 14.2%; Score 358; DB 2; Length 454;
 Best Local Similarity 25.8%; Pred. No. 4.3e-23;
 Matches 117; Conservative 61; Mismatches 177; Indels 98; Gaps 18;

QY 35 DDLWISISGDVYDVTWMLPHHPGDLPLITLAGODATDAFAAYHP----- 79
 Db 16 DGMKQCIDDAV-----LRSHPGS-AITTYKMDATVYFHTHGSKEAYOMTELKKE 68
 QY 80 -PSARP-----LRRFPVGRISDVAVSPASADYR-RLAQ--LSSAGLP 119
 Db 69 CPTQBEIPDKIDDPKIGIDVNMGTGFNISSEKSAQINISFTDLRRVRABEGMDGSPLE 128
 QY 120 ERVGFPKQVLMAVLF-----YALYLVLACASAMAHLLAGLIGFWIWSGMMGHS 174
 Db 129 Y-----IRKLEITFTILFAFYLYQHTYVLPAL-----LMGVAMQOLGMLIHIF 173
 QY 175 GHHRTGHPVLDVVVQVLSGNCL-----TGLSIAMWKCNHNTTHIACNSLDHDPDLQ 227
 Db 174 AHHQLFKRRYNDLASYPVGNFLQVSHIFNNFSSGGMKEQHNHAAATNVVGRDGDLDL 233
 QY 228 MFLFVSPKLFENINISYFQRTLAFDAASKFISYQHTFYPVMCIARINLAQSLFVL 287
 Db 234 VEFYATVAEHLNYSQDSVMTL-----FRQGVHMTF--MLPFLRLSWLLQSIIFV- 283
 QY 288 TEKRVFOR-----LLEIAGVATFMAVPLVLSLPMWMEVAVLFESFTICG--IQ 336
 Db 284 --SQMPTHYDYRTATIEVGLSLHMASLQVLFPLPDMSTRIMFVLVSHVVGGLLS 341
 QY 337 HVQFCINHFSDDVY-VGPRKNDMEFEKQTAGTLIDILCSPMWMDHGGLOQFOIEHNLPRRL 395
 Db 342 HV-VTFNHSYVEKFAISSNINSNYACLOIMTTRNMRPGRFIDMLWGLNGLYQIEHNLFTFM 400
 QY 396 PRCHLRKVAAPVARDLCKKGLTYSA-----ATFM 424
 Db 401 PRHNLNTVMPVKEFAAANGLPYMDYFTGFW 433

RESULT 11
 S35157
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - *Synechocystis* sp.
 C:Species: *Synechocystis* sp.
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S35157; S76243
 R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

Plant Mol. Biol. 22, 293-300, 1993
 A:Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium *Synechocystis* s.
 A:Reference number: S35157; PMID:93283633; PMID:8388613
 A:Accession: S35157
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <RED>
 A:Cross-references: GB:L11421; NID:g349563; P1DN:AAA27286.1; PID:g349563
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okunura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-116, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 s.
 A:Reference number: S74322; PMID:97061201; PMID:8905231
 A:Accession: S76243
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <KAN>
 A:Cross-references: EMBL:D09014; GB:AB001339; NID:g1653477; P1DN:BA18502.1; PID:d1019222
 A:Experimental source: PCC 6803
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 *Keywords: oxidoreductase, unsaturated fatty acid biosynthesis

Query March 9.8%; Score 247.5; DB 2; Length 359;
 Best local similarity 23.9%; Pred. 1.2e-13;
 Matches 92; Conservative 57; Mismatches 137; Indels 99; Gaps 19;

QY	106	YRLLAQLSSA----	GLFERVGETPKQVLVAVLFRYAALYLVLACASAWHLLAG--	157
		: :	: :	
DB	15	FRRLVLRVDVAFPAEHGILQRDNP-----	MYLKLIIIVMLFSAFAFLFAPVI	64
		: :	: :	
QY	158	---GLIFVWVQ-----	SGMWGHDGSHRIITHPHVLDRVQVVLGSGCINGSLIAMKCN	208
		: :	: :	
DB	65	FRVALLCGVLAIALMAAFSEVVGHDANNAYSNPHINRVLGAMYD--	PVGLSSFELRWYR	122
		: :	: :	
QY	209	HN-THHIACNLSLHD-----	PDLQHWLFAVSPKLFGNINISYFYQRTIAFDAA	255
		: :	: :	
DB	123	HNVLHHTYTNLIGHDVEIHGDGAVRMSPEQGHVIGYRFQDY--	INGLY-----	169
		: :	: :	
QY	256	SKPFIISQHWTFYVVMCLARINLLAQSLFVLTEKRV-----	PQRLLELNGVATFW	306
		: :	: :	
DB	170	--LEIPF-YWFLVDV-----	YLLNKGXKHDKIRPPQPLLELASLLGIFLWL	213
		: :	: :	
QY	307	AMV---PLIVA-SLPN--	MWERVAFVLEFPTIGIOHVQFCUNHFSFSDVYVGPBK--	356
		: :	: :	
DB	214	LGIVFGRLPGLGSEIFREVLIGASTYMTYIGIVCTI----	FMLANHULESEFELTRDDESG	269
		: :	: :	
QY	357	---NDWEFKQTAGTLILC--	SPMMDWFHQIGIQFOIEHHLEPRRLRCHLRKVAAPARDLCK	412
		: :	: :	
DB	270	AIDDEMAICQIRLTANPATNNPFMNWFCGGLNHQVTHHLPFNICHIVPOLENIKDVCQ		329
		: :	: :	
QY	413	KHGLTYSA-ATFWGANVLWTKTLPA	436	
		: :	: :	
DB	330	EFGEVEKYVPTFEKKAIAISNTRMLEA	354	

RESULT 12
T36617
probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces
C,Species: Streptomyces coelicolor
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C,Accession: T36617
R/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Raebstream, M.A.
submitted to the EMBL Data Library, June 1999
A,Reference number: Z21610
A,Accession: T36617
A,Status: preliminary; translated from GB/EMBL/DBJ
A,Molecule type: DNA
A,Residues: 1-345
A,Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCODEB: SCH35.42c
A,Experimental source: strain AJ(2)
C,Genetics:
A,Gene: SCODEB: SCH35.42c

C; Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

	Query Match	9.7%;	Score 245.5;	DB 2;	Length 345;	
	Best Local Similarity	24.3%;	Pred. 1.1-7e-13;			
	Matches	81;	Conservative	55;	Mismatches 156;	Indels 41; Gaps 11
QY	100 SPASADYRRLLAQSAGLFEFVGPPTPKVLMAVLFLVALYLVLACASAMAHLLAGGL	159				
Db	12 TPGS-DPARLSKRYADAGLLGRBPRGYTLRTITAVGTGVAAGMAAFVLGGASMTLTAAAF	70				
QY	160 IGFPMWISGMWGHDHSGHHRIITGHVLDVRVGVSG---NCLTGISIAWWKCNHTNHIIAC	216				
Db	71 LAVNYGOALVAHMARHQVERR-----RRASELSGRIGAGSIGMSYGWMQDKHTRHHNP	126				
QY	217 NSLHPDPLQMPLEAVSPKLFGNIWSFYORTLATFDASKEFTSYOHMTEFPVMCIARI	276				
Db	127 NTEUDDPD-----IGFDLL--VMSBDQR--AATGLPRLILGRMQAFLEFFLLITLEGF	174				
QY	277 NLTAQSALFVLTREKRVORLLE-----IAGVATFWAMYPLLVSLLPNMERVAFLV	327				
Db	175 NLHVASGR-AMANRRLKRRAIDGALLLAHCAYVTALTAEFWLPVPCGMA-----IAFLA	224				
QY	328 FSLFITCGIQ-HVGQCIMHFSSDYVVGPPKGDMEVEKQTAGTLDLCSPPMDWFHGLOPQ	386				
Db	225 VHOCLFGYLGSAFAAPHKKMPIILTADR-PDLRRÖVLTSRNVNGGLETTDALGGLWHQ	283				
QY	387 IEHLFPRLPRCHLRKVAPAVRDCKXKHGLYS	419				
Db	284 IEHLFPSMSPENLRKARAIYRKRCROLDGVDTA	316				

[illegible]

```

Db      289 NFIIMWYGGINLYQGVTHLPHICH1HYPKIAPILAEVCEBQVNVAVHQTFFGALANY 348
QY      432 KTLRAALQART 443
Db      349 SWLKXKMSINPEP 360

```

RESULT 14

```

JCI422
nitrate reductase (NADH) (EC 1.7.1.1) - Volvox carteri
C:Species: Volvox carteri
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C:Accession: JCI422; S22192
R:Gruber, H.; Goetlink, S.D.; Kirk, D.L.; Schmitt, R.
Gene 120, 75-83, 1992
Article: The nitrate reductase-encoding gene of Volvox carteri. Map location, sequence
A:Reference number: JCI422; WUID:93013022; PMID:1398126
A:Accession: JCI422
A:Molecule type: DNA
A:Residues: 1-864 <GR2>
A:Cross-references: EMBL:X64136; NID:g21993; PIDN:CAA45497.1; PID:g21994
A:Note: submitted to the EMBL Data Library, January 1992
A:Gene: nitrA
A:Map position: linkage group IX
A:Introns: 183/3; 234/2; 295/1; 339/1; 372/1; 425/2; 521/3; 593/3; 677/3; 797/2
C:Function:
A:Description: catalyzes the reduction of nitrate to nitrite
C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
C:Keywords: dimer; electron transfer; FAD; flavoprotein; heme; iron; metalloprotein; mol
F:36-425/Domain: molybdopterin-binding domain homology <PCO>
F:497-571/Domain: cytochrome b5 core homology <CB5>
F:613-864/Domain: cytochrome-b5 reductase homology <CBR>
F:1139/Binding site: molybdopterin (Cys) (covalent) #status predicted
F:532,555/Binding site: heme iron (His) (axial ligands) #status predicted

```

Query Match 7.4%; Score 185.5; DB 1; Length 864;

Best Local Similarity 36.4%; Pred. No. 7,9e-08;

Matches 48; Conservative 22; Mismatches 57; Indels 5; Gaps 3;

```

QY      7 AMPAPGDAAGA-GDYRMISSEKELRAHASADDLWISIGDYDVTPLPHHGGDLPLTL 65
Db      483 AAPPPVAAANAGGPRQYTMEEVAANTBESCMFVHGKVDATPYLDHPGABSLIV 542
QY      66 AGQDITDAFAAYHPSARPLRRFFVGRU--SDYAVSPASADYRRLAQLSSAGLFERY- 122
Db      543 AGADATDEFNSIHSSKAKMLAQYIGDVLVASKPAAGATVPEPQVASTSSPAVDPLVV 602
QY      123 -GPTPKVQVLVM 133
Db      603 LNPQKVKLPLI 614

```

RESULT 15

A86390

hypothetical protein TIK7_28 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: A86390

R:Theologis, A.; Ecker, J.R.; Palm, C.U.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; WUID:21016719; PMID:11130712

A:Accession: A86390

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-135 <STO>
A:Cross-references: GB:A8005172; NID:g9797763; PIDN:AAF98581.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1
C:Superfamily: cytochrome b5; cytochrome b5 core homology

C:Keywords: heme; iron; metalloprotein

F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 7.3%; Score 184.5; DB 2; Length 135;

Best Local Similarity 36.5%; Pred. No. 1.1e-08;

Matches 46; Conservative 23; Mismatches 48; Indels 9; Gaps 4;

```

QY      21 RMISSEKELRAHASADDLWISIGDYDVTPLPHHGGDLPLTLAGODATDAPA-AVHP 79
Db      6 KLYSHEEAATNKKQDDCNVVDGKTYDVSSYNDHPGGDDVLLAVAGKDATDDEFDAGHS 65
QY      80 PSARPLRRFPVGRLSDYAVS--PASADYRRLAQLSSAGLFERY-----VGPTPKVQL-V 131
Db      66 KDARELMKRYFGLDESSLPETPELKTKYKKQPDQSVQKLPDLTKQYVWVVSITISV 125
QY      132 LMAVLP 137
Db      126 AVSVLP 131

```

Search completed: January 1, 2004, 06:39:40

UO time : 18.385 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 10.1656 Seconds
(without alignments)
2137.240 Million cell updates/sec

Title: US-09-857-524B-4
Perfect score: 2521
Sequence: 1 MPPSYDAMPAPDAGAGDV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	16.8	444	1	FADS_BRARE
2	247.5	9.8	359	1	LICD_SYNY3
3	185.5	7.4	864	1	NIA_VOICA
4	183.5	7.3	387	1	FD61_SOYBN
5	180	7.1	134	1	CYS1_ARATH
6	180	7.1	136	1	CYB5_TOBAC
7	178.5	7.1	894	1	NIA_BEABA
8	176.5	7.0	905	1	NIA_FUOX
9	175	6.9	134	1	CYB5_BRAOL
10	172.5	6.8	318	1	NIA_CHLVU
11	170	6.7	891	1	NIA_HORVU
12	170	6.7	904	1	NIA_TOBAC
13	169.5	6.7	911	1	NIA_BRANA
14	168.5	6.7	448	1	FD6C_ARATH
15	167	6.6	904	1	NIA2_TOBAC
16	166.5	6.6	930	1	NIA_CICIN
17	166	6.6	917	1	NIA1_ARATH
18	164.5	6.5	911	1	NIA2_BRANA
19	164.5	6.5	982	1	NIA_NEUCR
20	163.5	6.5	134	1	CYS2_ARATH
21	163	6.5	146	1	CYB5_RAT
22	162.5	6.4	443	1	FD6C_BRANA
23	162	6.4	917	1	NIA2_ARATH
24	161.5	6.4	889	1	NIA1_MAIZE
25	161	6.4	926	1	NIA_SPIOI
26	160	6.3	135	1	CYB5_TOBAC
27	160	6.3	909	1	NIA_PERYU
28	159	6.3	132	1	CYB5_BOROF
29	158.5	6.3	916	1	NIA1_ORISA
30	158	6.3	137	1	CYB5_ORYSA
31	157	6.2	902	1	NIA1_PHYIN
32	157	6.2	881	1	NIA1_PHAVU
33	155	6.1	424	1	FD6C_SOYBN

34	155	6.1	911	1	NIA_LYCES	P17570 lycopersico
35	154.5	6.1	414	1	CYB2_DROME	P19967 dirosophila
36	154	6.1	890	1	NIA2_PHAVU	P19866 phaseolus v
37	153.5	6.1	912	1	NIA2_HORVU	P27869 hortum vul
38	153.5	6.1	915	1	NIA1_HORVU	P27867 hortum vul
39	152	6.0	900	1	NIA1_LOTJA	P27869 lotus japon
40	151.5	6.0	898	1	NIA_BETVE	P27783 betula verr
41	151	6.0	573	1	CYB2_HANAN	P09437 hansenula a
42	151	6.0	908	1	NIA_USTMA	O05531 ustilago ma
43	150.5	6.0	893	1	NIA1_LERPM	P36842 leprophaer
44	149	5.9	890	1	NIA2_SOYBN	P39870 glycine max
45	148.5	5.9	147	1	YDAA_SCHPO	O10352 schizosacch

ALIGNMENTS

RESULT 1	ID	FADS_BRARE	STANDARD	PRT	444 AA.
AC	Q9DEX7				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-)				
GN	FADS2 OR FADS2D6				
OS	Brachydanio rerio (Zebrafish) (Danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OX	Cyprinidae; Danio.				
OX	NCBI_TaxID=7955;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=21592990; PubMed=11724940;				
RA	Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,				
RA	Sargent J.R., Teale A.J.;				
RT	"A vertebrate fatty acid desaturase with deltas and deltas				
RT	activities."				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).				
CC	-1- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6				
CC	activities. May represent a component of the polyunsaturated fatty				
CC	acid biosynthesis pathway.				
CC	-1- PATHWAY: Polyunsaturated fatty acid biosynthesis.				
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.				
CC	-1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: AF309556; AAC25710.1; ..				
DR	HSSP: P00173; JEX.				
DR	ZFIN: ZDB-GENE-011212-1; fads2.				
DR	InterPro: IPR001199; Cyt B5.				
DR	InterPro: IPR005804; FA_desat fam.				
DR	Pfam: PF00487; FA_desaturase; 1.				
DR	Pfam: PF00173; heme_1; 1.				
DR	ProDom: PD000612; Cyt_B5; 1.				
DR	ProDom: PD001081; FA_desat fam; 2.				
DR	PROSITE: PS00191; CYTOCHROME_B5_1; FALSE_NEG.				
DR	PROSITE: PS00255; CYTOCHROME_B5_2; 1.				
KW	Fatty acid biosynthesis; Oxidoreductase; Heme.				
FT	DOMAIN 18 95				
FT	DOMAIN 53 53				
FT	METAL 76 76				
FT	SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1C0F65 CRC64;				
SQ	SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1C0F65 CRC64;				

Query Match 16.8%; Score 424; DB 1; Length 444;

```

Best LocalSimilarity: 27.7%; Pred. No. 2,1e-27;
Matches 124; Conservative 63; Mismatches 166; Indels 94; Gaps 16

QY      26 KELRAHASADLWISISGDVYDVTWMLRPHNPGDLP.LLTLAGQATDAFAAHP--PSAR 83
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      24 EEVQNGHTGSDQWVVERKVYVVSQWVKRHPGGLIHLGHVAGEDATTEAFAPHLQLVR 83
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      84 PLLRFFPGRSLSDVAVSPAS-----ADYRLLAQLSSAGLFEVRGPTKYVQ----- 129
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      84 KYLKLPLLLGGELE--ASEPSDRKXNALVEDPRALRERLEAGSCF-----KTPLRFA 134
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      130 -----LVLMANVFYAALYLVLACASAMAH--LLAGGLIGFVVISGSMGHDGSHRITGH 182
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      135 LHLGHIILLBELAIFMMWYF----GTGMINTLIVAVIILATASQAGMLCHDHGHLISVFEET 190
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      183 PVLDRVVOVLSGNCITGLSIAWKKCNHNTHTIACNSLDHPDLQHPPLFAVSPKLGNITM 242
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      191 SGMNHLVHKFVYLGHLKGSAGAMWNRHRHQHAKPNI FKDPDVNNMLNAFVV-----GNVQ 245
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      243 SYFYO---RTLAFLPAASKF-----ISYQHWTPYPMCTAR--INLLAQSALFPL 287
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      246 PVEGVGVKKIKHLRYNHQHKYFFFFIGRPLRIPYFQFOIFNNMI SHGMWDLMLCISYYV-- 304
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      288 TEKRVQRLLTEIAGVATFMAWYRLLVASLPHNWERVAFLVFSPTLGGIHOVFCINHF-- 345
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      305 ---RYFLCYTQPYGV--FW-----ATLLEFP-----VAFMSHWNV 335
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      346 -----SSDVYVGRPKGNDWFEKQTAGTLDILCSBMDWFIHGLQFOIENHLFRPLRCH 399
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      336 WYTGQSHIRPMNIDYERKQNDWLSMQVLVATCNISQSAFNDFSGHLNFOLEHHLFFVYPRHN 395
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      400 LRKAFAVRDLCCKGGLTYSAATFPGA 426
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      396 YWRAAPRVRALCEKGVKYQEXTLLGA 422
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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	RESULT 2			
ID	_LINC3	STANDARD:	PRT;	359 AA.
AC	Q08871;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Linooleoyl-CoA desaturase [EC 1.14.19.3] (Delta(6)-desaturase).			
GN	DSE6 OR SLU0262.			
OS	Synechocystis sp. (strain PCC 6803).			
OC	Bacteria; Cyanobacteriales; Chroococcales; Synechocystis.			
OX	NCBI_TaxID=1148;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93283633; PubMed=8389613;			
RA	Reddy A.S., Nucchio M.L., Gross L.M., Thomas T.L.;			
RT	"Isolation of a delta 6-desaturase gene from the cyanobacterium			
RT	Synechocystis sp. strain PCC 6803 by gain-of-function expression in			
RL	Anabaena sp. strain PCC 7120."			
	Plant Mol. Biol. 22:293-300(1993).			
	[2]			
RN	SEQUENCE FROM N.A.			
RP				
RX	MEDLINE=97061201; PubMed=8905231;			
RA	Kaneko T., Sato S., Korfani H., Tanaka A., Asamizu E., Nakamura Y.,			
RA	Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,			
RA	Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K.,			
RA	Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,			
RA	Yamada M., Yasuda M., Tabata S.;			
RT	"Sequence analysis of the genome of the unicellular cyanobacterium			
RT	Synechocystis sp. strain PCC6803. II. Sequence determination of the			
RT	entire genome and assignment of potential protein-coding regions."			
RL	DNA Res. 3:109-136(1996).			
CC	-I- CATALYTIC ACTIVITY: Linooleoyl-CoA + AH(2) + O(2) = gamma-			
CC	linoelnoyl-CoA + A + 2 H(2)O.			
CC	-I- COFACTOR: IRON.			
CC				
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CC -----
CC EMBL; L11421; AAA27286.1; -.
DR EMBL; D90914; BAA16502.1; -.
DR InterPro; IPR005804; PA_desatc_fam.
DR Pfam; PF00487; PA_desaturase; 1.
DR ProDom; PD001081; PA_desat_fam; 1.
KW Oxidoreductase; Iron; Complete proteome.
SQ SEQUENCE 359 AA; 41425 MW; 33FB165AEB98C05F CRC64;

Query Match	9.8%	Score 247.5	DB 1	Length 359
Best Local Similarity	23.9%	Pred. No. 5e-13		
Matches 92	Conservative 57	Mismatches 137	Indels 99	Gaps 19

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QY 106 YRLIACGSSA-----GFERRGPRTKQVLYLVAFYAAVLYVACASAMHLLAG----- 157
Db 15 FRRVLNQVVDVAFAEHGLTORDNS-----MYLKITLYLMLPSAMAFVLPAPV 64
QY 158 ---GLIGFWIQ-----SGMMGDSGHHRTGHEVLDREVVOVLSGNCULTGISIAWCKN 208
Db 65 FPRVLIGCMVALIALAASFVNGHDANNAVSNHNIRVLGMYD--FVGLSSFLMBVR 122
QY 209 HN-THHICNSLDHD-----PDLOMPLFAVSPKLFGINWSFFYORTLAFDA 255
Db 123 HNYLHHTVTLNLGHVEIHGDGAVRMSDEQEHVIGYRPOQFY--IWGLY----- 169
QY 256 SKFHSYOHMTFFYPWMCIAFINLQAQLFVTEGRV-----PQRLTEAGVTFM 306
Db 170 --LFIPI-YWFLYDV-----YLVNKGKTYHDHKLPRPQPLELASLGIKLIM 213
QY 307 AMY-----PLVA-SLPN--MWERVAFVLEFPTICGIOHVQCLNHFSSDVIYVPPKG--- 356
Db 214 LGVYFGDLALGFSIPEVLIGASVYMYMGIIVCTI----FWLAVLSESTEFITPDGESSG 269
QY 357 ---NDMEFKQTAGTIDILIC-SPMMDWFPGGLOFOJENHLPRLPRCHLAKVAPAYDLCK 412
Db 270 AIDDEWALCOQRTTANFATNNPFWMMFCGGLNHQVTHLFPNICHIHQPLENIIKDVCO 329
QY 413 KHGLTYSA-ATEFGANVLTWKTLRA 436
Db 330 EFGVEIKVYPTFKALIASNYRLEA 354

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RESULT 3			
N1A_VOLCA			
ID	N1A_VOLCA	STANDARD;	PTI; 864 AA.
AC	P36841;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Nitrate reductase [NADH] (EC 1.7.1.1) (NR).		
GN	N1TA.		
OS	<i>Volvox carteri</i> ;		
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;		
OC	Volvocaceae; Volvox.		
OX	NCBI_TaxId=3067;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=f. Nagariensis / HK10;		
RX	MEDLINE=93013022; PubMed=1398126;		
RA	Gruber H., Goetlink S.D., Kirk D.L., Schmitt R.;		
RT	"The nitrate reductase-encoding gene of <i>Volvox carteri</i> : map location,		
RT	sequence and induction kinetics."		
RL	Gene 120:75-83(1992).		
CC	-1- FUNCTION: Nitrate reductase is a key enzyme involved in the first		
CC	step of nitrate assimilation in plants, fungi and bacteria.		
CC	-1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2O) = nitrate + NADH.		
CC	-1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD		

CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- INDUCTION: By nitrate.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC EMBL; X64136; CAA45497.1; -.
 CC PIR; JCI422; JCI422.
 CC HSSP; P04166; 1B5M.
 CC InterPro; IPR001199; Cyt_B5.
 CC InterPro; IPR001834; Cyt_B5_reductase.
 CC InterPro; IPR000572; Bnk_Mb_oxred.
 CC InterPro; IPR001709; FPN_Cyt_reductase.
 CC InterPro; IPR005066; Mo-co_dimer.
 CC InterPro; IPR004433; Oxred_FAD/NAD(P).
 CC Pfam; PF00970; FAD_binding_6; 1.
 CC Pfam; PF00173; heme_1; 1.
 CC Pfam; PF03404; Mo-co_dimer; 1.
 CC Pfam; PF00175; NAD_binding_1; 1.
 CC Pfam; PF00174; oxidored_molyb; 1.
 CC PRINTS; PR00406; CYTBSRDITASE.
 CC PRINTS; PR00363; CYTOCHROMEBS..
 CC PRINTS; PR00407; EUMOPTERIN..
 CC PRINTS; PR00371; FPNCR.
 CC ProDom; PD000612; Cyt_B5; 1.
 CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE; PS00255; CYTOCHROME_B5_2; 1.
 CC PROSITE; PS00559; MOLYBDOTERIN_EUK; 1.
 CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 CC Nitrate assimilation.
 CC FT METAL 139 139 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT METAL 193 193 INTERCHAIN (POTENTIAL).
 CC FT DISULFID 376 376 INTERCHAIN (POTENTIAL).
 CC FT METAL 532 532 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 555 555 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 864 AA; 96402 MW; 499529652CDDIC7 CRC64;
 CC -----
 CC Query Match 7.4%; Score 185.5; DB 1; Length 864;
 CC Best Local Similarity 36.4%; Pred. No. 1.7e-07;
 CC Matches 48; Conservative 22; Mismatches 57; Indels 5; Gaps 3;
 CC -----
 CC Db 7 AMPAPGAPAGA-GDVWISSKELRAHASADDLWISGVDVYVTPWLFPHPGDLPLTLT 65
 CC 483 AARPVVAANAANGPRQYTMEEVAHNTBSCMFVHGKGYDATTPIDEHFGAESTLIIV 542
 CC Qy 66 AGQDADTAPAAVPPSARPLLRPFVGR--SDVAVSPASADYRRLIAQLQSAGLEFVY 122
 CC Db 543 AGDADTDEFNSIHSSKAKMLAQYIGDLVASKRAAGATVPEGPVASTSSDAVDPLIV 602
 CC Qy 123 -GPTPKVQLVLM 133
 CC Db 603 LNPQKVKPLPI 614
 CC -----
 CC RESULT 4
 CC FD61-SOYBN STANDARD; PRT; 387 AA.
 CC AC P48630;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1
 DE (EC 1.14.19.-).
 GN FAD2-1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Seed.
 RX MEDLINE=96151506; PubMed=8587990;
 RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;
 RT "Developmental and growth temperature regulation of two different
 RT microsomal omega-6 desaturase genes in soybeans.";
 RL Plant Physiol. 110:311-319(1996).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; I43920; AAB0859.1; -.
 CC PIR; T07687; T07687.
 CC InterPro; IPR005804; FA_desat_fam.
 CC Pfam; PF00487; FA_desaturase; 1.
 CC ProDom; PD001081; FA_desat_fam; 2.
 CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 CC Transmembrane.
 CC FT TRANSMEM 54 74 POTENTIAL.
 CC FT TRANSMEM 87 107 POTENTIAL.
 CC FT TRANSMEM 121 141 POTENTIAL.
 CC FT TRANSMEM 183 203 POTENTIAL.
 CC FT TRANSMEM 227 247 POTENTIAL.
 CC FT TRANSMEM 251 271 POTENTIAL.
 CC FT DOMAIN 109 113 HISTIDINE BOX-1.
 CC FT DOMAIN 145 149 HISTIDINE BOX-2.
 CC FT DOMAIN 319 323 HISTIDINE BOX-3.
 CC SQ SEQUENCE 387 AA; 44662 MW; 49068805C21A1C31 CRC64;
 CC -----
 CC Query Match 7.3%; Score 183.5; DB 1; Length 387;
 CC Best Local Similarity 23.1%; Pred. No. 9.8e-08;
 CC Matches 96; Conservative 53; Mismatches 165; Indels 101; Gaps 22;
 CC -----
 CC Db 80 PSARPLLRPFVGR--SDVAVSPASADYRRLIAQLQSAGLEFVYGPVQLVMAVLFYA 139
 CC Qy 30 PNTKP--PFTYGQLK--KAIRPHCFGRSLNLSFSIV-----YDLSFAIFPIY 73
 CC Db 140 AL-----YLVLAASAMALLAGLIGFVWIGSGMGKHDGSHRRITGHPVLDVVQ 190
 CC Qy 74 ATTYFHLPLPQPSLIMPIY--VLGGCLLTGVV--IAHECGHARSKYQWVDVVG 127
 CC Db 191 VLSGNCLTGLSLAMWKCNTHTHIACTSDHPDLOHMLFAVSPRL-----F 238
 CC Qy 128 LTLHSTLL-VVPFSWKISHRRHSNTGSLDRD-----EVFPPKPSKYAWPSKYLNPL 180
 CC Db 239 GNWISYFQRT-----LAFDAASKFISY-QHWTFYPMWCARIMLT--AQSALEFVLT 288

DB 181 GRAVSLVLTLLTGMPTLAFVNSGRPYDSFASHYHPAPYISNRERLLIYVSVALFSVT 240
 QY 289 EKVPQRLLEIAGVATFWMY--PLIVASLPNMNERAFULFSFTICIGIHQVFCINHS 346
 DB 241 YSL--YRVATLTKGLVLLCYGVPLLVN-----GPIVTTYLVLOHTHPALPHYD 287
 QY 347 SDVYVGPKNQDNWFEKOTAGTLDILCSPMMDW-----FHGQIQFQIENHLPRLPCHL 400
 DB 288 SSSW-----DWL-KGALATMD-----RDYGLNVFHHIDHTVAHLLFSTMPHYHA 333
 QY 401 RKAPAVRDLCKHGLTYSATFWGANVLTKTLRAAALQARTATSGAPKPLVW 455
 DB 334 MEATNAIKPIIGBY-YQFDDTPEYKA---LMREARECLYV--EPDEGTSEKGYW 382

RESULT 5
 CYSL_ARATH STANDARD; PRT; 134 AA.
 ID CYSL_ARATH STANDARD; PRT; 134 AA.
 AC Q42342; Q9SB05;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5 isoform 1.
 GN AT5G53560 OR MNC6.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RX MEDLINE=99087071; PubMed=9889378;
 RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.;
 RT "Mitochondrial electron transfer in higher plants: Cloning and
 RT heterologous expression of NADH-cytochrome b5 reductase from
 RT Arabidopsis.";
 RL Plant Physiol. 119:353-361 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=99087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:297-308 (1998).
 RN [3]
 RP SEQUENCE OF 1-113 FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Cooke R., Laurie M., Raynal M., Delyeny M.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (by similarity).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC
 CC EMBL: AB007801; BA74839.1; -
 CC EMBL: AB015476; BAB09732.1; -
 CC EMBL: F20001; CAA23377.1; -
 CC PIR: T52469; T52469.
 CC HSSP: P00171; IEHB.
 CC InterPro: IPR001199; Cyt_B5.

DR Pfam; PF00173; heme 1; 1.
 DR PRINTS: PR00363; CYTOCHROME5.
 DR PRODOM: PD000612; Cyt_B5_1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 KW Electron transport; transmembrane; Heme; Iron; Microsome;
 KW Multigene family.
 FT TRANSMEM 107 127 POTENTIAL.
 FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 1 3 MS -> AKA (IN REF. 3).
 SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60FC873FD CRC64;
 Query Match 7.1%; Score 180; DB 1; Length 134;
 Best Local Similarity 39.6%; Pred. No. 5.5e-08;
 Matches 36; Conservative 21; Mismatches 32; Indels 2; Gaps 2;
 QY 17 AGDVRMISSEKELRAHSAADLWISIGDYVDYTPWLPNHPGDLPLTLTAGODATDFA- 75
 DB 2 SSDRKVLSPFEVSKNKTKDCWLLISGKYVDYTPFMDHDPGDEVLSSGKDATNDFED 61
 QY 76 AYHPSPAPLRRFPYGRSLDVAVSPASADY 106
 DB 62 VGHSDTARDMDKCYFGEIDSSSV-PATRY 91

RESULT 6
 CYBS_TOBAC STANDARD; PRT; 136 AA.
 ID CYBS_TOBAC STANDARD; PRT; 136 AA.
 AC P49098;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting.";
 RL Plant Mol. Biol. 25:527-537 (1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
 CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
 CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
 CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
 CC LEVELS IN THE LEAF.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC
 CC EMBL: X71441; CAA50575.1; ALU_INIT.
 CC EMBL: X68140; CAA48240.1; -
 CC HSSP: P04166; 1BSM.

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DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR Electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 10 11 LA -> EF (IN REF. 1; CAA48240).
FT CONFLICT 105 105 MISSING (IN REF. 1; CAA48240).
SQ SEQUENCE 136 AA; 14979 MW; DACE9AE695B2835F CRC64;

Query Match 7.1%; Score 180; DB 1; Length 136;
Best Local Similarity 43.3%; Pred. No. 5.6e-08;
Matches 39; Conservative 14; Mismatches 35; Indels 2; Gaps 2;

QY 18 GDVRLMISKEPLRAHSAADLMISIGDYDVTPLPHHPCGDLPLTLGADATDAFA-A 76
DB 3 GERTKFTLAEVSGHNAKCMWLISGKYVDVTFKLDHDEGDEVLSATGKATDDEFDV 62
QY 77 YHPSAPPLRRFFVGRSLSDVAVSPASADY 106
DB 63 GHSSSARMLDEYVGDIDSATIPRTKTY 91

RESULT 7
NIA_BEABA STANDARD; PRT; 894 AA.
AC P43100;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).
GN NIA.
OS Beauveria bassiana (Trichothium shioteae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Cordyceps.
OX NCBI_TaxId=176275;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BB147;
RA Maurer P.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.
CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC AND ONE MOLYBDENUM ATOM.
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SIMILARITY: TO EDUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X84950; CAA59336.1; -.
CC PIR; S52857; S52857.
CC HSSP; P04166; 1EUF.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR000572; Btk_Mb_oxred.
CC InterPro; IPR001709; FPN_Cyt_reductase.
CC InterPro; IPR005066; Mo-co_dimer.

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DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; oxidored_molyb; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PRINTS; PR00407; EMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
KW Nitrate assimilation.
FT METAL 169 169 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 220 220 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 418 418 INTERCHAIN (POTENTIAL).
FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 894 AA; 99934 MW; D0ED234BF1B1322B CRC64;

Query Match 7.1%; Score 178.5; DB 1; Length 894;
Best Local Similarity 36.3%; Pred. No. 6.7e-07;
Matches 37; Conservative 21; Mismatches 35; Indels 9; Gaps 1;

QY 20 VEMISKEPLRAHSAADLMISIGDYDVTPLPHHPCGDLPLTLGADATDAFAAHP 79
DB 535 VRIISLEELKAHEGMEPWFVNGHYVNGTPLYLDHPCGATSIINAAQDATEEFWTIHS 594
QY 80 PSAPPLRRFFVGRSLSDVAVSPASADYRRLLAQ 112
DB 595 ENAKMMPQYHIGTLNDAARKALBGSABESPASDPTRAVFLQ 636

RESULT 8
NIA_FUSOX STANDARD; PRT; 905 AA.
AC P39863;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).
GN NIA.
OS Fusarium oxysporum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxId=5507;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=FOM24;
RX MEDLINE=93380674; PubMed=8370541;
RA Dhole A., Langin C., Gerlinger C., Brygoo Y., Daboussi M.-J.;
RT "The nia gene of Fusarium oxysporum: isolation, sequence and
RT development of a homologous transformation system.";
RL Gene 131:61-67(1993).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.
CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC AND ONE MOLYBDENUM ATOM.
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SIMILARITY: TO EDUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
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DR EMBL; Z22549; CA90270.1; -.
 DR PIR; JN0803; JN0803.
 DR HSSP; P04166; 1EUB.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR000573; Bk_Mb_oxred.
 DR InterPro; IPR001709; FFW_Cyt_redctase.
 DR InterPro; IPR005066; Mo-co-dimer.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD binding_6; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co dimer; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR Pfam; PF00174; oxidored_molp; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
 KM Nitrate assimilation.
 FT DOMAIN 3
 FT METAL 179 179 POLY-THR.
 FT METAL 230 230 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 428 428 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DOMAIN 550 620 INTERCHAIN (POTENTIAL).
 FT METAL 581 581 HEME-BINDING (BY SIMILARITY).
 FT METAL 604 604 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 645 905 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT DOMAIN 875 884 FLAVIN-BINDING DOMAIN (BY SIMILARITY).
 FT NP BIND 875 884 NADP (BY SIMILARITY).
 SQ SEQUENCE 905 AA; 101898 MW; D5D8E23F7971ACDA CRC64;

Query Match 7.0%; Score 176.5; DB 1; Length 905;
 Best Local Similarity 31.4%; Pred. No. 9.9e-07;
 Matches 36; Conservative 26; Mismatches 44; Indels 13; Gaps 2;

QY 21 RMISSEKELRAHASADDLWISGSDYDVTPLPHHPCGDLPLTLAAGDADAFAPAAVHP 80
 DB 547 RKITIELKKAHSGEEFVVKGEVDTCTPLSGHGAASIFCAAGQDAIEEFMAIHSR 606
 QY 81 SARPLLRFFVGRISDYAVSPASADYR-----LLAQLSAGLPER--VGPTPK 127
 DB 607 NAKAMLPYHIGTDESSRAILSGDATKNTDDADREVFLOAKTWSKAILDKTGISPDTK 666
 QY 128 V 128
 DB 667 I 667

RESULT 9
 CYB5_BRAOL STANDARD; PRT; 134 AA.
 ID CYB5_BRAOL
 AC P40934;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome B5.
 GN CYB5.
 OS Brassica oleracea (Cauliflower).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Eusteroideae; Brassicales; Brassicaceae; Brassica.
 CC NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 6-47 AND 75-89.
 RC STRAIN=cv. Cauliflora;

RA Kearns E.V., Keck P., Somerville C.R.;
 RT "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
 RT (Brassica oleracea L.).";
 RL Plant Physiol. 99:1254-1257(1992).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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DR EMBL; M87514; AAA32990.1; -.
 DR PIR; T14454; T14454.
 DR HSSP; P00171; 1EHB.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome.
 KM TRANSMEM 107 127 POTENTIAL.
 FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT VARIANT 5 5 K -> N.
 SQ SEQUENCE 134 AA; 15062 MW; 764DC24A4CDD591 CRC64;

Query Match 6.9%; Score 175; DB 1; Length 134;
 Best Local Similarity 37.4%; Pred. No. 1.4e-07;
 Matches 34; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 17 AGDVRMISSEKELRAHASADDLWISGSDYDVTPLPHHPCGDLPLTLAAGDADAFAPAAVHP 75
 DB 2 ASKKVGLGFEFVSQHNKTKDCLWISGKYDVTPLPHHPCGDLPLTLAAGDADAFAPAAVHP 61
 QY 76 AVHPSARPLLRFFVGRISDYAVSPASADY 106
 DB 62 VGHSDTARDMEKXYIGET-DSSTVPRATRY 91

RESULT 10
 NIA_CHLVU STANDARD; PRT; 318 AA.
 ID NIA_CHLVU
 AC O01170;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
 OS Chlorella vulgaris.
 CC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 CC Chlorellaceae; Chlorella.
 CC NCBI_TaxID=3077;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91354204; PubMed=1883330;
 RA "Expression of a cDNA clone encoding the haem-binding domain of
 RT Chlorella nitrate reductase.";
 RL Biochem. J. 278:203-209(1991).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- SUBUNIT: Homodimer.

CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 CC EMBL: X56771; CAA40090.1; -
 CC PIR: S17197; S17197.
 CC HSSP: P04166; 1BSW.
 CC InterPro: IPR001199; Cyt_B5.
 CC InterPro: IPR000572; Euk_Mb_oxred.
 CC InterPro: IPR005066; Mo-co_dimer.
 CC Pfam: PF00173; heme_1; 1.
 CC Pfam: PF03404; Mo-co_dimer; 1.
 CC PRINTS: PR00363; CYTOCHROMEBS.
 CC PRINTS: PR00407; EUMOPTERIN.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS00255; CYTOCHROME_B5_2; 1.
 CC PROSITE: PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
 CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 CC Nitrate assimilation.
 CC FT NON TER 1 1
 CC FT METAL 251 251 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 274 274 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT NON TER 318 318
 CC SQ SEQUENCE 318 AA; 34830 MW; E60D82FE1E98292A CRC64;
 CC
 CC Query Match 6.8%; Score 172.5; DB 1; Length 318;
 CC Best Local Similarity 36.5%; Pred. No. 6,2e-07;
 CC Matches 38; Conservative 17; Mismatches 38; Indels 11; Gaps 3;
 CC
 CC QY 2 PPSVDMAPAGAGAGVYRMISSKELRAHASADDLWISGVDYDPTWLPNHPGADLP 61
 CC Db 209 PP-----PAP---AGA---KSFTMAVEHTHTWESAMFVVDGKYDPTFLKDPGAGDS 257
 CC
 CC QY 62 LLTLAGODATDAFAAHPPSARPLRRFFVGRISDVAVSPASAD 105
 CC Db 258 ILTVAGIDATDEFNAHSLKAKKQLLYEYIGELAEBCQEAASD 301
 CC
 CC RESULT 11
 CC NIA7_HORVU STANDARD; PRT; 891 AA.
 CC ID NIA7_HORVU STANDARD; PRT; 891 AA.
 CC AC P27968;
 CC DT 01-AUG-1992 (Rel. 23, Created)
 CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Nitrate reductase [NAD(P)H] (EC 1.7.1.2).
 CC GN NAR-7.
 CC OS Hordeum vulgare (Barley).
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC OC Triticeae; Hordeum.
 CC NCBI_TaxID=4513;
 CC RN (1)
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=cv. Himalaya;
 CC RX MEDLINE=91375416; PubMed=1896007;
 CC RA Miyazaki J., Juricek M., Angelis K., Schnorr K.M., Kleinhofs A.,
 CC Warner R.L.;
 CC RT Characterization and sequence of a novel nitrate reductase from
 CC RT barley.";
 CC RL Mol. Gen. Genet. 228:329-334(1991).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first

CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(P)(+) + H(2)O = nitrate +
 CC NAD(P)H.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- SUBUNIT: Homodimer.
 CC -1- INDUCTION: By nitrate.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 CC EMBL: X60173; CAA42739.1; -
 CC PIR: S16895; RDBNHP.
 CC HSSP: P1571; 2CND.
 CC InterPro: IPR001199; Cyt_B5.
 CC InterPro: IPR001834; Cyt_B5_reductase.
 CC InterPro: IPR000572; Euk_Mb_oxred.
 CC InterPro: IPR001709; FPN_cyt_redctase.
 CC InterPro: IPR005066; Mo-co_dimer.
 CC InterPro: IPR001433; Oxred_FAD/NAD(P).
 CC InterPro: IPR001221; Phe_hydroxylase.
 CC Pfam: PF00970; FAD_binding_6; 1.
 CC Pfam: PF00173; heme_1; 1.
 CC Pfam: PF03404; Mo-co_dimer; 1.
 CC Pfam: PF00175; NAD_binding_1; 1.
 CC Pfam: PF00174; oxidored_molb; 1.
 CC PRINTS: PR00406; CYTB5BDYAS.
 CC PRINTS: PR00363; CYTOCHROMEBS.
 CC PRINTS: PR00407; EUMOPTERIN.
 CC PRINTS: PR00371; PPNCR.
 CC PRINTS: PR00410; PHEHYDRYLASE.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS00255; CYTOCHROME_B5_2; 1.
 CC PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
 CC Oxidoreductase; Flavoprotein; FAD; NAD; NADP; Heme; Molybdenum;
 CC Nitrate assimilation; Multigene family.
 CC FT METAL 168 168 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT METAL 221 221 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT DISULFID 406 406 INTERCHAIN (POTENTIAL).
 CC FT METAL 550 550 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 891 AA; 98630 MW; AA47EC52FC1EFD13 CRC64;
 CC
 CC Query Match 6.7%; Score 170; DB 1; Length 891;
 CC Best Local Similarity 44.6%; Pred. No. 3,3e-06;
 CC Matches 37; Conservative 10; Mismatches 32; Indels 4; Gaps 1;
 CC
 CC QY 27 ELRVASADDLWISGVDYDPTWLPNHPGADLPPLTLAAGDADPAFAAHPPSARPL 86
 CC Db 522 EVRRHASKDSAMIVVGHVYDCTAFLKDPGAGDSILINAGSDCTEEFADIAHSAKRGLL 581
 CC
 CC QY 87 RRFVGRPL----SDYAVSPASAD 105
 CC Db 582 EMYRVGELLVTGNDYSPQSSNAD 604
 CC
 CC RESULT 12
 CC NIA1_TOBAC STANDARD; PRT; 904 AA.
 CC ID NIA1_TOBAC STANDARD; PRT; 904 AA.
 CC AC P1605;
 CC DT 01-OCT-1989 (Rel. 12, Created)

01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NRL).
GN NIAL.
05 Nicotiana tabacum (Common tobacco).
06 Euryotia viridiplanthea; Streptophyta; Embryophyta; Tracheophyta;
07 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
08 Ascertidae; Jamids; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Xanthi; TISSUE=leaf;
RA Vancheret H., Kronenberger J., Rouze P., Caboche M.;
RT "Complete nucleotide sequence of the two homeologous tobacco nitrate
reductase genes";
PL Plant Mol. Biol. 12:597-600 (1989).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2O) = nitrate + NADH.
CC -1- COPROCTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF PAD,
HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
GROUP IS CALLED CYTOCHROME B5-57.
CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
BY THE CIRCULAN RHYTHM.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO PAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
C-TERMINAL DOMAIN.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X14058; CAA32216.1; -
DR PIR; S04838; RDNTNT.
DR HSSP; P17571; 2CND.
DR InterPro; IPR0011199; Cyt B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR000572; Euk_Mb_oxred.
DR InterPro; IPR001709; FPN_Cyt_reductse.
DR InterPro; IPR005066; Mo-co_dimer.
DR InterPro; IPR001433; Oxred_FAD/NMD (P).
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR Pfam; PF00174; oxidored_molyb; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EDMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS02055; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
Molybdenum-pterin; Multigene family.
FT METAL 183 183 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 237 237 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 422 422 INTERCHAIN (POTENTIAL).
FT METAL 566 566 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 589 589 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 904 AA; 101907 MW; 85642BDA723EE154 CRC64;
Query March 6.7%; Score 170; DB 1; Length 904;
Best Local Similarity 44.6%; Pred. No. 3,4e-06;
Matches 33; Conservative 10; Mismatches 31; Indels 0; Gaps 0

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0Y      21  RM1SSKELRAHSA5DDLM1SISGVYVYFWMLPHHPEGCDLPLTLAAGQDITDPAFAAHP  80
Db      532  KMYSMSVVRKHSADSAM1VHGHTYDATTFRFLXADHPGSPSIL1NAGTCTEEFDATISD  591
0Y      81  SARDLRRFFFGRL  94
Db      592  KAKULLEFPRIEGL  605

RESULT 13
NIAL_NIAL BRANA STANDARD; PRT; 911 AA.
AC      P39867;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Nitrate reductase (NADH), clone PBNBR1405 (EC 1.7.1.1) (NR).
GN      NIAL.
OS      Brassica napus (Rape).
OC      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
OC      Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae;
OC      eustoids II, Brassicales, Brassicaceae, Brassica.
OX      NCBI_TaxID=3708;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. lisandra;
RX      MEDLINE=96222419; PubMed=8685274;
RA      Fukuoka H., Ogawa T., Minami H., Yano H., Ohkawa Y.;
RT      "Developmental stage-specific and nitrate-independent regulation of
RL      nitrate reductase gene expression in rapeseed.";
RL      Plant Physiol. 111:39-47(1996).
CC      -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC      step of nitrate assimilation in plants, fungi and bacteria.
CC      -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC      -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC      AND ONE MOLYBDENUM ATOM.
CC      -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC      N-TERMINAL DOMAIN.
CC      -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC      C-TERMINAL DOMAIN.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, D38219; BAA07394.1; -.
DR      PIR, T08105; T08105.
DR      HSSP, P17571; 2CND.
DR      InterPro: IPR001199, Cyt_B5.
DR      InterPro: IPR001834, Cyt_B5 reductase.
DR      InterPro: IPR000572; Btk_Mb_oxred.
DR      InterPro: IPR001709, PPN_Cyt_reductse.
DR      InterPro: IPR005066; Mo-co_dimer.
DR      InterPro: IPR001433, Oxred_FAD/NAD(P).
DR      InterPro: IPR001221, Phe_hydroxylase.
DR      Pfam: PF00970, FAD_binding_6; 1.
DR      Pfam: PF00173; heme_1; 1.
DR      Pfam: PF03404; Mo-co_dimer; 1.
DR      Pfam: PF00175; NAD_binding_1; 1.
DR      Pfam: PF00174; oxidored_moiyb_1.
DR      PRINTS, PR00406; CYTB5RDTASE.
DR      PRINTS, PR00363; CYTOCHROMEBS.
DR      PRINTS, PR00407; EUMOPTERIN.
DR      PRINTS, PR00371; PPNCR.
DR      PRINTS, PR00410; PPHHDXRLASE.
DR      ProDom, PD000612; Cyt_B5; 1.

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DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOTERIN EUK; 1.
 KM Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 Nitrile assimilation; Multigene family;
 FT METAL 191 191 MOLYBDENUM-PTERIN (POTENTIAL).
 FT METAL 245 245 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 430 430 INTERCHAIN (POTENTIAL).
 FT METAL 574 574 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 597 597 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 911 AA; 102252 MW; BBAEI9835B03D8C CRC64;
 Query Match 6.7%; Score 169.5; DB 1; Length 911;
 Best Local Similarity 34.7%; Pred. No. 3.7e-06;
 Matches 41; Conservative 17; Mismatches 47; Indels 13; Gaps 3;
 QY 21 RMSSSELRHAAADIMISGDVDTVPLPHHGGDLPLTLGQDTAPPAVHP 80
 DB 540 KMSMEVRKGNASQAMITVHGHIDCTFLKDHDPGSGSITLNGTDEEFPAIHS 599
 QY 81 SARPLRFFVGR--SDVAVSP----ASADYRLIAQLQSAGLEFRRVGPTEKQLV 131
 DB 600 KAKKLEDRIGELITTTGYDSFNVSVHGSSVMSLAPI-----ROLAPYKNIALV 651
 RESULT 14
 FD6C ARATH STANDARD; PRT; 448 AA.
 AC P46312; O9N094;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 GN FAD6 OR FAD6 OR ATG30950 OR F6118.140.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE OF 1-418 FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95148736; PubMed=7846158;
 RA Falcone D.L., Gibson S., Lemieux B., Somerville C.R.;
 RT "Identification of a gene that complements an Arabidopsis mutant
 RL deficient in chloroplast omega 6 desaturase activity.";
 RL Plant Physiol. 106:1453-1459(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schnellier C., Wandout R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Anserge W., Brandt P., Grivell L., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtkeith T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnsbeil U., Zimmermann W., Weiler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schuren J., Grymonprez B., Chuang Y.-J., Vandenberghe F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitsengger T., Bothe G., Rampersingh U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke P.,
 RA Moolman P., Klein Lankhorst R., Rose W., Haut J., Koeltter P.,
 RA Bernieris S., Hempel S., Feldpausch M., Lambers S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McElroy K., Mayes R.,
 RA Pettit A., Rajandream M.A., Lyne M., Bens V., Reichmann S.,
 RA Borkova D., Blocher H., Scharte M., Grimm M., Loehner T.-H.,
 RA Dose S., De Haan M., Maarse A., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Partmann B., Grandérath K., Danner D., Herzi A.,
 RA Neumann S., Argirou A., Vitale D., Ligouri R., Piravandi E.,

RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lechman A., Aubourg S.,
 RA Chefor F., Cooke R., Berger C., Monfort A., Casaburga E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bietke C.,
 RA Fishman D., Haase D., Lemcke K., Mewes H.-W., Stoeck S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dehja N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sehkon M., Murray J., Shee P., Cordes M., Abu-Threiden U.,
 RA Stoneking T., Kallick J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mux P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramar J., Fulton L., Mardie E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Splich J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Dione K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamer B., Yordan C.,
 RA Ma P., Zhong Y., Preston R., Vili D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
 RA Chen E., Marra M., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RL thaliana.";
 RL Nature 402:769-777(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RL SFP consortium (Salk/Stanford/PGE).";
 CC Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE. INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST. MEMBRANE-BOUND (PROBABLY).
 CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC
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 CC
 CC EMBL; U09503; AAA92800.1; -
 CC EMBL; AL022198; CA18198.1; -
 CC EMBL; AL161578; CAB79813.1; -
 CC EMBL; AY045621; AAK73979.1; -
 CC EMBL; AY058078; AAL24186.1; -
 CC EMBL; AY058852; AAL24240.1; -
 CC EMBL; AY058852; AAL24240.1; -
 CC PIR; D85362; D85362.
 CC InterPro: IPR005804; FA desat fam.
 CC Pfam: PF00487; FA desaturase; 1.
 CC Prodom: PD001081; FA desat fam; 2.
 DR Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KM Transist peptide.
 FT TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 70 448 OMEGA-6 FATTY ACID DESATURASE.
 FT DOMAIN 171 175 HISTIDINE BOX-1.
 FT DOMAIN 207 211 HISTIDINE BOX-2.
 FT DOMAIN 367 371 HISTIDINE BOX-3.
 SQ SEQUENCE 448 AA; 51225 MW; C3AC72PB28F8F287 CRC64;
 Query Match 6.7%; Score 168.5; DB 1; Length 448;
 Best Local Similarity 21.8%; Pred. No. 2e-06;
 Matches 87; Conservative 64; Mismatches 140; Indels 109; Gaps 22;

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QY 84 PLTRFFVGLSDYA--VSPADYRRLAQLSSAGLFEVGV-----PTPK 127
DB 59 PVKRR--IGCIKAVAPAPPSADSDRQLAESYFROIGEDLPENNTLKOIMTLPK 116
QY 128 -----VOLVMAVLFYALVYLACASAMHLLAGLIGFWVIOGSM-----M 170
DB 117 EVEIDDLKALKSVLISVTSY-FLGLFMIAKSPMY-----LPLAMAMGTATIGFVFI 169
QY 171 GHDSGHHRIIGHVLDVRLVGVLSGNCITGLSIAM-----KCNTHHIIACNSLDHPDLQ 226
DB 170 GHDCAKHSFKKNLVEDIV-----GTLAFLPLVYPPEPMFKIDRHAKTNMIVHDPAWQ 224
QY 227 HMLPFAVSPCLFGNMSYFQRTIAPD-AASKFFISYQHTFYPVMCIARINLLAQSLF 285
DB 225 PIV-----PEEFSS--SPVKKAIIFGYPRIPLWLSAHVNM-----HPLKKPRA-- 269
QY 286 VLTEKVPORLLEIAGVATFWA-WYPLL-V-ASLPMN-----WERVAFVLSFTICGI 335
DB 270 ----SEVNRVKISILACVFAFMAVGMPLIVYKVGILGVKFMWLPWLGXHFWMSTFTM--- 322
QY 336 QHVQCLNHSSDVYVGPPEKNDW--FEKQTAGTLIDILCSPPMDWFHGLQFOLEHHLF 393
DB 323 -----VHHTAPRIPEKP--ADEMNAAQAOQNGTVHCDYPSWTEILCHDINVHI PHHISP 374
QY 394 RLPRCHLRKVAAPAVRDCKGGLTYSATFWG--ANVLTM 431
DB 375 RIPSYNLRRAHESIQE-----NMGKTYLATW 401

RESULT 15
NIA2 TOBAC STANDARD; PRT; 904 AA.
ID NIA2 TOBAC STANDARD; PRT; 904 AA.
AC P08509;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1989 (Rel. 12, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR2).
GN NIA2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4097;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=cv. Xanthi; TISSUE=leaf;
RA Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
RT "Complete nucleotide sequence of the two homologous tobacco nitrate
RT reductase genes.";
RT plant Mol. Biol. 12:597-600(1989).
RN [2]
RP SEQUENCE OF 171-724 FROM N.A.
RA Calza R., Huttner E., Vincentz M., Rouze P., Galangau F.,
RA Vaucheret H., Cheret I., Meyer C., Kronenberger J., Caboche M.;
RT "Cloning of DNA fragments complementary to tobacco nitrate reductase
RT mRNA and encoding epitopes common to the nitrate reductases from
RT higher plants.";
Mol. Gen. Genet. 209:552-562(1987).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
CC BY THE CIRCADIAN RHYTHM.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.

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CC -----
DR EMBL; X14059; CA32217.1; -.
DR EMBL; X06134; CA29497.1; -.
DR PIR; S04839; RDNTNS.
DR HSSP; P17571; 2CND.
DR InterPro; IPR001189; Cyt B5.
DR InterPro; IPR001834; Cyt B5.
DR InterPro; IPR000572; Euk_Mb_oxred.
DR InterPro; IPR001709; FPN_cyt_redctase.
DR InterPro; IPR005066; Mo-co_dimer.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; oxidored_molyb; 1.
DR PRINTS; PR00406; CYTB5RDYASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS02555; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family;
KW METAL.
FT METAL 183
FT METAL 237
FT DISULFID 422
FT METAL 566
FT METAL 589
SQ SEQUENCE 904 AA; 101957 MW; 75196875A3561D69 CRC64;

Query Match 6.6%; Score 167; DB 1; Length 904;
Best local Similarity 44.6%; Pred. No. 5.9e-06;
Matches 33; Conservative 10; Mismatches 31; Indels 0; Gaps 0;
QY 21 RMSSKELRAHSAADLWISGSDVDTVPWLPNHHGDLPLTLTAGQATDAFAAYHP 80
DB 532 KMSMSVEVKHSADSAWITVGHIVDAPFLKDHPGDTSDILINAGTCTEERFAIHS 591
QY 81 SARPLRRFFVGL 94
DB 592 KAKKLEDFRIGEL 605

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Search completed: January 1, 2004, 06:30:54
 Job time : 11.1656 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 41.465 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-4
Perfect score: 2521
Sequence: 1 MPPSYDAMPAPGDAGADV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_ricent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061	81.8	469	10 Q92TU8	Q92TU8 triticum ae
2	1500.5	59.5	446	10 Q92TV9	Q92TV9 ricinus com
3	1457	57.8	448	10 Q8VZ22	Q8VZ22 echium gent
4	1443	57.2	448	10 Q8VZ21	Q8VZ21 echium pita
5	1429	56.7	449	10 Q92RP8	Q92RP8 brassica na
6	1427.5	56.6	458	10 Q92RP8	Q92RP8 brassica na
7	1424.5	56.5	446	10 Q92RP8	Q92RP8 brassica na
8	1393	55.3	448	10 Q92RP8	Q92RP8 brassica na
9	1392	55.2	448	10 Q92RP8	Q92RP8 brassica na
10	1387	54.8	449	10 Q92RP8	Q92RP8 brassica na
11	1382	54.8	449	10 Q92RP8	Q92RP8 brassica na
12	1363.5	54.1	446	10 Q92RP8	Q92RP8 brassica na
13	1340	53.2	448	10 Q92RP8	Q92RP8 brassica na
14	738	29.3	523	3 Q9HDG8	Q9HDG8 mucor rouxi
15	620	24.6	568	3 Q8NKG9	Q8NKG9 saccharomyc
16	612	24.3	459	10 Q944W4	Q944W4 psidium lrr

17	605.5	24.0	573	3 Q8NKG8	Q8NKG8 kluyveromyc
18	564.5	22.4	483	10 Q9LENO	Q9LENO ceratodon p
19	552	21.9	520	10 Q9LENO	Q9LENO ceratodon p
20	536	21.3	457	3 Q8X173	Q8X173 mortierella
21	535	21.2	457	3 Q9UVY3	Q9UVY3 mortierella
22	535	21.2	477	10 Q8RXB0	Q8RXB0 phaeodactyl
23	532	21.1	457	3 Q9HEV1	Q9HEV1 mortierella
24	532	21.1	457	3 Q8X174	Q8X174 mortierella
25	523	20.7	457	3 Q9UVV3	Q9UVV3 mortierella
26	521	20.7	457	3 Q9HEV4	Q9HEV4 mortierella
27	506.5	20.1	467	3 Q96VC3	Q96VC3 mucor circi
28	495.5	19.7	525	10 Q92NM2	Q92NM2 physcomitri
29	462.5	18.3	443	5 Q61388	Q61388 caenorhabdi
30	461.5	18.3	443	5 Q23221	Q23221 caenorhabdi
31	437	17.3	452	13 Q8QNM5	Q8QNM5 oncorhynch
32	435	17.3	357	3 Q9HDF4	Q9HDF4 mortierella
33	433	17.2	454	13 Q98SW7	Q98SW7 oncorhynch
34	431.5	17.1	445	4 Q9Y5Q0	Q9Y5Q0 homo sapien
35	431.5	17.1	445	13 Q8AY64	Q8AY64 sparus aura
36	429	17.0	454	13 Q90Z88	Q90Z88 oncorhynch
37	425	16.9	454	13 Q8QGE2	Q8QGE2 salmo salar
38	414.5	16.4	444	4 Q96T10	Q96T10 homo sapien
39	414	16.4	501	4 Q8NCG0	Q8NCG0 homo sapien
40	413.5	16.4	449	11 Q9JUE7	Q9JUE7 mus musculu
41	413.5	16.4	449	11 Q8K1P9	Q8K1P9 rattus norv
42	413	16.4	444	4 Q96T13	Q96T13 homo sapien
43	412.5	16.4	449	11 Q8CDZ4	Q8CDZ4 mus musculu
44	412.5	16.4	449	11 Q8C4Y5	Q8C4Y5 mus musculu
45	412	16.3	444	4 Q60427	Q60427 homo sapien

ALIGNMENTS

RESULT 1	ID	Q92TU8	PRELIMINARY;	PRT;	469 AA.
AC	Q92TU8	01-MAY-1999 (TRENBLrel. 10, Created)			
DT	01-MAY-1999 (TRENBLrel. 10, Last sequence update)				
DT	01-MAR-2003 (TRENBLrel. 23, Last annotation update)				
DE	S276.				
GN	S276.				
OS	Triticum aestivum (wheat).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;				
OC	Triticaceae; Triticum.				
OX	NCBI_TaxID=4565;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=cv. ET3;				
RA	Delhalize E., Hebb D.M., Gardner R.C., Richards K.D.;				
RT	"Aluminum tolerance in yeast conferred by over-expression of wheat				
RT	genes."				
RI	Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.				
CC	-I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.				
DR	EMBL; AF031194; AAD10250.1; -.				
DR	HSSP; P00171; 115U.				
DR	InterPro; IPR001199; Cyt B5.				
DR	InterPro; IPR005804; FA_desat fam.				
DR	InterPro; IPR001092; H4_desat fam.				
DR	Pfam; PF00487; FA_desaturase; 1.				
DR	Pfam; PF00173; heme_1; 1.				
DR	PRINTS; PR001363; CYTOCHROME B5.				
DR	ProDom; PD00612; Cyt B5; 1.				
DR	ProDom; PD001081; FA_desat fam; 1.				
DR	PROSITE; PS00255; CYTOCHROME_B5_2; 1.				
DR	PROSITE; PS00038; H4_1; 1.				
KW	Heme.				
SQ	SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;				
Query Match	81.8%; Score 2061; DB 10; Length 469;				
Best Local Similarity	80.7%; Pred. No. 5.8e-169;				

Matches	371; Conservative	36; Mismatches	51, Indels	2; Gaps	1
QY	3	PSVAMPA	PGDAAGDVRMTSSKRLAAASADLDLMISGIVYDTWPLPHNPGGDLPL	62	
Db	12	PEADMPAA--SKDAADVRMTSTKELQAAADADLMISGIVYDTWPLPHNPGGDLPL	69		
QY	63	LTLAQADATDAFAA	YHPPSAPRLRRFFGVGSLDVAVSPASADYRRLLAQLSSAGLFEKV	122	
Db	70	ITLGGQATDAFMA	YHPPSVRLRRFFVGRITDVTTPPASADPFRLLAQLSSAGLFEKV	129	
QY	123	GPTREVQVLMAV	LYFYAALYLVLCASAMAHLLAGLIGFWITQSGMGHDSGHHRTGH	182	
Db	130	GHTPFFLLVMAVS	LYFCIALYCVLASGSAHMFAGLIGFWITQSGMGHDSGHHQDITTH	189	
QY	183	PVLDRVNOVLS	NGNCLTGTGSIAMWKNNHTHTHACNSLDHPDPLQHPPLPAVSPKLFGNTH	242	
Db	190	PALNRLLQVAV	SGNCLTGTGSIAMWKNNHTHTHACNSLDHPDPLQHPPLPAVSTKLPFNTH	249	
QY	243	SYFYORTLAF	DAASKFPTSYOHWTFYVWCJARINLLAQSALFVLTEKRVFORLLIAGV	302	
Db	250	SVCCERTLAF	PAISKFPVSYOHWTFYVWVGAFARINLLVOSIVFLITQKVRORWEIAGV	309	
QY	303	ATFMAWYELV	LAASLPNNMERVAFLVLFSPITGSIQHOVQCLNHFSSDYYVGPCKNDMPKX	362	
Db	310	AAFWWYELVLS	CLPNNMERVAFLVLAFLVITGSIQHOVQCLNHFSSDYYVGPCKNDMPKX	369	
QY	363	QTAGTLIDLCS	PMWDMFPGLOLOFQIETHNLFRPLRPHCHLRKVAFAVADLCKKHGLTYSAAT	422	
Db	370	QTAGTLIDLCS	PMWDMFPGLOLOFQVETHNLFRPLRPHCHYRMVARIVRDLCKKHGLSYGAAT	429	
QY	423	FMGANVL	TWTKTLRAALQARTASGAPRNVLWEALNTHG	462	
Db	430	FWEANVMTK	TLRAALQAREKTTGAAPRNVLWEALNTHG	469	

	RESULT 2		
ID	Q9ZTY9	PRELIMINARY;	PRT; 446 AA.
AC	Q9ZTY9		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)	
DE	Desaturase/cytochrome b5 protein.		
OS	Ricinus communis (Castor bean).		
OC	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae		
OC	eucosids I; Malpighiales; Euphorbiaceae; Ricinus.		
OX	NCBI_TaxID=3988;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Seed endosperm;		
RX	MEDLINE=97268723; PubMed=9108131.		
RA	Savanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,		
RA	Christie W.W., Shewry P.R., Napier J.A.;		
RT	"Expression of a borage desaturase cDNA containing an N-terminal		
RT	cytochrome b5 domain results in the accumulation of high levels of		
RT	delta-desaturated fatty acids in transgenic tobacco."		
RL	Proc. Natl. Acad. Sci. U.S.A. 94(4211-4216(1997)).		
CC	-1-SMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.		
CC	EMBL; AF005096; AAD01240.1; -.		
DR	HSSP; P00171.1f5U.		
DR	InterPro; IPR001199; Cyt_B5.		
DR	InterPro; IPR005804; FA_desat.fam.		
DR	Pfam; PF00487; FA_desaturase; 1.		
DR	Pfam; PF00173; heme_1; 1.		
DR	Prodrom; PD000612; Cyt_B5; 1.		
DR	Prodrom; PD001081; FA_desat.fam; 1.		
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.		
KW	Heme.		
SQ	SEQUENCE 446 AA; 51418 MW; AI954FDB32DB600F CRC64;		
Query Match	59.5%; Score 1500.5; DB 10; Length 446;		
Best Local Similarity	63.0%; Pred. No. 9.je-121;		

Matches	279;	Conservative	49;	Mismatches	112;	Indels	3;	Gaps	3									
QY	21	RMISKKELRAH	ASAD	LDLMI	SSG	VYD	TPYLPH	HH	PGD	LPL	TL	AGD	AD	AD	AA	Y	80	
Db	6	KYIKREDE	L	ERKNN	GG	DL	MI	SI	Q	KI	Y	NT	D	MS	K	H	PG	65
QY	81	SAR	ELRR	FF	VG	-	R	LS	D	Y	A	V	S	P	A	D	Y	139
Db	66	T	A	W	Y	D	K	F	F	G	Y	N	L	K	D	Y	S	124
QY	140	A	L	Y	V	L	A	C	A	S	A	M	A	L	L	A	G	199
Db	125	S	V	E	V	L	S	N	S	T	M	V	H	L	I	S	G	184
QY	200	L	S	I	A	M	M	C	N	N	H	T	H	I	A	C	N	259
Db	185	I	S	I	A	M	M	C	N	N	H	T	H	I	A	C	N	244
QY	260	I	S	Y	O	H	M	T	F	P	P	M	C	I	A	R	I	319
Db	245	V	S	Y	O	H	L	T	F	P	P	M	C	E	A	R	I	304
QY	320	M	E	R	A	F	L	E	S	T	I	G	I	O	V	O	F	379
Db	305	G	E	R	M	F	A	A	S	T	V	R	I	O	H	O	F	364
QY	380	H	G	L	O	F	O	I	E	N	H	L	P	R	L	P	R	439
Db	365	H	G	L	O	F	O	E	N	H	L	P	R	L	P	R	V	424
QY	440	Q	A	R	T	A	T	S	G	A	P	K	N	L	V	E	A	462
Db	425	Q	A	R	D	-	L	S	N	P	L	P	K	N	L	V	E	446

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RESULT 3
Q8VZ22
ID Q8VZ22 PRELIMINARY; PRT; 448 AA.
AC Q8VZ22;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Delta-6-desaturase.
GN D6DS.
OS Echinium gentianoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Boraginaceae; Echinium.
OX NCBI_TaxID=173991;
RN [1]
RP SEQUENCE FROM N.A.
RA Martore F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
RT "Cloning and Molecular Characterization of the D6-Desaturase from
RT Echinium: Functional Expression in Yeast and Tobacco."
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL, AY055117; AAL23580.1; -.
DR InterPro; IPR011199; Cyt_B5.
DR InterPro; IPR005804; FA_desac_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desac_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 448 AA; 51428 MW; CZA937951E87C183 CRC64;
Query Match 57.8%; Score 1457; DB 10; Length 448;
Best Local Similarity 57.8%; Pred. No. 5.2e-117;
Matches 256; Conservative 76; Mismatches 109; Indels 2; Gaps 2;
21 RMISKKLRLKASADLDLWISGQVYVTPVLRPHHRCQDRLYLTLAQDADTDAFAAYRPR 80
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Db      7 KYTAAELKHKDEGLWISIOCKYVSDWMLKDHGKRPPLISLAGOEVTDFAVAFHSG 66
Qy      81 SARPLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLPERVGPPTPKVOLVMAVLFA 139
Db      67 STMKLDSFETGYLLKDYVSSEVSKDYRKLVFEFNKMGLEFDKKGHVLVTVLFIAMFPM 126
Qy      140 ALYVLACASAMAHLLAGLIGFVMIOSGMWHDGHHRTGHPVLDRVVOVLSGNCLTG 199
Db      127 SVYGVLFCEGVVLVHLLAGLGMFVMIOSGMIGHDAGHYIYMPNPKLNMKGIVASNCISG 186
Qy      200 LSIAMWKCNHNTHTIACNSLDHDPDLQHPPLFAVSPKLGNIWISYFYQRTLAFDAASKFP 259
Db      187 ISIGMKNHNAHNTIACNSLDYDPDQYIPFLVSSKLSFSSLSHFYEKKLTFDSLSRFF 246
Qy      260 ISYQWTFYPVWCARINILNLAOSALFVTEKRVPOSLLIAGVATFMAVPLVLSLPMW 319
Db      247 VSHQWTFYPVWCASARVNFVQSLIMLTKRNVFYRSQELLGLVFWIWPPLVSCLPWM 306
Qy      320 WERVAFLVPSFTICGLOHVOFCLNHPSDYVYGPCKGNDMFEKQTAGTLDILCSPMWDMF 379
Db      307 GERIMEVVASLSTVGMOQVQFSLNHFSAVYVGQPKGNDMFEKQTGTLDISCPMWMDF 366
Qy      380 HGGLOFOIEHHLFPLRPRCHLRKVAVARDLCKKGLTYSATFGANVLTWKTLLAAL 439
Db      367 HGGLOFOVEHHLFPLRPRCHLRKISPFVWELCKKGNLSYNCSFSEANEMTLRTLDL 426
Qy      440 QARTATSGCAPKULVWEAVNTHG 462
Db      427 QARDLTK-PLPKULVWEALNTHG 448

RESULT 4
Q9VZ21 PRELIMINARY; PRT; 448 AA.
AC Q9VZ21;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Delta-6-deacaturase.
GN D6DBS.
OS Echium pitardii var. pitardii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Boraginaceae; Echium.
OX NCBI_Taxid=174255;
RN (1)
RP SEQUENCE FROM N.A.
RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.,
RT "Cloning and Molecular Characterization of the D6-Deacaturase from
RT Echium: Functional Expression in Yeast and Tobacco."
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AY055118; AAL23581.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_deacat_fam.
DR Pfam; PF00487; FA_deacaturase_1.
DR Pfam; PF00173; heme_1.1.
DR ProDom; PD000612; Cyt_B5_1.
DR ProDom; PD001081; FA_deacat_fam_1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 448 AA; 51394 MW; 4B6DEA4905DE263 CRC64;

Query Match 57.2%; Score 1443; DB 10; Length 448;
Best Local Similarity 57.3%; Pred. No. 8.3e-116;
Matches 254; Conservative 76; Mismatches 111; Indels 2; Gaps 2;

Qy 21 RMISSELRANASADLWISISGVYDVYPMPLPHHGGDLPLITLAGODATFAFAVHP 80
Db 7 KYTAAELKHKDEGLWISIOCKYVSDWMLKDHGKRPPLISLAGOEVTDFAVAFHSG 66
Qy 81 SARPLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLPERVGPPTPKVOLVMAVLFA 139
Db 68 TAMRHLNHNHNGYHKKHVDVSRDYRRLAABFGRGLFDKKGHVTLYTLGVAAMLAA 127

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Db      67 STMKLDSFETGYLLKDYVSSEVSKDYRKLVFEFNKMGLEFDKKGHVLVTVLFIAMFPM 126
Qy      140 ALYVLACASAMAHLLAGLIGFVMIOSGMWHDGHHRTGHPVLDRVVOVLSGNCLTG 199
Db      127 SVYGVLFCEGVVLVHLLAGLGMFVMIOSGMIGHDAGHYIYMPNPKLNMKGIVASNCISG 186
Qy      200 LSIAMWKCNHNTHTIACNSLDHDPDLQHPPLFAVSPKLGNIWISYFYQRTLAFDAASKFP 259
Db      187 ISIGMKNHNAHNTIACNSLDYDPDQYIPFLVSSKLSFSSLSHFYEKKLTFDSLSRFF 246
Qy      260 ISYQWTFYPVWCARINILNLAOSALFVTEKRVPOSLLIAGVATFMAVPLVLSLPMW 319
Db      247 VSHQWTFYPVWCASARVNFVQSLIMLTKRNVFYRSQELLGLVFWIWPPLVSCLPWM 306
Qy      320 WERVAFLVPSFTICGLOHVOFCLNHPSDYVYGPCKGNDMFEKQTAGTLDILCSPMWDMF 379
Db      307 GERIMEVVASLSTVGMOQVQFSLNHFSAVYVGQPKGNDMFEKQTGTLDISCPMWMDF 366
Qy      380 HGGLOFOIEHHLFPLRPRCHLRKVAVARDLCKKGLTYSATFGANVLTWKTLLAAL 439
Db      367 HGGLOFOVEHHLFPLRPRCHLRKISPFVWELCKKGNLSYNCSFSEANEMTLRTLDL 426
Qy      440 QARTATSGCAPKULVWEAVNTHG 462
Db      427 QARDLTK-PLPKULVWEALNTHG 448

RESULT 5
Q9ZRP8 PRELIMINARY; PRT; 449 AA.
AC Q9ZRP8;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Delta-8 sphingolipid desaturase.
GN SIDL.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosida II; Brassicales; Brassicaceae; Brassica.
OX NCBI_Taxid=3708;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Drakkar; TISSUE=ripening embryos;
RX MEDLINE=99003197; PubMed=9786850;
RA Sperling P., Zaehneringer U., Heinz E.,
RT "A sphingolipid Desaturase from Higher Plants Identification of a New
RT Cytochrome b5 Fusion Protein."
RT J. Biol. Chem. 273:28590-28596(1998).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ224160; CA11857.1; -.
DR HSP; P82291; ICXY.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_deacat_fam.
DR Pfam; PF00487; FA_deacaturase_1.
DR Pfam; PF00173; heme_1.1.
DR ProDom; PD000612; Cyt_B5_1.
DR ProDom; PD001081; FA_deacat_fam_1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 449 AA; 51490 MW; FEEF37AF9D390C1 CRC64;

Query Match 56.7%; Score 1429; DB 10; Length 449;
Best Local Similarity 57.3%; Pred. No. 1.3e-114;
Matches 254; Conservative 66; Mismatches 121; Indels 2; Gaps 2;

Qy 21 RMISSELRANASADLWISISGVYDVYPMPLPHHGGDLPLITLAGODATFAFAVHP 80
Db 8 RFTSDDLKKNQPGDLWISIOCKYVSDWMLKDHGKRPPLISLAGOEVTDFAVAFHSG 67
Qy 81 SARPLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLPERVGPPTPKVOLVMAVLFA 139
Db 68 TAMRHLNHNHNGYHKKHVDVSRDYRRLAABFGRGLFDKKGHVTLYTLGVAAMLAA 127

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Qy	140	ALVYLACSAANHLAAGLIGFVWQSGMGGHDSGHHRTGPHVLDREVQVYVSGNCLTG	199
Db	128	VVYGVACTISYAHILISAVLLGELWQSAVYGHDSGHVNTSTKPCNKVOLLSGNCITG	187
Qy	200	LSIAWKCNCNHTHTHACNSLDHDDPDIQHPMLPAVSPKLFNGTWSYFYQRTLAFAASKFF	259
Db	188	ISIAWKTWTHNAHHTSCNSLDHDDPDIQHPMLPAVSPKLFNGTWSYFYQRTLAFAASKFF	247
Qy	260	ISYQWTFPVWVCICIRINLTLAASALFVLTREKVPOLLELAGATATWAWPLLVASLPMW	319
Db	248	ISYQWTFPVWVCICIRINLTLAASALFVLTREKVPOLLELAGATATWAWPLLVASLPMW	307
Qy	320	WERVAFVLFSPFICIGIOHVOFCFLNHPSSDPVYVGP PKGNDFMEKQTAGTLDILCSPMWDMF	379
Db	308	QERIFVFLMSAVTALQHVOFCFLNHPAAVYVGP PKGNDFMEKQTAGTLDILCSRTMDWF	367
Qy	380	HGGLQFOIEHHLPRLPRCHLRKRVADAVDLCKHGLTVSAATFGWANVLTWKTLRAAL	439
Db	368	FGGLQFOLEHHLPRLPRCHLRKRVADAVDLCKHGLTVSAATFGWANVLTWKTLRAAL	427
Qy	440	QARTATSGAPAKNLWEAVNTHG	462
Db	428	QARDVTN-PVLENLMEALNTHG	449
RESULT 6			
ID	Q43469	PRELIMINARY; PRT;	458 AA.
AC	Q43469;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	Delta-8 sphingolipid desaturase.		
GN	SLD1.		
OS	Helianthus annuus (Common sunflower).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;		
OC	Heliantheae; Helianthus.		
NC	NCBI_TaxId=4232;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. inbred line HA89;		
RC	TISSUE=Cotyledons of developing sunflower fruits;		
RC	MEDLINE=96028121; PubMed=7588718;		
RA	Spearling P., Schmidt H., Heinz E.		
RT	"A cytochrome b5-containing fusion protein similar to plant acyl lipid		
RT	desaturases.";		
RL	Eur. J. Biochem. 232:798-805(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. inbred line HA89;		
RC	TISSUE=Cotyledons of developing sunflower fruits;		
RC	MEDLINE=21116801; PubMed=1171153;		
RA	Spearling P., Blume A., Zaehlinger U., Heinz E.;		
RT	"Further characterization of delta 8-sphingolipid desaturases from		
RT	higher plants.";		
RL	Biochem. Soc. Trans. 28:638-641(2000).		
RC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.		
DR	EMBL; X87143; CAA60621.1; -.		
DR	HSSP; P00171; 1F03.		
DR	InterPro; IPR001199; Cyt B5.		
DR	InterPro; IPR005804; FA_desat_fam.		
DR	Pfam; PF00487; FA_desaturase; 1.		
DR	Pfam; PF00173; heme_1; 1.		
DR	ProDom; PD00612; Cyt_B5; 1.		
DR	ProDom; PD001081; Cyt_desat_fam; 1.		
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.		
KW	Heme.		
SO	SEQUENCE	458 AA; 52231 MW; .D182827AB0E99245 CRC64;	
Query Match			
56.6%; Score 1427.5; DB 10; Length 458;			

Best Local Similarity 55.1%, Pred. No. 1,8e-114;
Matches 254; Conservative 77; Mismatches 123; Indels 7; Gaps 3

OY 3 PSVDAMPAGDAAAGDVMMISSELELRHAASADDLMISGDVYDTFWMLEPHHGGDLPL 62
:::
Db 4 PSEIVLNSIADGK-----KYITSKSELKKHNPNPDLMLISLKVVYVTWEAKENPGCDAPL 58
:::
OY 63 LTLAAGQATDAFAAYHPSPARPLLRRFPVG-RLSDYANVPASAPDRRLLAQLSAGLPER 121
:::
Db 59 INLLAQDQTDPAFLNHPETAKWKHLDKLFETYGLXLDYOVSISRDRKLASEPAKGMFEK 118
:::
OY 122 VGPTPKVOLVMAMLYFYALYLVLACASAMAHLLAGLGIFGVWIOSGMGHDSGHHRTTG 181
:::
Db 119 KGHGVYSLCVSVILLSACVYGVLYSGSFWIMHLSGALLGLAMMQLALGLHDAGHYQMA 178
:::
OY 182 HPVLDRVVOVLISGNCLTGLSLIAWKKCNHNTTHIACNSIDHDPIQHMPLFVSPKLPNT 241
:::
Db 179 TRGNKKFGAFIGINCITGISIAWKKMTNAHIICNSIDYDPDLQHLPEMLAVSSKLPNSI 238
:::
OY 242 WSYRYQRRLTAADAASKPFISYQHTFFPYVMCIATINLLAQSALFVLETKRPPRLLETAG 301
:::
Db 239 TSVEYGOQLTDPILARFVSYOHLYPRMCVARVNLYLTOTLLISKRKIPRGNLTLG 298
:::
OY 302 VATFMAMPPLVLVASLPMWERVAFLVFSTTCGIQHVQFCLNHFSSDVYVGPCKNDWFE 361
:::
Db 239 TLIWTWMPPLVSLRPNNPREVALVLSFCYTGIQHOIPLTNHRSBGDYVGPCKDNWFE 358
:::
OY 362 KQTAGTIDLICSPPMDWFHGGLQFOIEHNLEPRRLPRCLRKRVAPVRDLCKKHGLTYSAA 421
:::
Db 359 KQTGTIDIACSSNMDFEGGLQFOLEHNLEPRRLPRCLRKRLSRISPCRECLKKNLYPVSL 418
:::
OY 422 TFMGANVLTWKTLLRAALQAARTATSGCAPKRLWAEAVNTHG 462
:::
Db 419 SFYDANVTYTKTRTALQAARDLTN-PAPQNLAWEAFTVTHG 458
:::

RESULT 7
OBLDD7 PRELIMINARY; PRT; 446 AA.
ID OBLDD7 AC OBLDD7;
DT 01-OCT-2002 (TREMBREL. 22, Created)
DT 01-OCT-2002 (TREMBREL. 22, Last sequence update)
DT 01-MAR-2003 (TREMBREL. 23, Last annotation update)
DE Spingolipid long chain base delta 8 desaturase.
OS Aquilegia vulgaris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatocypae; Magnoliophyta; eudicotyledons; Ranunculales;
OC Ranunculaceae; Aquilegia.
NCBI_TaxID=3451;
RN NCBI_SEQUENCE FROM N.A.
RP Longman A.J., Michaelson L.V., Napier J.A.;
RA "Isolation and characterization of a cDNA encoding a delta 8
RT sphingolipid desaturase from Aquilegia vulgaris";
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
Dr EMBL; AF046816; AAN03619.1; -!
Dr InterPro; IPR001199; Cyt_B5.
Dr InterPro; IPR005804; PA_desat_fam.
Dr Pfam; PF00487; PA_desaturase_1.
Dr Pfam; PF00173; heme_1; 1.
Dr PRINTS; PR00363; CYTOCHROMEBS.
Dr ProDom; PD000612; Cyt_B5; 1.
Dr ProDom; PD001081; PA_desat_fam; 1.
Dr PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;

Query Match 56.8%; Score 1424.5; DB 10; Length 446;
Best Local Similarity 55.8%; Pred. No. 3,2e-114;
Matches 251; Conservative 68; Mismatches 122; Indels 1; Gaps 1.

21 RMISKELRAHASADDMISISGDVYDTFWMLEPHHGGDLPLTLAAGQATDAFAAHNP 80

Best Local Similarity 55.1%, Pred. No. 1,8e-114;
Matches 254; Conservative 77; Mismatches 123; Indels 7; Gaps 3

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OY      3 PSVDAMPAGDAAAGDVMMISSEKELRAHASADLMWISGDDVDTFWMLEPHHGGDLPL 62
          |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      4 PSEIVLNSIADGK-----KYITSEKELKHNNPNPMDLWISLKVVYVTWEAKENPGGDAPL 58
OY      63 LTLAAGQATDAFAAYHPSPARPLLRPFVG-RLSDYANVPASAPDRRLLAQLSAGLPFR 121
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      59 INLLAQODTDAFIAFHPEGTAKWKHLDKLFETGYHLKDYOVSISRDRKLASEPAKGMFEK 118
OY      122 VGPTPKVOLVMAMLYFYALYLVLACASAMAHLLAGGLIGFWIQSGMNGHDSGHRRITG 181
          |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      119 KGHGVYSLCVSVSLLSACVYGVLYSGSFWIMHLSGALLGLAMNQIALYLGHDAGHYQMA 178
OY      182 HPVLDRVVOVLISGNCLTGSLIAMKKCNHNTHIACNSLDHDPDIQHMPLEAVSPKLFNT 241
          ::::|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      179 TRGNMKFPAGIFIGINCITGISIAMKKMTNHAHIACNSLDYPDILQHLPMILAVSSKLFNSI 238
OY      242 WSYTYQRILTADAASKRPISTQHTFFPYVMCIATINLLAQSALFLYTEKRPORLLETAG 301
Db      239 TSVEYGOQLTDPLARFPVSYOHLYPRMCVARVNLYLTOTLLISRKXIPRGNLIG 298
OY      302 VATFMAMPPLVLVASLPMWERVAFLVFSTTCGIQHOVFCUNHFSSDYYVGPCKNDWFE 361
Db      299 TLIWTWMPPLVSLRPNMPEVAVLVSFCYTGIQHOILOFTLNHSRGDYVGPCKDNWFE 358
OY      362 KQTAGTIDILCSPPMWDFHGGLQFOIEHHLEPRLPRCLRKAAPAVRDCLKKGITYSAA 421
Db      359 KQTGTIDIACSSWNWDFGGLQFOLEHHLEPRLPRCLRKLSISPICRECLKKNLYPVSL 418
OY      422 TFMGANVLTWKTLLRAALQAARTATSCGAPKRLUWEAVNTHG 462
Db      419 SFYDANVTYTKTRTAALQAARDLTN-PAPQNLAWEAFTNHG 458
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RESULT 7

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QBLLD7 PRELIMINARY; PRT; 446 AA.
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ID QBLLD7 AC

DB 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Spingolipid long chain base delta 8 desaturase.

OS Aquilegia vulgaris.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatocladaceae; Magnoliophyta; eudicotyledons; Ranunculales;

OC Ranunculaceae; Aquilegia.

OX NCBI_TaxID=3451;

RN (1)

RP SEQUENCE FROM N.A.

RA Longman A.J., Michaelson L.V., Napier J.A.;

RT "Isolation and characterization of a cDNA encoding a delta 8

RT spingolipid desaturase from Aquilegia vulgaris."

RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

DR EMBL; AF046816; AAN03619.1; -.

DR InterPro; IPR001199; Cyt B5.

DR InterPro; IPR005804; PA_desat fam.

DR Pfam; PF00487; PA_desaturase_1.

DR Pfam; PF00173; heme_1; 1.

DR PRINTS; PR00363; CYTOCHROMEBS.

DR ProDom; PD000612; Cyt_B5; 1.

DR ProDom; PD001081; PA_desat fam; 1.

DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.

KM Heme.

SQ SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;

Query Match 56.5%; Score 1424.5; DB 10; Length 446;

Best Local Similarity 56.8%; Pred. No. 3,2e-114;

Matches 251; Conservative 68; Mismatches 122; Indels 1; Gaps 1;

21 RMISKELRAHASADLMWISGDDVDTFWMLEPHHGGDLPLTLAAGQATDAFAAHNP 80

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Db      6 RETISELKKGNKGDWISIOGKIDYVSEWIKDHPGEGAPLNLTAGQDVTDAFVAFHFG 65
Qy      81 SARPLLRFRFVGLSDVAVPASADYRRLAOLSSAGLFEFVGPTRPVOLVMAVLFYA 140
Db      66 SAKRTLDKFFITGLKDTTISEVSKDYRKLVAFESKAGLYDKGHHILFSLTFVTLMAIS 125
Qy      141 LYLVLACASAMHLLAGGLIGFWVIOGMMGHDGSHHRTIGHVPLDRVVOVLSGNCITGL 200
Db      126 VMGVLSQDKTWAMHLASAVALGGLMQLGFGHDSGHNNILTKLRNFMQIFGNCITGI 185
Qy      201 SIAMKCNHNTNHHIACNSLDHDDPDLQHMLFAVSPKLFGNIMSYFQRTLAFAASKFT 260
Db      186 SIQMMKNNHNAHIAVNSLDYDPDLQHIPELAVSSDIFSSLTSEKFGYKRTFDPIDARFLI 245
Qy      261 SYQHMTFYPVNCIARINILNLAOSALFVTEKRVQRLLEIAGVATFMAVYLLVLAASLPNW 320
Db      246 SFQHMFTFYPMAIARINLFAQSFLLLSKRPVTDRALELLGLMFWCWSYLLAACLPMWG 305
Qy      321 ERVAVFLSFITIGIOHVQFCNLNHFSSDVYVPPKGNDFEKOAGTGLDILCSPPMMDWFH 380
Db      306 ERAMVAVMSFAVSGYQIOTFCNLNHFSAHTYVGPPCNDWFEKOTKGFDPDISCTMDWFH 365
Qy      381 GGLQFOIEHHLFPRLPKRLKVAAPAVRDLCKKGLTYSATFGANVLTWKTLLRAALQ 440
Db      366 GGLQFOVEHHLFPRLPKRLKRTKISPYKELCRKGNLPYISVSFEANQKMTIATLLRAALQ 425
Qy      441 ARTATSGAPKXUWMEAVNTHG 462
Db      426 ARDLTN-PIPKNLWMEAVNTHG 446

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RESULT 8

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OQSAS5; PRELIMINARY; PRT; 448 AA.
ID 09SAS5;
AC 09SAS5;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Delta 6-desaturase.
OS Borage officinalis (Borraghe) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Boraginaceae; Borage.
OX NCBI_TaxID=13363;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Seed;
RA Nunberg A.N., Beremand P.D., Thomas T.L.;
RT "Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
RT (GLA).";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF007561; AAD01410.1; -
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 448 AA; 51626 MW; EAC3F0BF22E0DE00 CRC64;
Query Match 55.3%; Score 1393; DB 10; Length 448;
Best Local Similarity 55.8%; Pred. No. 1.7e-111;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;
Qy 21 RMISSEKELAAHSAADLWISISGDVYDTPWMLPHNPGGDLPLTLTAGODATDPAAYHNP 80
Db 7 KYTSELKNDKRGDLWISIOGKAYDVSDWKDHPGGSFPLKSLAGQEVTDFAFVAFHFA 66
Qy 81 SARPLLRFRFVGLSDVAVPASADYRRLAOLSSAGLFEFVGPTRPVOLVMAVLFYA 139

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Db      67 STWKNDKFFFTGYLLKDYVSEVSKDYRKLVFEFSKGLYDKKHIMFATLCFIAMLFAM 126
Qy      140 ALYLVLACASAMHLLAGGLIGFWVIOGMMGHDGSHHRTIGHVPLDRVVOVLSGNCITGL 129
Db      127 SYGVGLFCEGVVHLFSSGLCMGLFWIOGMIQGDACHVAVSDSRINKFMGTGIFAAACLSG 186
Qy      200 LSIAMKCNHNTNHHIACNSLDHDDPDLQHMLFAVSPKLFGNIMSYFQRTLAFAASKFP 259
Db      187 ISIGMMKNNHNAHIAVNSLDYDPDLQHIPELAVSSDIFSSLTSEKFGYKRTFDPIDARFLI 246
Qy      260 ISYQHMTFYPVNCIARINILNLAOSALFVTEKRVQRLLEIAGVATFMAVYLLVLAASLPNW 319
Db      247 VSYQHMTFYPVNCIARINILNLAOSALFVTEKRVQRLLEIAGVATFMAVYLLVLAASLPNW 306
Qy      320 WERVAVFLSFITIGIOHVQFCNLNHFSSDVYVPPKGNDFEKOAGTGLDILCSPPMMDWFH 379
Db      307 GERIMFVIALSLVSTGQOQVFSLNHFSSSVYVGPCKGNWFEKOTGTTDILSCPMMMDWF 366
Qy      380 HGLQFOIEHHLFPRLPKRLKVAAPAVRDLCKKGLTYSATFGANVLTWKTLLRAAL 439
Db      367 HGLQFOIEHHLFPRLPKRLKRTKISPYKELCRKGNLPYISVSFEANQKMTIATLLRAAL 426
Qy      440 QARTATSGAPKXUWMEAVNTHG 462
Db      427 QARDITK-PLPKNLWMEALHTHG 448

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RESULT 9

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O04353; PRELIMINARY; PRT; 448 AA.
ID 004353;
AC 004353;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Delta 6-desaturase.
OS Borage officinalis (Borraghe) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Boraginaceae; Borage.
OX NCBI_TaxID=13363;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97268723; PubMed=9108131;
RA Sayanova O., Smith M.A., Lapinakas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; U79010; AAC49700.1; -
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 448 AA; 51635 MW; B62EEF701680909F CRC64;
Query Match 55.2%; Score 1392; DB 10; Length 448;
Best Local Similarity 55.8%; Pred. No. 2e-111;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;
Qy 21 RMISSEKELAAHSAADLWISISGDVYDTPWMLPHNPGGDLPLTLTAGODATDPAAYHNP 80
Db 7 KYTSELKNDKRGDLWISIOGKAYDVSDWKDHPGGSFPLKSLAGQEVTDFAFVAFHFA 66
Qy 81 SARPLLRFRFVGLSDVAVPASADYRRLAOLSSAGLFEFVGPTRPVOLVMAVLFYA 139
Db 67 STWKNDKFFFTGYLLKDYVSEVSKDYRKLVFEFSKGLYDKKHIMFATLCFIAMLFAM 126

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QY 140 ATYLVACASAMAHLLAGLIGFVWIOSGMWGHDSGHRITGHPVLDRVVQVLSGNCITG 139
 DB 127 SVYGVLFCEBVLVHLBSGCLMGFMIOSSGIGHDAGYVWVSRLKMKMGPANCLSG 136
 QY 200 LSIAMWKCNHNTHTIACNSLDHDPDLQHMPLFAVSPRLFGNINSYFYQRTIAPDAASKPF 259
 DB 187 ISIGWKMKNNAHIIACNSLEYPDLQYIFLVVSAKFSFSLSHFEXKLTDPDSJRRF 246
 QY 260 ISYQHTFFVPMVCARINLAQSLFVLTREKVPQLLEIAGVATFAMVPLVASLPMW 319
 DB 247 VSYQHTFFVPMVCARINLAQSLFVLTREKVPQLLEIAGVATFAMVPLVASLPMW 306
 QY 320 WERVAVLFSFTTIGIHOVFCINHFSSDYVGPCKGDMPEKOTAGTLIDILCSPPMMDWF 379
 DB 307 GERIMFVIALSTGMOQVPSLNHFSSSYVYGPCKGNMFEKOTDGLTIDILCSPPMMDWF 366
 QY 380 HGGLOFOIEHHLFPRRLPRCHLRKVPAPVBDLCKKGLTYSATFWGANVLTWKTLLRAAL 439
 DB 367 HGGLOFOIEHHLFPRRLPRCHLRKVPAPVBDLCKKGLTYSATFWGANVLTWKTLLRAAL 426
 QY 440 QARTATSGAPKXULVWEAVNTHG 462
 DB 427 QARDITK-PLPKXULVWEALHTHG 448
 RESULT 10
 Q9ZRP7 PRELIMINARY; PRT; 449 AA.
 ID Q9ZRP7
 AC Q9ZRP7
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase (AT1G61580/F2A19_180).
 GN SUD1 OR F2A19.180 OR AT1G61580.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbia II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxID=3702;
 RX MEDLINE=99003197; PubMed=9786850;
 RA Speirling P., Zaehring U., Heinz E.;
 RT "A sphingolipid desaturase from higher plants. Identification of a new
 cytochrome b5 fusion protein.";
 RL J. Biol. Chem. 273:28590-28596(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA De Haan M., Maere A.C., Grievell L.A., Mewes H.W., Lemcke K.,
 Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narisaka M.,
 Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.U., Sakurai T.,
 Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 Becker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
 Kawai J., Kim C.J., Narisaka M., Quach H.U., Sakurai T., Satou M.,
 Seki M., Shin P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
 Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Becker J.,
 RA Theologis A., Davis R.W.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AJ224161; CA11858.1; -;
 DR EMBL: AL132962; CAB71088.1; -;
 DR EMBL: AF428420; AAL16189.1; -;
 DR EMBL: BT000442; AAN17419.1; -;
 DR HSSP: P00171; 1150.
 DR InterPro: IPR001159; Cyt B5.
 DR InterPro: IPR005804; FA desat fam.
 DR Pfam: PF00487; FA desaturase_1.
 DR Pfam: PF00173; heme_1.1.
 DR ProDom: PD000612; Cyt B5; 1.
 DR ProDom: PD001081; FA desat fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51675 MW; 145048F9FD35964 CRC64;
 Query Match 55.0%; Score 1387; DB 10; Length 449;
 Best Local Similarity 55.8%; Pred. No. 5e-111;
 Matches 247; Conservative 69; Mismatches 125; Indels 2; Gaps 2;
 QY 21 RMISKELEPAHASADLWISGSDYDVPWLPBPHRGSDPLTLTAGODATPAFAAYHP 80
 DB 8 KYTNEDLKKHNSGGLMTALIQKYNVSDWIKTHGGGVTLNLVGODVDAFLAHFG 67
 QY 81 SARPLRPFVVG-RLSDVAVSPASADYRLRLAQLSSAGLFEFVGPPTKQVLVMAVLYA 139
 DB 68 TANHHDHLFTGHTIDPQVSEVSRDYRMAAFRLGLGFENKGHVTLTLTFAVMAFLG 127
 QY 140 ATYLVACASAMAHLLAGLIGFVWIOSGMWGHDSGHRITGHPVLDRVVQVLSGNCITG 139
 DB 128 VLYGVLAAGTSVFPAHQIAALLGLMTIOSAVYIGHDSGHVYIMSNKSYNRPAQLSGNCITG 187
 QY 200 LSIAMWKCNHNTHTIACNSLDHDPDLQHMPLFAVSPRLFGNINSYFYQRTIAPDAASKPF 259
 DB 188 ISIAMWKCNHNTHTIACNSLDHDPDLQHMPLFAVSPRLFGNINSYFYQRTIAPDAASKPF 247
 QY 260 ISYQHTFFVPMVCARINLAQSLFVLTREKVPQLLEIAGVATFAMVPLVASLPMW 319
 DB 248 VSYQHTFFVPMVCARINLAQSLFVLTREKVPQLLEIAGVATFAMVPLVASLPMW 307
 QY 320 WERVAVLFSFTTIGIHOVFCINHFSSDYVGPCKGDMPEKOTAGTLIDILCSPPMMDWF 379
 DB 308 PERFFVFTSFVTALQHOFTLNHPADVYVGPPTGSDWFEKQAGTIDISGRSYMDWF 367
 QY 380 HGGLOFOIEHHLFPRRLPRCHLRKVPAPVBDLCKKGLTYSATFWGANVLTWKTLLRAAL 439
 DB 368 HGGLOFOIEHHLFPRRLPRCHLRKVPAPVBDLCKKGLTYSATFWGANVLTWKTLLRAAL 427
 QY 440 QARTATSGAPKXULVWEAVNTHG 462
 DB 428 QARD-VAAPVXKULVWEALHTHG 449
 RESULT 11
 Q8LB96 PRELIMINARY; PRT; 449 AA.
 ID Q8LB96
 AC Q8LB96
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 23, Last sequence update)
 DE Delta-8 sphingolipid desaturase.
 GN SUD1 OR F2A19.180 OR AT1G61580.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbia II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxID=3702;
 RX MEDLINE=99003197; PubMed=9786850;
 RA Speirling P., Zaehring U., Heinz E.;
 RT "A sphingolipid desaturase from higher plants. Identification of a new
 cytochrome b5 fusion protein.";
 RL J. Biol. Chem. 273:28590-28596(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA De Haan M., Maere A.C., Grievell L.A., Mewes H.W., Lemcke K.,
 Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narisaka M.,
 Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.U., Sakurai T.,
 Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 Becker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

RP	SEQUENCE FROM N.A.
RA	Haes B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA	Feldmann K.A., Flavell R.B., White O., Selzberg S.L.;
RT	"Full-length messenger RNA sequences greatly improve genome
RT	annotation.";
Rt	Genome Biol. 0:0-0(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA	Feldmann K.;
RT	"Full-length cDNA from Arabidopsis thaliana.";
RL	Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
CC	-I-SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR	EMBL; AY087345; AA64895.1; -
DR	InterPro; IPR001199; Cyf_B5.
DR	InterPro; IPR005804; FA_desatase fam.
DR	Pfam; PF00487; FA_desaturase; 1.
DR	Pfam; PF00173; heme_1; 1.
DR	ProDom; PD000612; Cyf_B5; 1.
DR	ProDom; PD001081; FA_desat_fam; 1.
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW	Heme.
SQ	SEQUENCE 449 AA; 51744 MW; ALEB557B8CE03E18 CRC64;
Query Match	54.8%; Score 1382; DB 10; Length 449;
Best Local Similarity	55.5%; Pred. No. 1.5e-110;
Matches 246; Conservative 69; Mismatches 126; Indels 2; Gaps 2	
OY	21 RMISKELEAASADDLTMSIGVDVDTPLPHHGGDLPILTLAGODATAPFAAYHP 80
Dd	8 KYINEDDKKNGSGDDMLAIQGKYNNVSDMKTHPGDVTYLVNLVGDDVDAFIAHPG 67
OY	81 SARPLRRFEVFG-RISDYAVSPASADYRRLLAQLSSAGLFERVGPTPKVOLVMAVFYA 139
Dd	68 TAMHLIDLFTGYHIRDPQVSEVSRDYRMMAEFPKGLFERKGHTVLTTLAFVAMFLR 127
OY	140 ALTVYLACASAMHLIAGLGIFGWIOSGMGHDSGNHRIRIGHVLDRVVQVLSGNCITG 199
Dd	128 VLGVLCSTVPAFQIAAALLGLMIOSAYIGHDSGHVIVMNSKNYNFPADLLSNCITG 187
OY	200 LSIAMWKNNHTHHIACSNDLHDPDLOMPLEAVSPKLFGNIMSYFYORTLAFDAASKF 259
Dd	188 ISIAMKKTNNAHLACSLDYDLDQIHPPVAYSTKFSSILTSFFYRKLTDFDVAREL 247
OY	260 ISYQHWTFYPWCJARINLNLQAOLSFVLTEKRVPORLLEIGVATFWAMYPLVASLBNW 319
Dd	248 VSQHFTFYTPWCGRIQLFIQTFLFRSKREVPBRALNPAGILVFMWPFLLVASCLENW 307
OY	320 WERAFAVLFSITGICIOHVQCCLNHSSDDVYVGPCKGDWDWEKOTAGTLIDICSFMDWF 379
Dd	308 PERFFFTGTFTVALOHIOETLNHFADVYGPTGSDWEEKOAAGTIDISCRYMDWF 367
OY	380 HGGLOFOIEHNLFPRLPRCHLRKAPAYARDICKHGGLYSATFPGAVLTMKTARAAL 439
Dd	368 FGGLOFQIEHNLFPRLPRCHLRKSVPVOELCKKANLPYRSKSWPEANVLTINTIKTAAY 427
OY	440 QARTATSGAGAKNLWEBAVNTHG 462
Dd	428 QARD-VANPVVKNLWEALNTHG 449
RESULT 12	
Q9FR82	PRELIMINARY; PRT; 446 AA.
AC	Q9FR82;
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	Delta 8-sphingolipid desaturase.
GN	SLD1.
OC	Borage officinalis (Bourrache) (Borage);
OC	Eukaryota Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC	Asteridae; lamids; Boraginaceae; Borage.
CX	NCBI_TaxID=13363;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21092516; PubMed=11162428;
RA	Ishisch B., Michaelson L.V., Lewis M.J., Shewry P.R., Napier J.A.;
RT	"Chimeras of Delta-6-fatty acid and Delta-8-sphingolipid desaturases";
RL	Biochem. Biophys. Res. Commun. 279:779-785(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21260464; PubMed=11368168;
RA	Sperling P., Ishisch B., Zaehring U., Napier J.A., Heinz B.;
RT	"Functional identification of a delta 8-sphingolipid desaturase from
RL	Borago officinalis.";
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR	EMBL; AF133728; AAC43277.1; "
DR	HSSP; P00171; 115U.
DR	InterPro; IPR001199; Cyt_B5.
DR	InterPro; IPR005804; PA_desat.fam.
DR	Pfam; PF00487; PA_desaturase; 1.
DR	Pfam; PF00173; heme_1; 1.
DR	Prodrom; PD000612; Cyt_B5; 1.
DR	Prodrom; PD001081; PA_desat.fam; 1.
DR	PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
SR	Heme.
KW	SEQUENCE 446 AA; 50926 MW; BBD579F035A3AFOC CRC64;
Query Match	54.1%; Score 1363.5; DB 10; Length 446;
Best Local Similarity	55.4%; Pred. No. 5.8e-109;
Matches 247;	Conservative 64; Mismatches 132; Indels 3; Gaps 2.
QY	18 GDVAMISKEELRAHASADDLMISIGDVIDVTPLPHHGGDLRLTLGAGDATDAFAAY 77
DB	3 GTKKYIVSEGLKHNQGVDWVISIQKVNVNTDWIKKHGGDVDMNLACGDATDAFAIY 62
QY	78 HPSBARLRLRRFPFG-RLSDYANSPASADYRRLLAQLSSAGLFERVPPTPKVLYLVAVL 136
DB	63 HPGTAMRNLENLPFGYHLIEDYLVEISEKDYRKLASSEPSKAGLFEPKGHTVYYCLSFALL 122
QY	137 FYAALYVLVCASMAHLLAGLGIFPWIOSGMGHSGHHIRINGHPYLDVVVOVLSGNC 196
DB	123 LCGGVVLCSNSLMVMMLSGAMLCMPICDAAYIGHDSGHTMMSSSKGYNFPAOVLNENC 182
QY	197 LTGISIAMMKCNTHIHIA CNSLDHDELOHMPLFAVSPKXFGNIWSFYORTLAFDAAS 256
DB	183 LTGISIAMMKMTNAHHIA CNSLDYDDLOHLPFAVPSSEFFSLSTRFYORELTFLDLS 242
QY	257 KPFISYOHMTFYPVPCITARIINLLAQSLFVLTEKRVFORLLEAGVATFMAYPLVLVASL 316
DB	243 RFLVSYOHFTIYVLMIFGRINLYVQTFLTFSTKVDPRALNIIIGILVYMWTFYVLSCL 302
QY	317 PNMMERYAPFLFSFTTCIGIQHVQCINHSDDVVGPPKNDWEKQTAGTDLTLCSPWM 376
DB	303 PNMMERYAPFLTGESVALDHIOFTLNHFADADVVGPPGTNMWEKQAAGTIDISCSSWM 362
QY	377 DMFPGLOPOIEHNLFRPLPRCHLRKYAPVRDLCCKGKGLTYSATPFMGANVLTMKTJRA 436
DB	363 DMFPGLOPOIEHNLFRPMRCQQRNISPVIQDYCKGNLPRKSLSPFDANVAITKLIRT 422
QY	437 AALQARTATSGAPKNLWEAVNTHG 462
DB	423 AALQARDLTV--VFQNLLMEAFNTHG 446
RESULT 13	
ID Q8L717	PRELIMINARY; PRT; 448 AA.
AC Q8L717;	
DT 01-OCT-2002 (TtEMBLrel. 22, Created)	
DT 01-OCT-2002 (TtEMBLrel. 22, Last sequence update)	
DT 01-MAR-2003 (TtEMBLrel. 23, Last annotation update)	
DE Delta-6-desaturase.	

OS Argania spinosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Sapotaceae; Argania.
 OC NCBI_TaxID=85884;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA El Filali A., Anderson M., Abbas K.;
 RT "Characterization and cloning of delta-6-desaturase in Argania spinosa
 RT fruit";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY131238; AA94345.1; -;
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW Heme.
 SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;
 Query Match 53.2%; Score 1340; DB 10; Length 448;
 Best Local Similarity 54.2%; Pred. No. 6.1e-107;
 Matches 240; Conservative 72; Mismatches 129; Indels 2; Gaps 2;
 QY 21 RMSSSKLRRAHAAADDMISGSDYVVTWLPNHPGDDPLTLAQQDTDAFAAYHPP 80
 DB 7 KYTSDRLKNDKDKDGMISILGRAYDVSDWVTDHPGSSPFLKSLAQEYTDFAVAHPA 66
 QY 81 SARPLRRFFVVG-RISDYAVSPASADYRRLAQLSAGLPERVGPRTKVOVLMAVLEVA 139
 DB 67 STWNLKDFFTGYLYLKDYSEVSKYSLVFEFSKNGLDKAGHMFATLCTFAMLFAM 126
 QY 140 ALYLVLCASAMALLAGLIGFWIIOGWMGHDGSHRITGHPVLDVVQVLSGCLTG 199
 DB 127 SVGVLCCEGVLYVLFSGCLMGFLMIOGMIQHDPGHYVYVDSRLMKFMGIFAANLCSG 186
 QY 200 LSTAMKCNNTHTHIAQNSLDHPDLQMPFAVSPKLFNGINWYFFQRTLAFAASKFF 259
 DB 187 ISIGMSKMNNAHAIACNSLEYDLDLQYIPFLVVSXKFFSGSLTSHFEKRLTIDSLRFF 246
 QY 260 ISYOHMFYFVPCARINLTAQSLAFVLTREKRVQRLLEIAGVATFWAMYPILVASLBNV 319
 DB 247 VSYOHMFYFVPCARINLTAQSLAFVLTREKRVQRLLEIAGVATFWAMYPILVASLBNV 306
 QY 320 WERVAFLVFTTCIGIOHVQCLNHFSSDYVVPKGNDFEKOAGTGLDILCSPPMNDWF 379
 DB 307 GERIMFYIASLVYGMQOVQSLNHFSSVYVGRKNGNMEFQTGTLDISCPMMNDWF 366
 QY 380 HGGIOFOIEHNLFRRLRCHLRKAPAVRDLCCKGGLTYSNATYWGAVNLTWKTLRAAL 439
 DB 367 HGGIOFOIEHNLFRRLRCHLRKAPAVRDLCCKGGLTYSNATYWGAVNLTWKTLRAAL 426
 QY 440 QARTATSGAPKYLWEAVNTHG 462
 DB 427 QARDITK-PLPKNLWMBELHTHG 448

RESULT 14

Q9HDS8 PRELIMINARY; PRT; 523 AA.
 AC Q9HDS8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Delta-6 desaturase.
 OS Mucor rouxii.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 OC NCBI_TaxID=29923;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 24905;
 RX MEDLINE=20563795; PubMed=1112411;
 RA Laoteng K., Mammottarat R., Tanticharoen M., Cheevadhanarak S.;
 RT "Delta(6)-desaturase of Mucor rouxii with high similarity to plant
 RT delta(6)-desaturase and its heterologous expression in Saccharomyces
 RT cerevisiae";
 RL Biochem. Biophys. Res. Commun. 279:17-22(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF296076; AAG36960.1; -;
 DR EMBL: AF290983; AAG36959.1; -;
 DR HSPS: P00173; ITEX.
 DR InterPro: IPR001525; C5_DNA_meth.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS00095; C5_MTASE_2; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW Heme.
 SQ SEQUENCE 523 AA; 60622 MW; A03727AF39EB7857 CRC64;
 Query Match 29.3%; Score 738; DB 3; Length 523;
 Best Local Similarity 31.4%; Pred. No. 4.7e-55;
 Matches 164; Conservative 78; Mismatches 175; Indels 106; Gaps 10;
 QY 1 MPSPVDMPAPGADAGDVRMISRELAH-----ASADLMISGSDYV 48
 DB 1 MPENT-----AAD-RLISSTSSNIVTEKEFOELIKQDSVFI-YEQKVVHV 47
 QY 49 TPLPLNHPGDDPLTLAQQDTDAFAAYHPPSA----- 82
 DB 48 NMFAGHGGEBALRLSALRDVTDLRTMHPQVYERKMINLYCIGDMPDVIRPASKQ 107
 QY 83 -----RPLRRFFVGRISDYAVSPASAD-----Y 106
 DB 108 HTTKREKEDKPVLTATWEGFTYQAYDDAIQDLKHSHNDLKDVAVLQKLDQDQIRNAY 167
 QY 107 RRLAQLSSAGLE-----RVGPTPKVQVLMVAVLFYAAVLVLCASAMALLAGGL 159
 DB 168 RKLAEVLAKGLKCYMKVYKAREG-----CRYTLILFLSLMFTLKGTETHWYMGAAF 220
 QY 160 IGVFWIQSGMGHDSGHRITGHPVLDVVQVLSGCLGLSLAMKCNNTHTHIAQNSL 219
 DB 221 MAMFWQLVFTADAGHNEITGSEIDHVIQVIANFISGLSIGWKDNNHNVHIVTNRH 280
 QY 220 DHPDQHPMLFVSPKLFQGNISYFQRTLAFAASKFFISYOHMFYFVPCARINL 279
 DB 281 EHPDQHPMLFVSPKLFQGNISYFQRTLAFAASKFFISYOHMFYFVPCARINL 279
 QY 280 AQSALFVLTREKRVQRLLEIAGVATFWAMYPILVASLPPMWERVAFLVSPFTICGIOHVQ 339
 DB 341 RLSPFAVLITCKVARTLLELVGITFFVWFGSLSTLPTMNRIRAIYINVSYMLTFPLHVQ 400
 QY 340 FCNLNHFSSDYVVPKGNDFEKOAGTGLDILCSPPMNDWFHGGIOFOIEHNLFRRLR 397
 DB 401 ITLSHFQGST---EDRGDPDEFPAKMLRTTMDVDCDEWMLDFHGGIOFOYQVAVHLLFRPLR 457
 QY 398 CHLRKVAAPAVRDLCCKHGLTYSNATYWGAVNLTWKTLRAALQ 440
 DB 458 HNLKQCVLPVKKPCDEVGLHYMYNFTSTNGVGLTKLSVADQ 500

RESULT 15

Q8NKG9 PRELIMINARY; PRT; 568 AA.
 AC Q8NKG9;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)


```

DE Putative delta 8-sphingolipid desaturase.
OS Saccharomyces kluyveri (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4934;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1685;
RA Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
RT "Isolation and characterization of the genes encoding delta 8-
RT sphingolipid desaturase from Saccharomyces kluyveri and Kluyveromyces
RT lactis.";
CC Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AB085689; BAB93117.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; PA_desat_fam.
DR Pfam; PF00487; PA_desat_fam.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD001081; PA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 568 AA, 66465 MW, 115887B876D68EC CRC64;

Query Match 24.6%; Score 620; DB 3; Length 568;
Best Local Similarity 27.4%; Pred. No. 7,4e-45;
Matches 151; Conservative 87; Mismatches 166; Indels 148; Gaps 9;

QY 22 MISSEKELRAHASADLMISISGVDVTPWLPHPGGLPLTLAQDATDAFAAYHPS 81
DB 4 IISRGIEIDRIARGAQIVIEGVLNLEKWKIFPGDKAIHHMIGRDATDEMKAYHCD 63
QY 82 ARPLARFVGR-----LSDYAVSPASAD----- 105
DB 64 TWEIEFKMRIGRIDQEWENFLPRIGGVFERLNOQHDSTDLGSLNKMIAPISTSDQFKIK 123
QY 106 ----- 105
DB 124 NEKMGCEPDVKIYPIKPGVIPSLLKKEAYEKKVVTDPATVADNYDNELVRQDLETLPD 183
QY 106 -----YRLLAQLSAGLFE-----RVGPTPKVQLVIMAVLYAALY 142
DB 184 LDPKTOEWLSKEYNKNHNEIEAGLYQCVFRYKELTRIG-----LLFALSYLLVH 236
QY 143 LVLAACASAWAHLLAGLIGFWIQSMMGHDGHRITGHPVLDRAVVOVLSGCLTGLSI 202
DB 237 RQCKFSAFS-----MGCAMQQLVFIADAGHISITHHYOLDNIFGMIASWVGLSL 289
QY 203 AWMKCHNTHIACNSLDHPDLQHPMLFAVSPKLFGNISVYFQRTLAFDAASKFFISY 262
DB 290 GMMKRNHNHHLITNDPIHDPDICHLPFAVSTRFLDNITYSTYEKFLWFDAPAKKVPEW 349
QY 263 QHWTFYPVNCIARINLAQSALFVL-----TEKRVPORLLEIAGVATP--WAMYPLVA 314
DB 350 QNLYLYPMLAFGRFNLRLSMWHLVLLGPRGKAGMFRFELGGLIFNNYMEFYLLVGC 409
QY 315 SLPNMTERVAFVLFSTTIGIQHVQCLNHF---SSDVYVGPCKGDMPEKQTAGTLDTL 371
DB 410 KQGTGMDRFOYIMVSHITMLVHQITLSHFAMSTSDLGV---GEGFPMRQRTSMDDV 465
QY 372 CSPMMDPFGGLQFOLEHLLPRLPRCHLRKVAFAVRDLCKKHGLTYSATFGANVLTW 431
DB 466 CRRMLDFLHGLOFQVHHLPRLPRHNLRAAPVIEPEKVGIKYSIYGFSKNGVVL 525
QY 432 KTLRAAALQART 443
DB 526 TKLQEIAYOAKT 537

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 16.051 Seconds
(without alignments)
1217.848 Million cell updates/sec

Title: US-09-857-524B-4

Perfect score: 2521

Sequence: 1 MPSPVDAMPAPGDADAGDV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
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5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	55.0	448	1	US-08-366-779-5
2	1387	55.0	448	1	US-08-789-936-5
3	1387	55.0	448	4	US-08-934-254-5
4	1379	54.7	452	4	US-08-934-254-27
5	1370	54.3	446	2	US-08-833-610-5
6	1370	54.3	446	3	US-08-834-033A-15
7	881	34.9	252	2	US-08-834-655-7
8	881	34.9	252	3	US-08-834-033A-8
9	881	34.9	252	3	US-09-363-574-7
10	881	34.9	252	3	US-09-363-526-7
11	523	20.7	457	2	US-08-834-655-2
12	523	20.7	457	3	US-08-834-033A-2
13	523	20.7	457	3	US-09-363-574-2
14	523	20.7	457	4	US-09-363-526-2
15	523	20.7	457	4	US-09-330-235-18
16	523	20.7	458	4	US-09-439-261-10
17	523	20.7	458	4	US-09-439-261-44
18	523	20.7	458	4	US-09-439-261-11
19	523	20.7	458	4	US-09-439-261-11
20	521	20.7	457	2	US-09-227-613-41
21	521	20.7	457	2	US-08-833-610-41
22	443	17.6	125	3	US-08-834-033A-14
23	443	17.6	125	3	US-08-834-033A-9
24	443	17.6	125	3	US-09-363-574-8
25	443	17.6	125	3	US-09-363-526-8
26	431.5	17.1	445	4	US-09-488-888-1
27	408.5	16.2	323	4	US-09-439-261-17

28	408.5	16.2	323	4	US-09-227-613-17	Sequence 17, Appl
29	408.5	16.2	355	2	US-08-834-655-5	Sequence 5, Appl
30	408.5	16.2	355	3	US-08-834-033A-6	Sequence 6, Appl
31	408.5	16.2	355	3	US-09-363-574-5	Sequence 5, Appl
32	408.5	16.2	355	4	US-09-363-526-5	Sequence 4, Appl
33	406.5	16.1	444	4	US-09-227-613-42	Sequence 42, Appl
34	406.5	16.1	444	4	US-09-227-613-42	Sequence 42, Appl
35	406.5	16.1	444	4	US-09-488-888-3	Sequence 3, Appl
36	404	16.0	444	4	US-09-439-261-11	Sequence 11, Appl
37	404	16.0	444	4	US-09-227-613-12	Sequence 12, Appl
38	404	16.0	444	4	US-09-439-261-39	Sequence 39, Appl
39	404	16.0	444	4	US-09-439-261-45	Sequence 45, Appl
40	390	15.5	432	4	US-09-439-261-9	Sequence 9, Appl
41	390	15.5	432	4	US-09-227-613-9	Sequence 9, Appl
42	390	15.5	465	4	US-09-439-261-40	Sequence 40, Appl
43	390	15.5	465	4	US-09-227-613-38	Sequence 38, Appl
44	390	15.5	465	4	US-08-833-610-2	Sequence 2, Appl
45	320	12.7	446	2	US-08-834-033A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-366-779-5
Sequence 5, Application US/08366779
Patent No. 5614393
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Nuberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 838321XW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-366-779-5
Query Match 55.0%; Score 1387; DB 1; Length 448;
Best Local Similarity 55.5%; Pred. No. 1.1e-134;
Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;
21 RMISSEKELRAHNSADDLWISISGDVYDTPWLPHPGDLPLTLAAGDQATDAFAAYHP 80

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Db 7 KYTSDBLKNHCKPBDLWISIOGKAYDVSDBWVDHCGSEPLPLKSLAGQEVTDLFAVAFHPA 66
Qy 81 SARPLLRRFPVG-RUSDYAVSPASADYRRLLAQLSSAGLFEERVPTPKVOLVIMAVLYVA 139
Db 67 STWKLDKFFFTGYLKDYSVSEVSKDYRKLVFEPFSXMGJYDKKGHIMPATLCFIAMLFAM 126
Qy 140 ALYVLACASAMAHLLAGLIGFVWIOGSMGHDGSHHRTGHPVLDYRVQVLSGNCITG 199
Db 127 SYVGLAFCEGVLVHIFSQGLMGFLWIOGSMIGHDACHYVWSDSRINKFNGIIPAANCLSG 186
Qy 200 LSIAMWKNHNTHHIAACNSLDDPDLQHPPLFAVSPKLFNGIMSYFQRTLAFDAASKPF 259
Db 187 ISIGMKNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 246
Qy 260 ISYQHTFYPVNCIARINILAAOSALFVLTREKRPQRLBIAGVATWAMVPLTVASHPW 319
Db 247 VSYQHTFYPVNCIARINILAAOSALFVLTREKRPQRLBIAGVATWAMVPLTVASHPW 306
Qy 320 WERVAFLVFSPTTCGIIQHVQFCINHESSDYYVGPYKGNDFMEKQIAGTDLIDCSPMWDF 379
Db 307 GERIMFVIALSLVTGMQOVQFSLNHSSSVYVQKPKGNWFMFEKQTGDTLIDCSPMWDF 366
Qy 380 HGGLOFOLEHHLPRLPRCHLRKVAVAYDCLCKKHGLTISAATFWGNAVULTMKTIRAAAL 439
Db 367 HGGSOFOLEHHLPRLPRCHLRKVAVAYDCLCKKHGLTISAATFWGNAVULTMKTIRAAAL 426
Qy 440 QARTATSGGAPKULWEAVNTHG 462
Db 427 QARDITK-PLPKULWEALHTHG 448

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RESULT 2
 US-08-789-936-5
 ; Sequence 5, Application US/08789936
 ; Patent No. 5789220
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freybsinet, Georges L.
 ; APPLICANT: Nuberdy, Andre N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/789,936
 ; FILING DATE: 28-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/366,779
 ; FILING DATE: 30-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383ZYXW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
US-08-789-936-5

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Query Match	55.0%	Score 1387	DB 1	Length 448
Best Local Similarity	55.5%	Pred. No. 1.1e-134		
Matches 246	Conservative 73	Mismatches 122	Indels 2	Gaps 2

Qy	2	RMI\$SEI\$R\$H\$A\$S\$A\$D\$U\$M\$T\$S\$G\$D\$Y\$U\$D\$T\$P\$M\$P\$H\$P\$G\$D\$L\$P\$L\$T\$A\$G\$O\$D\$A\$P\$A\$A\$C\$H\$P\$R	80
Dd	7	K\$T\$S\$B\$E\$L\$K\$H\$D\$K\$P\$G\$D\$M\$I\$S\$T\$O\$G\$K\$A\$Y\$D\$V\$S\$D\$M\$K\$D\$H\$P\$G\$S\$P\$F\$K\$S\$A\$G\$O\$E\$V\$T\$D\$A\$V\$A\$H\$P\$R\$A	66
Qy	81	S\$A\$P\$P\$L\$R\$P\$P\$V\$G-\$R\$S\$D\$Y\$A\$V\$S\$P\$A\$S\$A\$D\$Y\$R\$R\$L\$A\$Q\$U\$S\$A\$G\$L\$F\$E\$R\$V\$G\$P\$T\$P\$K\$V\$O\$L\$M\$A\$V\$L\$F\$Y\$A	139
Dd	67	S\$T\$M\$K\$N\$D\$K\$F\$F\$T\$G\$Y\$U\$L\$K\$D\$Y\$S\$E\$V\$S\$K\$D\$Y\$K\$R\$L\$V\$E\$F\$K\$M\$G\$L\$Y\$K\$K\$H\$M\$E\$A\$T\$C\$F\$I\$A\$M\$L\$F\$A\$M	126
Qy	140	A\$T\$V\$L\$M\$L\$C\$A\$S\$A\$M\$H\$M\$L\$A\$G\$L\$G\$F\$P\$W\$T\$O\$S\$G\$M\$W\$C\$H\$S\$G\$H\$R\$I\$G\$H\$F\$V\$L\$D\$R\$V\$O\$V\$U\$S\$G\$N\$C\$L\$T\$G	139
Dd	127	S\$V\$G\$V\$L\$F\$C\$B\$G\$V\$L\$V\$H\$L\$P\$S\$G\$C\$L\$M\$G\$P\$M\$T\$O\$S\$G\$M\$I\$G\$H\$D\$G\$H\$M\$V\$S\$D\$S\$R\$L\$N\$F\$M\$K\$I\$F\$A\$N\$C\$L\$S\$G	166
Qy	200	I\$S\$T\$A\$M\$K\$C\$H\$N\$H\$T\$H\$L\$A\$C\$N\$S\$L\$D\$H\$D\$P\$L\$O\$M\$P\$L\$F\$A\$V\$S\$P\$K\$L\$F\$G\$N\$I\$M\$S\$Y\$F\$Y\$O\$R\$T\$L\$A\$P\$D\$A\$S\$K\$F\$	259
Dd	187	I\$S\$G\$M\$K\$M\$H\$N\$H\$A\$H\$L\$A\$C\$N\$S\$L\$E\$V\$D\$P\$D\$Q\$Y\$I\$P\$L\$V\$V\$S\$K\$F\$G\$S\$L\$T\$S\$H\$F\$E\$K\$R\$L\$T\$P\$D\$S\$L\$R\$F\$E	246
Qy	260	I\$S\$O\$H\$T\$F\$P\$W\$C\$I\$A\$R\$I\$N\$L\$A\$O\$A\$S\$L\$F\$V\$L\$T\$E\$K\$R\$V\$O\$R\$L\$E\$I\$G\$A\$V\$T\$P\$M\$A\$Y\$P\$L\$V\$A\$S\$L\$P\$W\$	319
Dd	247	V\$S\$O\$H\$T\$F\$P\$P\$I\$C\$M\$A\$L\$N\$M\$Y\$O\$S\$L\$I\$M\$L\$T\$K\$R\$V\$S\$Y\$R\$A\$O\$E\$L\$G\$C\$V\$F\$S\$I\$W\$P\$L\$V\$A\$S\$C\$P\$W\$	306
Qy	320	M\$E\$V\$A\$F\$L\$F\$S\$T\$C\$G\$I\$O\$H\$O\$F\$C\$L\$N\$H\$F\$S\$S\$D\$V\$V\$G\$P\$K\$G\$M\$D\$F\$E\$K\$O\$T\$A\$G\$T\$L\$D\$L\$C\$S\$P\$M\$D\$M\$F\$	379
Dd	307	G\$E\$I\$M\$V\$A\$S\$L\$S\$T\$G\$M\$Q\$Y\$O\$F\$S\$L\$N\$F\$S\$S\$Y\$V\$G\$K\$E\$K\$G\$N\$M\$E\$K\$O\$T\$D\$G\$L\$D\$S\$C\$P\$M\$D\$M\$F\$	366
Qy	380	H\$G\$L\$O\$F\$O\$I\$E\$H\$H\$L\$P\$R\$L\$P\$C\$H\$K\$R\$K\$V\$A\$P\$A\$V\$D\$L\$C\$K\$G\$L\$T\$Y\$S\$A\$T\$T\$G\$A\$N\$V\$L\$T\$W\$K\$L\$R\$A\$A\$L\$	439
Dd	367	H\$G\$S\$O\$F\$O\$I\$E\$H\$H\$L\$P\$K\$M\$P\$C\$N\$L\$R\$K\$I\$S\$P\$Y\$U\$E\$L\$C\$K\$G\$H\$N\$L\$P\$Y\$N\$A\$S\$K\$A\$N\$E\$M\$T\$L\$R\$L\$R\$M\$T\$A\$L\$	426
Qy	440	Q\$A\$R\$T\$A\$T\$S\$G\$A\$P\$K\$V\$L\$W\$E\$A\$N\$T\$H\$G\$462	
Dd	427	Q\$A\$R\$D\$I\$T\$K-\$P\$L\$P\$K\$V\$L\$W\$E\$A\$L\$H\$T\$H\$G448	

RESULT 3
 US-08-934-254-5
 Sequence 5, Application US/08934254
 Patent No. 6355861
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,254
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 839821YXWVU

TELECOMMUNICATION INFORMATION
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-934-254-5

Query Match	55.0%	Score 1387	DB 4:	Length 448
Best Local Similarity	55.5%	Pred. No. 1.1e-134		
Matches 246, Conservative	73	Mismatches 122	Indels 2	Gaps 2

Qy	21	RMSSSELEBAHSAADLMISISGVDYDTPLYPHHGGDLPLTLTGAODTADPAAYHP	80
Db	7	KYTSDELKNHDKPGLMISTIGKAYVDSDWKHGGSPFLKSLAGEYTDFAVAFHPA	66
Qy	81	SARPLLRPFVG-RUSDYAVSPASADYRRLLAQSSAGLFEFVGPTPKVOLVIMAVLFYA	139
Db	67	STWKNDKEFFGTGYLTKDYSEVSVDKRYLFEFESKMLYDKKHIMPATLCFIAMLFAM	126
Qy	140	ALVLYACASAMHLLAGGLIGFWIISGWSHDSGHHRIIGHVLDLRVYVULSGNLTG	139
Db	127	SVYGVLPFGCVLVHLPSSGCLMGPTLWISGWIIGHDGHMTVSDSLNKKFPIFANCLSG	166
Qy	200	LSIAMWCKNHNTHILACNSLDDPDLOHMPLEFAVSPKLFGNIWSFYQRTLAEPASKFF	259
Db	187	ISIGWKMNMHNAHILACNSLEYPDPLQYIPLVYSKRFSGLSLHFPEKRLTFPSSRFF	246
Qy	260	ISVQHTFPFWMCIAFINLLAOSALFVLTREKRVORLELTAGVATFWMAIPLVASLPPW	319
Db	247	VSVQHTFPFIMCAALNMYQSLIMLTLKRVVSRFOELGCVLFSIWPPLVSCCLPNW	306
Qy	320	MEVAVLVLSFTICGLOHVQFCILNHFSSDYYVGPFGKDMFEKOTDAGTLIDCSPPMDWF	379
Db	307	GERIMVIVLSLSTYGTGQVQVPSLNFSSVYVGRKXGNMWEKOTDGLTIDSCPPMDWF	366
Qy	380	HGGLFOIEHHLLFPRLLPRCHLRKVAIPAVRDLCKHGILTYSAATFWGANVLTWKTLRAAL	439
Db	367	HGGSQCFQIEHHLLFPKMPRCNLKRIISPYVETLCKGNILPYNVAASFKNEMWTLRTLRTAL	426
Qy	440	QARTATSGAPKNIVLEAVNTHG 462	
Db	427	QARDITK-PLPKNLWEALHTHG 448	

RESULT 4
US-08-934-254-27
Sequence 27, Application US/08934254
Patent No. 635861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentm Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:

```

1 CLASSIFICATION: 435
2
3 ATTORNEY/AGENT INFORMATION:
4
5 NAME: Presser, Leopold
6
7 REGISTRATION NUMBER: 19, 827
8
9 REFERENCE/DOCKET NUMBER: 8383ZXWVU
10
11 TELECOMMUNICATION INFORMATION:
12
13 TELEPHONE: (516) 742-4343
14
15 TELEFAX: (516) 742-4366
16
17 TELEEX: 230 901 SANS UR
18
19 INFORMATION FOR SEQ. ID NO: 27:
20
21 SEQUENCE CHARACTERISTICS:
22
23 LENGTH: 452 amino acids
24
25 TYPE: amino acid
26
27 TOPOLOGY: linear
28
29 MOLECULE TYPE: protein
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Query Match	54.7%	Score 1379;	DB 4;	Length 452;
Best Local Similarity	56.7%	Pred. No. 7	7e-134;	
Matches 253;	Conservative	64;	Mismatches 125;	Indels 4;
				Gaps 3

QY	21	RMSSEKELFAHSAADLWISTSGDYVDTPLYPHNPGDPLRLTLACQADTDAFAAHP	80
Db	7	KYTADBLRNHKSODLWISTQKYYDSCRAAHHPGEVPLSLAQQDTDAFIAHPG	66
QY	81	SARELLRREFVC--RLSDYAVSPASADYRLLAQLSSAGLFERVGPPLPKQVLMALFY	138
Db	67	TAMRLDLPLFTYYUKDFEVSLSKDYRRLLINEMSSGIFPEKKGHIIIMTFPGVAWMA	126
QY	139	ALLYLALACASAMALLAGLIGPWYIOSGMMGHDGHNRLTGHPLVDRVVOYLSGCLT	198
Db	127	ALYGVLSSESQVHMLGALGLIMTDAAGVHDSGYOVMPPRGYRNRTIQLAGIILT	186
QY	199	GSIAWKKCNHTHHIACNSLDHDPDLOHMLFAVSPKLFGNISYFYORTLAFDAASK	258
Db	187	GSIAWKKWTHNAHHIACNSLDYDPDLOHIEVPAVSTRFLFNSITSVFYGRVLKDEVARF	246
QY	259	FISYQHTWTFPIMCLARINLQAOSLFLYTEKRPORLLEAGVATWAWPRLVSLPN	318
Db	247	LVSQHTWTFYPMIGRVNLPLOTFLLLTLTRDVPDRLLIMGLAVMTWFLFVSLPN	306
QY	319	WMEVAVFLVFSTICIGIOHVOFCNLHFSDDVYVPPKNDWFEKQTAGTLDILCSPPMDN	378
Db	307	WPERREFVLISFAVNAIQHVOFTLNHFSGDLYYVERPPKDNWFBEQTKGTIDITCPRMDN	366
QY	379	FHGGLOFQLEHNLPRLLPRCHLRKVAVARDLCKKHGLTYSATFW--GANVLFWKTLRAA	437
Db	367	FFGGLOFQLEHNLPRLLPRGOLRKIAPLARDLCKKHGIMPRASFEGMDADVIRTILRDA	426
QY	438	ALQARTATSGAPKULVW--BAVNTHG 462	
Db	427	AVQARDLNSAPCPKULGTGEAYNTHG 452	

RESULT 5
 US-08-433-610-5
 : Sequence 5, Application US/08833610
 : Patent No. 5972664
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: KNOTZON, DEBORAH
 : APPLICANT: MURKERJI, PRADIP
 : APPLICANT: HUANG, YUNG-SHENG
 : APPLICANT: THURMOND, JENNIFER
 : APPLICANT: CHAUDHARY, SUNITA
 :
 : TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 : OF TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 :
 : NUMBER OF SEQUENCES: 12
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: RAE-VENTNER LAW GROUP, P. C.
 : STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 : CITY: PALO ALTO
 : STATE: CALIFORNIA
 : COUNTRY: USA

```

1      ZIP: 94306
2      COMPUTER READABLE FORM:
3      MEDIUM TYPE: Floppy disk
4      COMPUTER: IBM PC compatible
5      OPERATING SYSTEM: PC-DOS/MS-DOS
6      SOFTWARE: PatentIn Release #1.0, Version #1.30
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/08/833,610
9      FILING DATE: 11-APR-1997
10     CLASSIFICATION: 435
11     ATTORNEY/AGENT INFORMATION:
12     NAME: RAE-VENTER, BARBARA
13     REGISTRATION NUMBER: 32,750
14     REFERENCE/DOCKET NUMBER: CGNE.123.00US
15     TELECOMMUNICATION INFORMATION:
16     TELEPHONE: (650)328-4400
17     TELEFAX: (650)328-4477
18     TELEX: N/A
19     INFORMATION FOR SEQ ID NO: 5:
20     SEQUENCE CHARACTERISTICS:
21     LENGTH: 446 amino acids
22     TYPE: amino acid
23     STRANDEDNESS: not relevant
24     TOPOLOGY: linear
25     MOLECULE TYPE: peptide
26     OS-08-833-610-5

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	Query Match	Similarity	Score	DB	Length
	Best Local	55.3%	Pred. No. 6.4e-133		446
	Matches	244	Conservative	73	Mismatches 122
				Indels	2
				Gaps	2
QY	21	RMISSEKLRAHASADMLWISISGDVYDTPWLPHHPGDLPLTLTGADATDAFAAYHP	80		
DB	7	KYISDELKNDKDKDGLWISIQKXAYDSDWVKHPGSPFLKSLAGQEVTDFAFAHPDA	66		
QY	81	SARPLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFEFVGFTPKVQLVMAVLEYA	139		
DB	67	STWNLKDFPGYYLKDYVSEVSKVYRKLVFEFSKMLYDKKHIMEATLCEFIIMLEFAM	126		
QY	140	ALYVLACASAMAHLLAGGLIGFWIISGMMGHDSGHRIRGHVPVLDBVNOVLSGNCITG	199		
DB	127	SVYVLECEGVYVHLPSCCLMGFLWISGMIGHDGHWVSDSLNNFMGIFAAKCLSG	186		
QY	200	LSIAWMKCNHTNHHIACNSLDHDPDLQHPLEFVSPKLEGNISYFYORTLAFDAASKFF	259		
DB	187	ISIGMMKNNAHHIACNSLEYPDLQYIPFLVYSSKFGSLSHFEYKRLTLPDLSKFF	246		
QY	260	ISYCHMTFFYPMCLARINLLAQSALFVLTKEKVPORLEIAGVATFMAWYPLLVASLEPNW	319		
DB	247	VSYCHMTFFYPMCLARINLVYQSILMLTLTKENVSYRAOELLGCVLFSIWPVLVSLCPENW	306		
QY	320	WERVAFPLFSTGIGIOHVQFCNLNHFSSDYYVGPKNDFWEKOTAGTLIDLCSPMDMF	379		
DB	307	GERIMFYIASLSTVGMOQVPSLNHFSSVYVGKPKGNWWEKQDGLDISCPMDMF	366		
QY	380	HGGHGFQIEHLLFPLRPRCHLRKYAPARADCKKHGLTYSATFEGANVLTWTKTLRAAAL	439		
DB	367	HGGHGFQIEHLLFPRMPCRNLRKISPLYIETCKKHNLFPYNAFSEKAMEMTLRTLRNAL	426		
QY	440	QARTATSGAGAPXULVWEAVNT	460		
DB	427	QARDITK-PLPKNLVWEALHT	446		

1 APPLICANT: CHAUDHARY, SUNITA
2 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
3 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
4 NUMBER OF SEQUENCES: 26
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
7 STREET: 2001 FERRY BUILDING
8 CITY: SAN FRANCISCO
9 STATE: CA
10 COUNTRY: USA
11 ZIP: 94111
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: WORDPERFECT 5.1
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/834,033A
19 FILING DATE: 11-APR-1997
20 CLASSIFICATION: 800
21 ATTORNEY/AGENT INFORMATION:
22 NAME: WARD, MICHAEL R.
23 REGISTRATION NUMBER: 38,651
24 REFERENCE/DOCKET NUMBER: CGAB-300. USA
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (415) 433-4150
27 TELEFAX: (415) 433-8716
28 TELETYPE: N/A
29 INFORMATION FOR SEQ ID NO: 15:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 446 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: not relevant
34 TOPOLOGY: linear
35 MOLECULE TYPE: peptide
36 OS-08-834-033A-15

[illegible]

Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-7

Query Match 34.9%; Score 881; DB 3; Length 252;
Best Local Similarity 59.6%; Pred. No. 8.8e-83;
Matches 149; Conservative 39; Mismatches 62; Indels 0; Gaps 0;

QY 141 LYLVLACASAMHLLAGLIGFWIWSGMMGHDGSHHRTGHPVLDREVVOVLSGNCITGL 200
DB 3 LYGVLACTSVFAHQIAAALLGLMIQSAVIGHDSGHVYVMSNKSYNRFAQLLSGNCITGL 62

QY 201 SIAMWKNHNTHTIACNSLDHDPDLOHMPPLFVSPKLFQINISYFYORTLAFDAASKFPI 260
DB 63 SIAMWKNHNTHTIACNSLDHDPDLOHMPPLFVSPKLFQINISYFYORTLAFDAASKFPI 122

QY 261 SYOHWTFYPMCIARINLLAQSALFVLTREKVPORLEIAGVATFWAWYPLVASLPMNW 320
DB 123 SYOHWTFYPMCIARINLLAQSALFVLTREKVPORLEIAGVATFWAWYPLVASLPMNW 182

QY 321 ERVAFVLFSTTCIGIOHVOPLCNHFSDDYVGPCKNDWPEKOTAGTLDLCSPPMDWPH 380
DB 183 ERVAFVLFSTTCIGIOHVOPLCNHFSDDYVGPCKNDWPEKOTAGTLDLCSPPMDWPH 242

QY 381 GGILOFOIEHH 390
DB 243 GGILOFOIEHH 252

RESULT 10
US-09-363-526-7
Sequence 7, Application US/09363526
Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-7

Query Match 34.9%; Score 881; DB 4; Length 252;
Best Local Similarity 59.6%; Pred. No. 8.8e-83;
Matches 149; Conservative 39; Mismatches 62; Indels 0; Gaps 0;

QY 141 LYLVLACASAMHLLAGLIGFWIWSGMMGHDGSHHRTGHPVLDREVVOVLSGNCITGL 200
DB 3 LYGVLACTSVFAHQIAAALLGLMIQSAVIGHDSGHVYVMSNKSYNRFAQLLSGNCITGL 62

QY 201 SIAMWKNHNTHTIACNSLDHDPDLOHMPPLFVSPKLFQINISYFYORTLAFDAASKFPI 260
DB 63 SIAMWKNHNTHTIACNSLDHDPDLOHMPPLFVSPKLFQINISYFYORTLAFDAASKFPI 122

QY 261 SYOHWTFYPMCIARINLLAQSALFVLTREKVPORLEIAGVATFWAWYPLVASLPMNW 320
DB 123 SYOHWTFYPMCIARINLLAQSALFVLTREKVPORLEIAGVATFWAWYPLVASLPMNW 182

QY 321 ERVAFVLFSTTCIGIOHVOPLCNHFSDDYVGPCKNDWPEKOTAGTLDLCSPPMDWPH 380
DB 183 ERVAFVLFSTTCIGIOHVOPLCNHFSDDYVGPCKNDWPEKOTAGTLDLCSPPMDWPH 242

QY 381 GGILOFOIEHH 390
DB 243 GGILOFOIEHH 252

RESULT 11
US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,655
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.124.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-2

Query Match 20.7%; Score 523; DB 2; Length 457;
 Best Local Similarity 30.2%; Pred. No. 2e-45;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRLMISKEL-----RAHASADLMISGDVYDTPWLRPHNPGDLPRLTL 65
 2 AARPSTRTTRAEVLAELNBSGKDAEAPFLMI-IDNKVYDVRREVPRHPGGSV-ILTH 59
 66 AGODATDAFAAYHPPSARPLRLRRFVGRIS---DYAVSPASADYRRLAQLSSAGLFR 121
 60 VGKDGTDVDTFHPRAAMETLANFYVGDI DESDRDIKNDPFAAEVAKLTLPQSLGYD- 118
 122 VGTPRVQVLMAVLFYA-----ALYVLAC---ASAMHLLAGLIGFWIQS 167
 119 -----SSKAYVAFKVSFNLCTIWLSTVIYAKWGQSTLANVLSAALLGLFWQC 167
 168 GNMGDSGHRITGHPVLDRLVQVLSGNCITGLSIAMWKCNHTHIIACNSLDHDPDLOH 227
 168 GMLADFLHLYQVQDFRFGWDLFGALFGVCGQFSSSMWKDKNTHTHAAPNVGEBDDIOT 227
 228 MFLFAVSP--KLFGNI-----WSYFYQRTLAFDAASKFPISYQHTFYVNCIARI 276
 228 HPLLTSEHALBMFSDVPDEELTRMW-----SRFMVNLQWTWFFPILSFAL 274
 277 NLLAGSALFVL-----TEKRVQRLLEIAGVATFWAMY-DLVAASLPMNMMERVAFVL 327
 275 SWLQSLILFLPVGQAKHKSAGARVPISTVQLSLAMNMTWYLAITWELFIKDIPVNLVYFL 334
 328 FSTTIGG-IQHVQFCNH-----FSSDYYVYGPCKNDWPEKOTAGTLDILCSMMWPF 381
 335 VSGAVCGNLAIATFSLNHNMGMPVYSKEAV---DMDFPKQIITGRDVHPLGLFANWFTG 390
 382 GLQFOLEHHLFRLPRCHLRKVAFAVADLCKKGLTY 418

DB 391 GLNYQIEHHLFSPMRHNFESKIQPAVETLCKKYNRY 427

RESULT 12
 US-08-834-033A-2
 Sequence 2, Application US/08834033A
 Patent No. 6075183
 GENERAL INFORMATION:
 APPLICANT: KUNTZON, DEBORAH
 APPLICANT: MIKERTI, PRADIP
 APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
 STREET: 2001 FERRY BUILDING
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,033A
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: WARD, MICHAEL R.
 REGISTRATION NUMBER: 38,651
 REFERENCE/DOCKET NUMBER: CGAB-300.USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-033A-2

Query Match 20.7%; Score 523; DB 3; Length 457;
 Best Local Similarity 30.2%; Pred. No. 2e-45;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRLMISKEL-----RAHASADLMISGDVYDTPWLRPHNPGDLPRLTL 65
 2 AARPSTRTTRAEVLAELNBSGKDAEAPFLMI-IDNKVYDVRREVPRHPGGSV-ILTH 59
 66 AGODATDAFAAYHPPSARPLRLRRFVGRIS---DYAVSPASADYRRLAQLSSAGLFR 121
 60 VGKDGTDVDTFHPRAAMETLANFYVGDI DESDRDIKNDPFAAEVAKLTLPQSLGYD- 118
 122 VGTPRVQVLMAVLFYA-----ALYVLAC---ASAMHLLAGLIGFWIQS 167
 119 -----SSKAYVAFKVSFNLCTIWLSTVIYAKWGQSTLANVLSAALLGLFWQC 167
 168 GNMGDSGHRITGHPVLDRLVQVLSGNCITGLSIAMWKCNHTHIIACNSLDHDPDLOH 227
 168 GMLADFLHLYQVQDFRFGWDLFGALFGVCGQFSSSMWKDKNTHTHAAPNVGEBDDIOT 227
 228 MFLFAVSP--KLFGNI-----WSYFYQRTLAFDAASKFPISYQHTFYVNCIARI 276
 228 HPLLTSEHALBMFSDVPDEELTRMW-----SRFMVNLQWTWFFPILSFAL 274


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Oy 27 NILAQSALFVL-----TEKRVPRBLEINGVATPWAAW-PLIVASLPMWERRVAVFL 327
      ||| |||
Db 275 SWCLQSLILEFENGQAHKPSGARVPISLVEQSLSMHMTWTIATIFLEFIKQPVNMLDYFL 334
      ||| |||
Oy 328 FSEFTIGS-IQHVQFCANH-----FSSDGVYVGPCKNDMFBEKQTAGTLDILCSPMMDWFHG 381
      ||| |||
Db 335 VSOAVQGNLTAIFYSLNHNGMFPVLSKEAV----DMDFFTQIITGRDVPGLFANWFTG 390
      ||| |||
Oy 382 GLOFOIEHHLFRLPRCHLRKVAFAVADLCCKGHGLTY 418
      ||| |||
Db 391 GLAVQIEHHLFPSMPRHNSKIQPAVETLCKCKINVRV 427
      ||| |||

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RESULT 13
US-09-363-574-2
; Sequence 2, Application US/09363574

1 APPLICANT: KNOTZON, DEBORAH
 2 APPLICANT: MURKERI, PRADIP
 3 APPLICANT: HUANG, YUNG-SHENG
 4 APPLICANT: THURMOND, JENNIFER
 5 APPLICANT: CHAUDHARY, SUNITA
 6
 7 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 8 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 9
 10 NUMBER OF SEQUENCES: 18
 11
 12 CORRESPONDENCE ADDRESS:

STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574

```

1 CLASSIFICATION:
2 ATTORNEY/AGENT INFORMATION:
3 NAME: WARD, MICHAEL R.
4 REGISTRATION NUMBER: 38,651
5 REFERENCE/DOCKET NUMBER: CGAB-202 USA
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (415) 433-4150
8 TELEFAX: (415) 433-8716
9 TELEX: N/A
10 INFORMATION FOR SEQ ID NO: 2:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 457 amino acids
13 TYPE: amino acid
14 STRANDEDNESS: not relevant
15 TOPOLOGY: linear
16 MOLECULE TYPE: peptide
17
18 OS-09-363-574-2

```

Query Match	20.7%	Score 523	DB 3	Length 457
Best Local Similarity	30.2%	Pred. NO. 2e-45		
Matches 138	Conservative 64	Mismatches 171	Indels 84	Gaps 15

QY 15 AGAGDVRLMISSEKL-----RHASADLMISIGDYDLYPYLHNGGGLRLYLT 65
Db 2 AAAPSRTRRAEVLNAEALNGKKDAEPLMT-IDNKVTDYAEFPVDHGGGV-ILTH 59
QY 66 AGODATDAFAAYHPESARPELRRPFVGRIS-----DYAVSPAADYRLLAQLSSAGFLER 121
Db 60 VGRDGTDFDTFHPPEAAWETLANFYVGQIDSDSDRDIKNDDPAALVRLKRLTFLQSLGYD- 118
QY 122 VGRTPKQVLMAVLFYA-----ALYIVLAC-----ASAAHLLAGGLIGFWIQS 167

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Db      119  -----SSKAYAPKVSFNLCIGSLSTVIAAKMGQSTLANVLSAALLGLFWQC 167
Qy      168  GMMGSGGSHRRITGHPVLDYRVQVYLSGCLTGLSTIAWKKCHNTHNTHACSLDHPDLOH 227
Db      168  GMLAHDFLHHQVPODRFMGDLFGAFLGGVCOGFSSSWVKDGNTHHAAAPVHGDDPIDT 227
Qy      228  MPEAVSP---KLFGNI-----WSFYQRTLAFDAASKFPISYOHTFYPVMIARI 276
Db      228  HPLLTYSBALFMFSDVPDEELTRM-----SRFWLNQTFYFPIISFARL 274
Qy      277  NLLAQSALFVL-----TEKRYQORLLETAGVATFWAW--PLTVASLNNMERAVFL 327
Db      275  SMCLOSILFVLENGCAHKPSGARVDSLVEQSLAMHTWYLAWEFLFDOPVNLVYFL 334
Qy      328  FSEFTIG-IQHVQFCINH-----FSSDYYVGPSPKNDMFEKQTATGIDLILCSFMMDFHG 381
Db      335  VSGAVCGNLLAVFSLNHNQMPVLSKEBAV---DMDFFTQILITGRDVAHGLFAVWFEG 390
Qy      382  GLQFOLEHLLPRLPRCHLRKVAAPVRDLCKKHGILTY 418
Db      391  GLNYQLEHHLFSPMRPNPSKIQPVAETLCKKINRY 427

```

RESULT 14
US-09-363-526-2
; Sequence 2, Application US/09363526

APPLICANT: KUNTZON, DEBORAH
APPLICANT: MURKERTJ, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO

```

1  COUNTRY: USA
2  ZIP: 94111
3
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: Floppy disk
6  COMPUTER: IBM PC compatible
7  OPERATING SYSTEM: PC-DOS/MS-DOS
8  SOFTWARE: Patent Release #1.0, Version #1.30
9  CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/09/363,526

```

CENSITIZATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: WARD, MICHAEL R.
 REGISTRATION NUMBER: 38,651
 REFERENCE/DOCKET NUMBER: CGAB-201 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PS-09-363-526-2

Query Match	20.7%	Score 523	DB 4	Length 457
Best Local Similarity	30.2%	Pred. No. 2e-45		
Matches 138	Conservative 64	Mismatches 17	Indels 84	Gaps 15

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QY 15 AGAGDVMMISSKEL-----RAHASADLWISISGDVYDVTPLPHHGGDLPLTL 65
DB 2 AASPVRTFTFRAVLNNAEALNEGKDAEAPFLMI-IDNKYVDREFFPDHGGSV-ILTH 59
QY 66 AGGDATDAPAAVYPPSARPLRRFFVGRLS---DVAVSPASADYRLLAQLSSAGLFE 121
DB 60 VGKDGIDVDFPTFHPPEAMETLANFVYGDIDESDRDIKNDDFAAEVRRLRTLFGSLGYD- 118
QY 122 VGFTPKVQLVLMVLFYA-----ALYVLAC---ASAMAHLLAGLIGFWWIOS 167
DB 119 -----SSKAYYAFVSVNLCIWSLSTYIVAKWGOTSTLANVLSAALIGLFWQOC 167
QY 168 GWMGHDGSHHRTGHPVLDREVVLVSGNCLTJLSIAMWKCNNHTHHIACNSLDHDPDLOH 227
DB 168 GMLAHDFLHHQVQODRPFWDGLFGAFIAGVCGQFSSSWMKDKNTHHAAPVHEDDIDT 227
QY 228 MPFAVSP---KLFGNI-----WSFYQRTLAEDAAKFEISYQHTFFVWCIA 276
DB 228 HPLLTSSEHALMFSDVPDEBLTRMW-----SRFVVLNQTFWFFPILSFARL 274
QY 277 NLLAQSALFVL-----TEKRVQRLLEIAGVATFWAMY-PLVVASLPMWMEVAFVL 327
DB 275 SWCLOSILFVLNPGQAHKPSGARVPISLVEQLSLAMHMTWYLATMELFTKDPVNMVLVYFL 334
QY 328 FSFTIGG-IQHVQFCLNH-----FSSDVYVGPCKNDWFEKOTAGTLDILCSPPMDWPHG 381
DB 335 VSGAVCGNLLAIVFSLNHNMPVISKEAV----DMDFTKQIITGRDVHPLGLFANWFTG 390
QY 382 GLQFOIEHHLPRLPRCHLRKVAFAVRDLCKKHGLTY 418
DB 391 GLNYQIEHHLPSPMRHNSKIQPAVETLCKKYNVRY 427

RESULT 15
US-09-330-235-18
; Sequence 18, Application US/09330235
; Patent No. 6459018
; GENERAL INFORMATION:
; APPLICANT: Knutson, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
; FILE REFERENCE: MOCO.156.000S
; CURRENT APPLICATION NUMBER: US/09/330.235
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/089,043
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 457
; TYPE: PRF
; ORGANISM: Mortierella alpina
US-09-330-235-18

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Query Match 20.7%; Score 523; DB 4; Length 457;
 Best Local Similarity 30.2%; Pred. No. 2e-45;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

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QY 15 AGAGDVMMISSKEL-----RAHASADLWISISGDVYDVTPLPHHGGDLPLTL 65
DB 2 AASPVRTFTFRAVLNNAEALNEGKDAEAPFLMI-IDNKYVDREFFPDHGGSV-ILTH 59
QY 66 AGGDATDAPAAVYPPSARPLRRFFVGRLS---DVAVSPASADYRLLAQLSSAGLFE 121
DB 60 VGKDGIDVDFPTFHPPEAMETLANFVYGDIDESDRDIKNDDFAAEVRRLRTLFGSLGYD- 118
QY 122 VGFTPKVQLVLMVLFYA-----ALYVLAC---ASAMAHLLAGLIGFWWIOS 167
DB 119 -----SSKAYYAFVSVNLCIWSLSTYIVAKWGOTSTLANVLSAALIGLFWQOC 167
QY 168 GWMGHDGSHHRTGHPVLDREVVLVSGNCLTJLSIAMWKCNNHTHHIACNSLDHDPDLOH 227
DB 168 GMLAHDFLHHQVQODRPFWDGLFGAFIAGVCGQFSSSWMKDKNTHHAAPVHEDDIDT 227

```

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QY 228 MPFAVSP---KLFGNI-----WSFYQRTLAEDAAKFEISYQHTFFVWCIA 276
DB 228 HPLLTSSEHALMFSDVPDEBLTRMW-----SRFVVLNQTFWFFPILSFARL 274
QY 277 NLLAQSALFVL-----TEKRVQRLLEIAGVATFWAMY-PLVVASLPMWMEVAFVL 327
DB 275 SWCLOSILFVLNPGQAHKPSGARVPISLVEQLSLAMHMTWYLATMELFTKDPVNMVLVYFL 334
QY 328 FSFTIGG-IQHVQFCLNH-----FSSDVYVGPCKNDWFEKOTAGTLDILCSPPMDWPHG 381
DB 335 VSGAVCGNLLAIVFSLNHNMPVISKEAV----DMDFTKQIITGRDVHPLGLFANWFTG 390
QY 382 GLQFOIEHHLPRLPRCHLRKVAFAVRDLCKKHGLTY 418
DB 391 GLNYQIEHHLPSPMRHNSKIQPAVETLCKKYNVRY 427

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Search completed: January 1, 2004, 06:38:13
 Job time: 17.251 secs


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Db      59 INLAGOVDTDAFIHFGHTAMKHLKDLFTGYHLKDYQVSDISRHYRKLASEFAKAGMFEK 118
Qy      122 VGPTRVQVLMVLYVLAALYLVLACASMAHLIAGLIGFVWIOSGWMGDSGHHRTG 181
Db      119 KGGVITVSLCFVSLISACVYGVLSGSEFTHMLSGALGLAMWQIAYIGHDGHYQMA 178
Qy      182 HPLADVVVQVLSGNCUTGLSIAMWKNHNTHTIACNSLDHDPDLQMPLEFVSPKIFGNI 241
Db      179 TKGWNNFAGIFGNCITGLSIAMWKNHNTHTIACNSLDVDPDLQHLPLMVLAVSKLFNSI 238
Qy      242 WSYFYORTAFAFASKEFISYQHTWYTPVNCIARINLAQSLFVLTEKRVORLLEIAG 301
Db      239 TSFVYGROLFDFDLAFVSVYQHYLYPIWCVARVNLVYQITILLISKRIIPRGANIIG 298
Qy      302 VAFEMVPLVLSLNMWNRVAVLFEFTICIQVQFCLNHFSSDVYVGPCKNDWPE 361
Db      299 TLIETWTFPLVRLPLWMPERVAVLVSFCVTGIQHIQFTLNHPGSDVYVGPCKNDWPE 358
Qy      362 KOTAGTLDILCSBMDMFHGLQFOIEHHLFPLPRCHLRKVAFAVADLCKKHGLTYSAA 421
Db      359 KOTRGITIDACSSMDMFPGLOFQLEHHLFPLPRCHLRISIPICRELCKTNLPVSL 418
Qy      422 TFGANVLTKTLRAALQARITATSGAPNVLWEAVNTHG 462
Db      419 SFYDANVTTLKTLRTALQARLDTN-PAPONLAMEAFNTHG 458

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RESULT 2

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US-10-340-779A-13
; Sequence 13, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: UK 9727256.1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Borago officinalis
; US-10-340-779A-13

```

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Query Match      55.2%; Score 1392; DB 12; Length 448;
Best Local Similarity 55.8%; Pred. No. 1,4e-127;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

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Qy      21 RMISSEKELRAHASADLMTISISGDVYDVTPMLPHHGGDLPLTLTAGODATDAFAAVNRP 80
Db      7 KYTSDCLKNKHDPGDMISIOGKAYVSDVNDHDPGSGFPLKSLAGQEVTDFAVAFHRA 66
Qy      81 SARPRLRRFFVG-RLSDYAVSPASADYRRLAQLSSAGLFEVGPTRPKVQVLMVAVLFYA 139
Db      67 STWKNDLKFPTGYLKYVSVSEVKDYRKLVFEFSKMGLYDKGHIMFATLCFIAMLFAM 126
Qy      140 ALVLYLACAAMAHLAGLIGFVWIOSGWMGDSGHHRTGHPVLDVRYVQVLSGNCITG 139
Db      127 SVYGVLFCEGVVHLFSGCLMGFLMTIQSGWIGHDAGHYMVVSDSRINKFNGIFRANCLSG 186
Qy      200 LSLAMWKNHNTHTIACNSLDHDPDLQMPLEFVSPKIFGNIYFYORTAFAFASKEF 259

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Db      187 ISIGWKNHNTHTIACNSLBYDPLQYIPLVSSKFFGSLTSHFEKRLTFDSLSRPF 246
Qy      260 ISYQHTWTFVNCIARINLAQSLFVLTEKRVORLLEIAGVAFPMWYPLVLSLPM 319
Db      247 VSYQHTWTFVNCIARINLAQSLFVLTEKRVORLLEIAGVAFPMWYPLVLSLPM 306
Qy      320 WERVAFVLSFTICIQVQFCLNHFSSDVYVGPCKNDWPEKQTAGTLDILCSBMDMF 379
Db      307 GERIMVIALSVTGMQVQFSLNHFSSDVYVGPCKNDWPEKQTAGTLDILCSBMDMF 366
Qy      380 HGLQFOIEHHLFPLPRCHLRKVAFAVADLCKKHGLTYSATFGANVLTKTLRAAL 439
Db      367 HGLQFOIEHHLFPLPRCHLRKVAFAVADLCKKHGLTYSATFGANVLTKTLRAAL 426
Qy      440 QARTNSGAPNVLWEAVNTHG 462
Db      427 QARDITK-PLPNVLWEALHTHG 448

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RESULT 3

```

US-10-029-756-5
; Sequence 5, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE

```

```

; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANG UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-10-029-756-5

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Query Match      55.0%; Score 1387; DB 14; Length 448;
Best Local Similarity 55.5%; Pred. No. 4,2e-127;
Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;

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Qy      21 RMISSEKELRAHASADLMTISISGDVYDVTPMLPHHGGDLPLTLTAGODATDAFAAVNRP 80
Db      7 KYTSDCLKNKHDPGDMISIOGKAYVSDVNDHDPGSGFPLKSLAGQEVTDFAVAFHRA 66
Qy      81 SARPRLRRFFVG-RLSDYAVSPASADYRRLAQLSSAGLFEVGPTRPKVQVLMVAVLFYA 139

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Db      67 STWKNDKFFFTGYLLKDYVSSEVSKDYRKLVFFFSKMGIDYDKGHIMFATLCFIAMLFAM 126
Qy      140 ATLVLVACASAMHLLAGLIGFVWIOSGMGHDGHHRTIGHPVLDVAVVQVLSGCLTG 199
Db      127 SVYGVFCEGVVHLVSGCLMGFLWIOSGWIIGHAGVIVVSDSRINKFGITFAANCLSG 186
Qy      200 LSIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPKLFNGINISYFYORTLAFDASKFP 259
Db      187 ISIGMKNMNAHNAHICNSLEVPDLOYPFLVSSKFFSGLSHYERKLTDSLSRFF 246
Qy      260 ISYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATWAMVPLVLSLPM 319
Db      247 VSYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATWAMVPLVLSLPM 306
Qy      320 MERVAVLVSFTICGLOHVOFCNLHFSDDVYVGPCKGNDWEKOTAGTLDIICSPMMDW 379
Db      307 GERIMFVLASLSTYGMQVQFSLNHFSDDVYVGPCKGNDWEKOTAGTLDIICSPMMDW 366
Qy      380 HGLQLOFQIEHHLFPLPRCHLRKVAAPAVRDLCKKGLTYSATFGANVLTWKTURAAL 439
Db      367 HGSQOQIEHHLFPLPRCHLRKVAAPAVRDLCKKGLTYSATFGANVLTWKTURAAL 426
Qy      440 QARTATSGAPKXUWVAVNTG 462
Db      427 QARDITK-PLPKXUWVAVNTG 448

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RESULT 4

US-10-029-756-27
Sequence 27, Application US/10029756
Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:

ADDRESSER: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza.
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 8383EYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-10-029-756-27

```

Query Match      54.7%; Score 1379; DB 14; Length 452;
Best Local Similarity 56.7%; Pred. No. 2,6e-126;
Matches 253; Conservative 64; Mismatches 125; Indels 4; Gaps 3;
Qy      21 RMISSEKELPAHASADDLWISIGDYDVTWPLPHHFGCLPLITLAGODATDAFAAYHP 80
Db      7 KYTAEDELRRNHSKGLMISIGKYDCSRMAEHPGGEVPLISLAGODVDAFAIYHFG 66
Qy      81 SARPLLRFFVCG-RLSDVAVSPASADYRRLAOLSSAGLFRVGVTPVAVVLAFLV 138
Db      67 TAMRHLDPLFTGYIKDQVESEISKDYRLINEMSRSGIFKKGHHIMTWFGVAVVMA 126
Qy      139 AALVVLACASAMHLLAGLIGFVWIOSGMGHDGHHRTIGHPVLDVAVVQVLSGCLTG 198
Db      127 ATVYGVLSASESVGMHLCALLGLMLQAAVYGHDSGHVQWPTGYNNTITGLAGNITL 186
Qy      199 GLSIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPKLFNGINISYFYORTLAFDASKF 258
Db      187 GISIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPKLFNGINISYFYORTLAFDASKF 246
Qy      259 FTSYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATWAMVPLVLSLPM 318
Db      247 LVSYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATWAMVPLVLSLPM 306
Qy      319 MERVAVLVSFTICGLOHVOFCNLHFSDDVYVGPCKGNDWEKOTAGTLDIICSPMMDW 378
Db      307 WPERRGFVLISFAVTAIGHVQFTLNHFSDDVYVGPCKGNDWEKOTAGTLDIICSPMMDW 366
Qy      379 FHGLOFQIEHHLFPLPRCHLRKVAAPAVRDLCKKGLTYSATFGANVLTWKTURAAL 437
Db      367 FHGLOFQIEHHLFPLPRCHLRKVAAPAVRDLCKKGLTYSATFGANVLTWKTURAAL 426
Qy      438 ALQARTATSGAPKXUWVAVNTG 462
Db      427 AVQARDLNSAPCPKXUWVAVNTG 452

```

RESULT 5

US-09-967-477B-8
Sequence 8, Application US/09967477B
Patent No. US20020156254A1

GENERAL INFORMATION:

APPLICANT: Xiao Qiu
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF

FILE REFERENCE: BNZ-001
CURRENT APPLICATION NUMBER: US/09/967,477B

PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8
LENGTH: 459
TYPE: PRT

ORGANISM: Thraustochytrium sp.
US-09-967-477B-8

Query Match 24.3%; Score 612; DB 10; Length 459;
Best Local Similarity 32.8%; Pred. No. 3.5e-51;
Matches 154; Conservative 74; Mismatches 157; Indels 84; Gaps 15;

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Qy      5 VDAMPAPGDAAGDVRMISSEKELPAHASADDLWISIGDYDVTWPLPHHFGCLPLIT 64
Db      2 VDLKP-----GVKRLVSKWEIKREHATPAWVIHHKVTIDISKV-DSHFGGSV-MLT 51
Qy      65 LAGODATDAFAAYHPSPARPLLRFFVGLSDYAVS-----PAS-----AD 105
Db      52 QAGEDATDAFAVHFPSALKLEQFYVGVDVETSAEIGCEPASDEBRARERINEFIAS 111

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QY 106 YRRLAQLQSLAGFE-----RGPPEKQVLTMAVLTFY---AALYLVLACASAAHL 154
Db 112 YRRLRVKVMGMGLYDLSALYVAMKLVSTFGIALVSMALCFPNPSFAMTV-----161
QY 155 LAGGLIGFWVIOGMMGHDSGHRIRITGHPVLDRVVQVLSGCLTGLSLAMKCNHTHHI 214
Db 162 -AGVINGLFWQSGMWLAHDFLNNQVCENRTLGNLGLCVGNAWQGSFYWMMKNKNHLLHA 220
QY 215 ACN-----SLDHDPLQHPMLFAVSPKLFNGINISYFYQRTLAFDAASKFISYQHTF 267
Db 221 VPLNLSAKDEGFIGDDEPIDTMLLA-----WSKEMARAFESAHGPFIRINQFLY 271
QY 268 YPWCILARINLQAOSLFLVLT-----KRVQRLLEIAGVATFAMVPLVLASLP---317
Db 272 FPLLLARLSMLWAOSEFFYVTEFGCIPDKVFEDEKAGILVHTWQ---LAIPLYFCN 327
QY 318 -NMNERVAFVLSFTTCG-IQHVQPLNFFSSDYYVVGPPKNDWFEKQTAETDILDSPW 375
Db 328 MSJFEGVAFWLMQOASGILLALVBSIGNGMSYVERETKDPFW-QLOVYTTNRIRASVF 386
QY 376 MDWFHGOLOFOIENHLEPRLPRCHLRKVAVPAVRDCKXGKGLYSAAATPW 424
Db 387 MDWFTGLANTQIDHHLFLVLPVRHNLKPVNVILKSLCKEEDIPFHEBTGW 435

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```

RESULT 6
US-09-769-863-14
: Sequence 14, Application US/09769863
: Publication NO. US20030157144A1
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Mukerji, Pradip
: APPLICANT: Huang, Yung-Sheng
: APPLICANT: Das, Tapas
: APPLICANT: Thurmond, Jennifer
: APPLICANT: Pereira, Suzette B.
: TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
: FILE REFERENCE: 6763.US.O1
: CURRENT APPLICATION NUMBER: US/09/769,863
: CURRENT FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 453
: TYPE: PRT
: ORGANISM: Saprolegnia diclina
US-09-769-863-14

Query Match      22.6%; Score 571; DB 12; Length 453;
Best Local Similarity 31.2%; Pred. No. 3,6e-47;
Matches 138; Conservative 77; Mismatches 163; Indels 64; Gaps 13

QY      23  ISSKELRHASADDWMISIGDYVYVTPWLPHPHFGDLPILTLAQDRTDARAAYHPSPA 82
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      10  ISMATIREHNRQDNAMIVIHKKVYDISAF-EDHPGG-VVMFTQAGEDADDAFAVHPSPA 67
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      83  RPLRRFVFG-----RLSDYAVSPA--ADYRLTAQTSAGLFE----- 120
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      68  LKLEQYVGVGDVOSTAANDVISISBEVKKSGSDFLASTRKALKYKRGCLYSSKLYLY 127
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      121 RVGPTPKQVLYLMAVLFY--AAUYLYLACASAMALLAGLLIGFVMIQSGMWGHDGHN 177
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      128  KCASTLSIALVSAIICLHPDSTAMTVAAV-----ILGFYQCCGWLADHDFLN 176
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      178 RITGHPVLDRVVQVLSGNCITGLSTAMWKCNNTHTIACN-----SLDHPDLOHPL 230
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      177  QVFENHLRGDVLGVVWGNLMQGFVSQVMKXKNTHTIALIPNLATBEIAFHGPDIDTMPI 236
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      231 FAVSPKLFNGNIISYFYORTLAFDASKFEFISYQHTWTFVWVCIGARINLLAQALFVL-- 287
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      237  LA-----WSLGMAGHAUDSPVGLFFPMRYQATVLYPIFLPAISWVIGSAMTAFTYV 287
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      288  ---TEKRPORLLEIAGVATFWAV-YPLLVASLBNMERVAFLVFSPTICGI-OHVQFC 341
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 288 GPGGIFDQVQPIFLERAGLLLYGNGNLGLVYAANNLSLQAAFLFVSQASCGFLFAMVPS 347

QY 342 LNHSSDYVYGPPKNDMFEKQTAGTLDILCSPMWDHFGCIQFOIEHHLLFRLPLPCHLR 401

Db 348 VGHNGMEVFDDXSKPDFV-KLQVLSTRVNTSLMIDWFGLNGIYQIDHLLFPMVRHNLPL 406

QY 402 KVAARVRLDCKKKGGLYSATF 423

Db 407 ALNLVLKSLCKQYDLPYHETGF 428

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RESULT 7
US-10-054-534B-14
? Sequence 14, Application US/10054534B
? Publication No. US20030167525A1
? GENERAL INFORMATION:
? APPLICANT: Abbott Laboratories
? APPLICANT: Mukerji, Pradiip
? APPLICANT: Huang, Yung-Sheng
? APPLICANT: Dae, Tapas
? APPLICANT: Thurmond, Jennifer M.
? APPLICANT: Pereira, Suzette L.
? TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
? FILE REFERENCE: 6763. US. P1
? CURRENT APPLICATION NUMBER: US/10/054.534B
? CURRENT FILING DATE: 2002-01-22
? PRIOR APPLICATION NUMBER: US 09/769,863
? PRIOR FILING DATE: 2001-01-25
? NUMBER OF SEQ ID NOS: 55
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 14
? LENGTH: 453
? TYPE: prt
? ORGANISM: Saprolengia dielina
US-10-054-534B-14

```

Query Match	22.6%	Score 571	DB 12	Length 453
Best Local Similarity	31.2%	Pred. No. 3.6e-47		
Matches 138	Conservative 77	Mismatches 163	Indels 64	Gaps 13
Qy	ISSKRLRPHASADLMWISISGDVVDVPMLEPHREGDPLFLLTLGADPTDAFAAHPPSA	82		
Db	10 ISMTATREHNRQDNAMIVIHKKVLDISAF-EDHFGG-VVMFTQAGEBATDAFAVHPESA	67		
Qy	83 RPLRRPFVGG-----RLSDYAVSPAS--ADYRLLAQLSSAGLE-----	120		
Db	68 LKLEQYVGGVDVDSTAAVDTSIDDEVKSGSDPLASRYKRLREVKRGVLDSSKLYLY	127		
Qy	121 RVGRTPKVQLVLMVLF--AALYLVLACASAMAHLLAGLIGFWAQSGMGHDSHH	177		
Db	128 KCASTLSIALVSAALICLHFDSTAMVMAAV-----ILGLFYQCCGMLAHDFLHH	176		
Qy	178 RITGHPIVLDRAVVOYLSGNCCLTGLSIAMWKKGNHTHTIACN-----SLDHDPDLQHPPL	230		
Db	177 QVFENHLEFGDVLGVGAVGNLMQGSFVQWKKGNKGNHTHTHALPMLDATTRELAFHGDPRDITMPFI	236		
Qy	231 FAVSPKLFGNIWISFYORTLTFADSAKFFPISYQHTFEPVWCICARINMLLAQSAFLV---	287		
Db	237 LA-----WSLKMQHADVDSVGLGFEMRYQVAVLVEPILLFPRISAVTISQAMVAFVNV	287		
Qy	288 ---TEKKVPRLLEIAGVATFWAM-YPLVLASLPMNMWERYAVLFSFTTIGI-OHVQFC	341		
Db	288 GPGGTFDFKVQPLLEIRAGLLILYYCMNLGLVYAANMSLLQAAAFVFSQASGGLFLAWFS	347		
Qy	342 LNHSSSDVYVPRPKGNDFEKOIAGTDILCSPPMMDWFHGGLOIOEHNLEPRKLPRCLXR	401		
Db	348 VGHNGMEVFEDSKSPDFW-KLQVLSIRAVTSSLIWDFMGGLNTQIDHHLPRMVRHMLP	406		
Qy	402 KVAPARDLCKKGGHGLTSAATF	423		
Db	407 ALANLVKSLCKQYDIPIYHETGF	428		

```

RESULT 8
US-10-431-952-14
; Sequence 14, Application US/10431952
; Publication No. US2003019073A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thummond, Jennifer
; APPLICANT: Perreira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/10/431,952
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/769,863
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match      22.6%; Score 571; DB 12; Length 453;
Best Local Similarity 31.2%; Pred. No. 3.6e-47;
Matches 138; Conservative 77; Mismatches 163; Indels 64; Gaps 13;

QY 23 ISSKELRAHSAADDELISIGDYDVTPLPHHGGDLPLTLAGODATDAFAAYHPRA 82
DB 10 ISWATIREHNRQDNAMIVIHKKYDLSAF-EDHPGG-VVMFTQAGSDATDAFAVHPESA 67
QY 83 RPLRRFFVG-----RLSDYAVSPAS--ADYRLLAQSSAGLFE----- 120
DB 68 LKLEGGYVGDVDQSTAAVDTSTISDEVKKSQSPFIASRYKRLREVRKLGLYDSSKLYLY 127
QY 121 RVGPPKQVLMAVLFY---ALYLVLA CASAMALLAGLIGFWISQGMGHSGHH 177
DB 128 KCASTISIALVSAIICLHPDSTIMVVAV-----ILGLFYQCGWLADHFLHH 176
QY 178 RTGHPVLDRVVQVLSGNCITGLSIAMKCNHTTHIACN-----SLDHPDLQHP 230
DB 177 QVFEHNLFGDLYGVMTGNLMOGSSVQWMAKKNHTTHAIFNLATPEIAFHGDDITMTI 236
QY 231 FAVSPRLFGNINISYFQRTLAADASKFPISYOHMTFYPVMCIARINLAQSAFLVL-- 287
DB 237 LA-----WSLKMAQHAVDSPVGLFFMRVQAYLYPRLIFARISWVLOSAMVAFYNV 287
QY 288 ----TEKRPQRLLETAGVATFWAM--YPLLVASLPMWMERVAFVLFSPITCGI-QHVQFC 341
DB 288 GPGGTFDKQVPLLEFAGLLYYGMNLGYVAAAMSLQAAAFLFVSOASCGFLAMVPS 347
QY 342 LNHFSDDVYVGPFGKNDWFEKQTAGTLDILCSPPMMDPFGLOFOYEHNLFPRLPCHIR 401
DB 348 VGHNGHEVDFDKSKPRPFM-KLQVLASTRANTVSLMIMWFGGLNYQIDHHLFPVPRHNLP 406
QY 402 KVAAPAVRDLCKKGGLTYSATF 423
DB 407 ALNLVAKSLCKQYDIPYHETGF 428

```

```

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4137
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4137

Query Match      22.6%; Score 568.5; DB 12; Length 366;
Best Local Similarity 35.1%; Pred. No. 4.7e-47;
Matches 123; Conservative 63; Mismatches 139; Indels 25; Gaps 9;

QY 106 YRLLAQSSAGLFRVGPTRPVQVLMAVLFYAALYVLACAS----AMA-HLLAGGL 160
DB 7 YRELNERIKAEGLVD-----CNVVAVAIBGFR--YTLIFGCGLLFLKMGVYVSAFCL 57
QY 161 GFVWTQSGMGHDSGHHRTGHPVLDRVVQVLSGNCITGLSIAMKCNHTTHIACNSLD 220
DB 58 GSFHWQLVFTAHADAGHMGIITHFHVDTVGIITADFIGLSIGWMAKKNHTTHIITNSPE 117
QY 221 HBDPLQHPFLVAVSKLFCNINISYFQRTLAADASKFPISYOHMTFYPVMCIARINLA 280
DB 118 HPDIEHLPEFAISRFTNLKSTYYDRWEMEDIFAKFVSLQHLVLYIIMPARNLVLR 177
QY 281 QSAFLVL---TEKRP---QRLLEIAGVATFWAM--YPLLVASLPMWMERVAFVLFSPIT 332
DB 178 LSWELILKQAGAKHGRPAWHRHLELVQVFFCWCYGYGMVYALIDGNMRFYPMISHAV 237
QY 333 CGIQHVQCLNHFS-SDVYVGPFGKNDWFEKQTAGTLDILCSPPMMDPFGLOFOYEHNL 391
DB 238 TSPRLHVLTLSPHASTSDIGPHE--SPQRMILRTTMDVDCPEMLDFFHGGLQFOAIHHL 295
QY 392 FRLRLCHLRKVAAPAVRDLCKKGGLTYSATFWGNVLTWKLTLRAALQA 441
DB 296 YRIRHNRHNRKTYQKLVDPCNDVGIYVALYGFVEGNKHYIGLADAVARA 345

RESULT 10
US-10-278-391-4
; Sequence 4, Application US/10278391
; Publication No. US2003015916A1
; GENERAL INFORMATION:
; APPLICANT: KODCHIK, JOHN J.
; KELLER, BRUCE
; HUANG, YUNG-SHENG
; KIRCHNER, STEPHEN J.
; MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
; PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,391
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: 800

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/087,578
FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-03348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030159164A1 Relevant
TOPOLOGY: No. US20030159164A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-278-391-4

Query Match 20.7%; Score 523; DB 12; Length 457;
Best Local Similarity 30.2%; Pred. No. 1,8e-42;
Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRMISSEKEL-----RAHASADLMISGVDVTPMLPHHGGDLPLTL 65
2 AAAPSVRTTTRAEVLAALNEGKDAEPFLMI-IDNKYDVREVPDPHGGSV-ILTH 59
66 AGODATDAFAAHPSPARPLRRFPVGRLS---DYAVSPASADYRRLAQLSSAGLPER 121
60 VGKDGTDVDTFTPEAAMETLANFYVGDIDESDRDIKNDPFAAEVRKRLTLFQSLGYD- 118
122 VGPTRVQLVLAVALFYA-----ALYVLAC---ASAMAHLLAGGLGFVWIOS 167
119 -----SSKAYAEKVSFNLCITWGLSTVIYAKWGQSTLANVLSAALLGLFWQOC 167
168 GNMGDSGHHRIIGHVLDLVDRVQVLSGNCLTGLSIAMWKCNHTTHIACNSLDHDDLOH 227
168 GMLADHFLHGVQDFRFGWGLDFGAFVGVCGQFSSSWMKDKNTHHAAPVHGEDDIDT 227
228 MFLFAVSP---KLFGNI-----WSYFYQRTLAFDAASKFFISYQHTFYPVMCIARI 276
228 HPLLTSEALHMFSDVPBELTRMW-----SRFWVLNQTFYFPIILSFARL 274
277 NLLAAGALFVL-----TEKRVQRLLEIAGVATFWAMY-PLVVASLPMNMEVAVFL 327
275 SMCLOSILFVLBNQGAHKPSGARVPISLVEQSLAMHMTWYLATMFLFIKDPVNMMLVFL 334
328 FSFTTCG-IQHVQFCLNH-----FSSDYYVVGPRKGDMEFEKOTAGTLDLCSPPMDMFG 381
335 VQAVCGNLALVFLSLNHGMFVISKAEV---DMDFTFKQIITGRDVHFGGLFANWFTG 390
382 GLQFOIEHHLFPLRPCHLRKVAFAVARDLCKKHGLTY 418
391 GLNYQIEHHLFSPMRHNSKIQPAVETLCKKYNRY 427

RESULT 11
US-10-191-513A-11
Sequence 11, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (458) ... (458)
OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-11

Query Match 20.7%; Score 523; DB 15; Length 458;
Best Local Similarity 30.2%; Pred. No. 1,8e-42;
Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRMISSEKEL-----RAHASADLMISGVDVTPMLPHHGGDLPLTL 65
2 AAAPSVRTTTRAEVLAALNEGKDAEPFLMI-IDNKYDVREVPDPHGGSV-ILTH 59
66 AGODATDAFAAHPSPARPLRRFPVGRLS---DYAVSPASADYRRLAQLSSAGLPER 121
60 VGKDGTDVDTFTPEAAMETLANFYVGDIDESDRDIKNDPFAAEVRKRLTLFQSLGYD- 118
122 VGPTRVQLVLAVALFYA-----ALYVLAC---ASAMAHLLAGGLGFVWIOS 167
119 -----SSKAYAEKVSFNLCITWGLSTVIYAKWGQSTLANVLSAALLGLFWQOC 167
168 GNMGDSGHHRIIGHVLDLVDRVQVLSGNCLTGLSIAMWKCNHTTHIACNSLDHDDLOH 227
168 GMLADHFLHGVQDFRFGWGLDFGAFVGVCGQFSSSWMKDKNTHHAAPVHGEDDIDT 227
228 MFLFAVSP---KLFGNI-----WSYFYQRTLAFDAASKFFISYQHTFYPVMCIARI 276
228 HPLLTSEALHMFSDVPBELTRMW-----SRFWVLNQTFYFPIILSFARL 274
277 NLLAAGALFVL-----TEKRVQRLLEIAGVATFWAMY-PLVVASLPMNMEVAVFL 327
275 SMCLOSILFVLBNQGAHKPSGARVPISLVEQSLAMHMTWYLATMFLFIKDPVNMMLVFL 334
328 FSFTTCG-IQHVQFCLNH-----FSSDYYVVGPRKGDMEFEKOTAGTLDLCSPPMDMFG 381
335 VQAVCGNLALVFLSLNHGMFVISKAEV---DMDFTFKQIITGRDVHFGGLFANWFTG 390
382 GLQFOIEHHLFPLRPCHLRKVAFAVARDLCKKHGLTY 418
391 GLNYQIEHHLFSPMRHNSKIQPAVETLCKKYNRY 427

RESULT 12
US-10-191-513A-41
Sequence 41, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11

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; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458) .. (458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41

```

```

Query Match      20.7%; Score 523; DB 15; Length 458;
Best Local Similarity 30.2%; Pred. No. 1.8e-42;
Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

```

```

QY 15 AGAGVRLMSSKEL-----RAHASADLMISIGGVYDTLPHLPHPGGDLPLTL 65
DB 2 AAPSRTPTTAEVLAALNKGKDAEAPFLMI-IDNVAVDVREFVDPHGGSV-ILTH 59
QY 66 AGODATAFAAHPSPARPLLRFPYGRUS---DYAVSPASADYRRLAQLSSAGLPER 121
DB 60 VKKDGTDFDTHTPEAMETTLANFYGDIDESDRDKNDFAAEVAKLTTLFQSLGYYD- 118
QY 122 VGPTKVLVLMAVLFLY-----ALYVLAC---ASAMAILLAGLIGFWIQS 167
DB 119 -----SSKAYAFKVSFNLCIMGLSTVIYAKMGOTSTLANVLSAALLGLFWQC 167
QY 168 GMMGDSGHRITGHPVLDLVVQVLSGNCITGLSIAMWKKNHTTHIACNSLDHDPDLOH 227
DB 168 GMLADHFLHQVFODRFMGDLFGAFLGVCGFSSSSMKDKINTTHAAENVHGEDDIDT 227
QY 228 MFLFVSP---KLFGNI-----WSYVQRTLAADASKFPISQHTFFPWCIAPI 276
DB 228 HBLTWSEHALMFSDVPDEELTRM-----SRFVNLQTFPFPILISFAL 274
QY 277 NLLAASALEVL-----TEKRVQRLIEIAGVATFAMY--PLVASLPNMWERAFLV 327
DB 275 SWCLOSLFLVLPNGAHRKSGARVPSISLVEQSLAMHTMYLATMELFKDVNMLVYTL 334
QY 328 PSFTTCG-IQHVQCLNH-----FSSDYYVGPCKGDMFEKQTAGTLDLCSPMWDFHG 381
DB 335 VQAACGMLAIVFSINHGMPVISKEEAV---DMDFPTKQIICRDVHPGLFANWFTG 390
QY 382 GIQFQIEHHLFRLPRCHLRKVAAPVRDLCCKHGGLY 418
DB 391 GLNYQIEHHLFSPMPRHNSKIQPAVETLCKKYNRY 427

```

```

RESULT 13
US-10-340-779A-20
; Sequence 20, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Jonathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 443

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; TYPE: PRT
; ORGANISM: C. elegans
US-10-340-779A-20

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```

Query Match      18.1%; Score 455.5; DB 12; Length 443;
Best Local Similarity 29.0%; Pred. No. 7.2e-36;
Matches 134; Conservative 70; Mismatches 173; Indels 85; Gaps 18;

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QY 35 DDLWISIGDYYDVTPWLPNHPGGLPLTLAAGDADTAFAAHPSPAR-----PLLRPF 89
DB 15 DKKMLYLSBEL-----VKGPQGAN-IBQYNSDATIHIFAHFHGSSQAYQDLDKGH 67
QY 90 -----FVGR-----LSDYAVSPAS---ADYRRLAQLSSAG-----L 118
DB 68 GEHDFLEKQLEKRLDKVDINSAIDVVAQCKRVSESEKRLQKLDHGGMLKANETVYL 127
QY 119 FERVGPTKVLVLMAVLFLY-----YAAVLVLACASAMAILLAGLIGFWIQSGMNGDSG 175
DB 128 FVAIS-----TLISAFAPVLYQLGMYITSAC-----LLALAMQCFGMLTHERC 171
QY 176 HHRITGHPVLDLVVQVLSGNCITGLSIAMWKKNHTTHIACNSLDHDPDLOHMPFVSP 235
DB 172 HQQPKNRPPLNDTISLFGNPLQGFSSRDWKKDKHTTHAATVNIHDDGIDILAPLPAFI 231
QY 236 KLFGNIWSYVQRTLAAPDAASKFPISYOHWPFPWCIAPIMLAQSALFVLTEKRVPR 295
DB 232 ---GDLCKY---KAFKALIKVYQHLVYTTAMLPHLRPSWTQSQVQWVKENOMEYK 284
QY 286 LL-----EIAGVATFAMYPPLVLVASLPNMWERAFLVPSFTTCG-IQHVQCLNHFS 347
DB 285 VQGRNAFWEQATIVGHMAMVVFQFLPLTPRLVAVFYISQGGGLLAAHV-VTFNHNVS 343
QY 348 DTVVPPRG---NDMFEKQTAGTLDLCSPMWDMHGGIQFQIEHHLFRLPRCHLRKA 404
DB 344 DKY--PANSRLNNPALQIILTRNMTSPFIDWLMGGIANTQIEHHLFPTWRCMLNACV 401
QY 405 PAVRDLCKKGIGLYTSAATFGANVLTWTLR--AAALQRTA 444
DB 402 KYVKEMCKENLPVLYVDYFDGGMNLQQLKMAHIAQKAA 443

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RESULT 14
US-10-369-493-6108
; Sequence 6108, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6108
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6108

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```

Query Match      18.0%; Score 454.5; DB 12; Length 473;
Best Local Similarity 28.1%; Pred. No. 9.8e-36;
Matches 138; Conservative 71; Mismatches 163; Indels 113; Gaps 20;

```

```

QY 35 DDLWISIGDYYDVTPWLPNHPGGLPLTLAAGDADTAFAAHPSPAR-----PLLRPF 89
DB 15 DKKMLYLSBEL-----VKGPQGANVIBQYISPLANKNIETRRGITTRGSSNALDILVY 68

```

QY 68 --ODATDAFAAHPPEAR-----PLRRF-----FVGR-----LSDYAVSPAS 103
 DB 69 RNSDATHIFPAFEGSSQAYKQDLKKGHEDEPLEKQLEKRLDKVDIVASVDYVAQ 128
 QY 104 -----ADYRRLAQLSSAG-----LFEVGPFPKVOVLMAVLF---YAALYVLA 146
 DB 129 EKKVSEFEBKLARKLHDDGIMKANETVFLPKAIS-----TLSIMAFAYLYQYIGWYITSA 183
 QY 147 CASAMWHLAAGLIGFVWIOSGMWGHDSCHNRTGHPVLDYRVVOVLSGNCITGLSIAMWK 206
 DB 184 C-----LALAMQOPGWLTHEFCHQOPKRNPLNDTISLFGNGLQSPSHDMWK 232
 QY 207 CNHNTHHIACNSLDHPDLOHMPLEFAVSPFLFGNIMSYFYQRTLAFDAASKFEISYQHW 266
 DB 233 DKNTHTHAATNVVDHGDIDLALFAFIP---GDLCY---KASPEKALIKVPIQHLX 285
 QY 267 FVFWCIRATINLAQSLFVLTERRVQRL-----ELGVATFWAMVPLVASLPMW 320
 DB 286 FTMLPMLRFSWTSQSVQWFKENOMEYKYORNAFMEQATIVGHMAWVYQULPTWP 345
 QY 321 ERVAFVLFSTIG--IGHVQFLNHFSSDYVYGPWK---NDMEKQTAGTLDILCSPW 375
 DB 346 LRVAFTIISOMGGGLIAHV-VTFNHSVDKY--PANSRLNPFALQIITTNMTPSPR 402
 QY 376 MDMFHGLOFQIBHHLFPLRCHLRKVAVARDLCKHGLTYSAAATFWGANVLTWKTJR 435
 DB 403 IDLMWGLNVIQIBHHLFPTMPCRLNACMKYVEMCKENNLPLYVDYFPGYAMNIQOLK 462
 QY 436 --AAALQART 444
 DB 463 NMAEHIOAKXA 473

RESULT 15

US-10-262-617-1
 ; Sequence 1, Application US/10262617
 ; Publication No. US2003007747A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
 ; FILE REFERENCE: PF-0494-1 DIV
 ; CURRENT APPLICATION NUMBER: US/10/262,617
 ; PRIOR FILING DATE: 2002-09-30
 ; PRIOR APPLICATION NUMBER: 09/048,888
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CD1
 US-10-262-617-1

Query Match 17.1%; Score 431.5; DB 15; Length 445;
 Best Local Similarity 28.6%; Pred. No. 1.6e-33;
 Matches 129; Conservative 72; Mismatches 199; Indels 51; Gaps 17;

QY 9 PARGDAAAGADVMSKELRAHASADDLWISGVDYDTFWLPHHFGDDLPLTLTAQ 68
 DB 9 PRGGPAPGAPLPTFCWEQIRAHDOEGDKWLVIERRYDISRWAQRHGGSRLLIGHGAE 68
 QY 69 DATDAFAAHP--SARPLRRFFVGRLSDYAVS---PASA---DYRRLAQLSSAGLF 119
 DB 69 DATDAFAAHPQDANFPAKFLQPLILIGLAPESQDGPLNAQVVEDFRALQAADMKLF 128
 QY 120 ERVGPFPKV---QLVLMAVLFYAALYLVACASAWA-HLLAGGLIGFVWIOSGMWGHDS 174

DB 129 D-ASPTFAFLIGHILAMEVLMLLYLL---GPGVPSALAAFIILAIQAQSWCLOHDL 184
 QY 175 GHHRIIGHVLDYRVVOVLSGNCITGLSIAMWKNHNTHHIACNSLDHPDLOHMPLEFAVS 234
 DB 185 GHASITKKSWMNHVAAKFPWGOLKGFSAHMMNFRHGHAKRNIIFHKDDVYVAVF--- 241
 QY 235 PFLFGNIMSYFYQRTLAFDAASKFEISY--QHWTFY---PWCIRATINLAQSLFVLT 288
 DB 242 --LLG-----ESSVEYKKRRRYLPYNOQLYFFLIGPPLTL--VNFVEENLAVML- 289
 QY 289 EKRVPORLLEIGVATFWAMVPLVASLPMWERRAFAVLFSTIGCIQHVQC---LW 344
 DB 290 ---VCMQMDLWMAASFYARF--FLSYLP-FYGVPGVLLFVAVARVLESHMFWMITQMNH 343
 QY 345 FSSDYVYGPWKNDMEKQTAGTLDILCSPMWDMFHGLOFQIBHHLFPLRCHLRKVA 404
 DB 344 IPKE--IGHEKRDWVSSQLAATCNVEBPLFTNWSGHLNFOLEHHLFPRMRYNSRVA 401
 QY 405 PAVRDLCKHGLTYSAAATFWGANVLTWKTJR 435
 DB 402 PLVKSICAHGHSYEVKPFLLTVLVDIVRSK 432

Search completed: January 1, 2004, 06:58:35
 Job time: 89.0127 secs

TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences (1)
 JOURNAL PERS Lett. 542 (1-3), 100-104 (2003)
 MEDLINE 22615586
 PUBMED 12729906
 REFERENCE 2 (bases 1 to 1385)
 AUTHORS Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK
 FEATURES
 source
 1. 1385
 /organism="Primula vitalii"
 /mol_type="mRNA"
 /db_xref="taxon:175103"
 27. 1385
 /note="cytochrome b5 fusion desaturase"
 /product="sphingolipid delta-8 desaturase"
 /codon_start=1
 /protein_id="AAP23035.1"
 /db_xref="GI:30350279"
 /translation="MADPPNPRTSYITSSDLKHNKAGNLWISIHGEVYDVSSWAGLHPGSAPIMLAGHDVTDALAYHPSTARLPLSTNLLQHSVSPSSDYRKLIHNPRIKLPOTKSHHTCTTFAVAVLFPILSYGFCSDSAVHLASGVGVAMIOSGM LGHDSGHYOIMSSRTNRPAOVLSGNCIAGISIAWKMHNAHLACNSLDVDPDIQHMPPFVSSKFPFSGILSRFYDRKLRPDSVSRFLVSYOHMFSPWCLARINLPQSGFML LFSRRKVPDRFOELFGIGVFWVYPLVSLPVMGRIMFVASFRVGTGIQHVQFCIN HPSAEVYGPPEGNDPFEKQTAGTINISCSNMWDPHGLOQIENHLPRLPRSQLR KVSPPVRDCKKINLAPYNTSTPTMANVLTFLKLRNAAIQARDLSNPTPNLWBEAVNT HG"
 BASE COUNT 294 a 392 c 341 g 358 t
 ORIGIN
 Query Match 37.7%; Score 331.8; DB 8; Length 1385;
 Best Local Similarity 65.5%; Pred. No. 1.2e-67;
 Matches 536; Conservative 0; Mismatches 278; Indels 4; Gaps 4;
 4 CCTCCCTCTCTCTCCCGGCTTCTCCACCTCCACCGCTCTTCCGACCAACCGCTCTCGG 63
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 124 GCAAGGCGCACACACCTCCATCTCTCTCTTATTTCTACCTTTTCTCTCTG 183
 361 CCAATCCCAACACTACATGCTGCTGCTGCGCAGTGAAGCTTGTCTCTCAGCC 420
 184 TCTGGCGGCTCTCTCTCTCGACAGCACTTCTGACAGCTTCTCGCTGCAATTGATG 243
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 AY234124
 VERSION
 KEYWORDS
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 ORGANISM
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Asteridae; Ericales; Primulaceae; Primula.
 1 (bases 1 to 1681)
 Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences (1)
 JOURNAL PERS Lett. 542 (1-3), 100-104 (2003)
 MEDLINE 22615586
 PUBMED 12729906
 REFERENCE 2 (bases 1 to 1681)
 AUTHORS Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK
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Best Local Similarity 65.0%; Pred. No. 1.9e-66;
Matches 534; Conservative 0; Mismatches 283; Indels 4; Gaps 4;

QY	1	CGCGCTCCCTCTCTCTCTCCCGCCTTCTCCACCTCCACCGCTTTTCCGACCGACCGCT	60
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Db	384	AGACCAAAATCCACACCAACTGCTTCAAGTGTGCGCAAGTAGTCTTGTCTTCTTCA	443
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Db	444	GCTGTCTGGGGGTCTTTTTCGACGACGACGACGTGGGTGACTTTGGCTACGGCGGGGTCA	503
QY	241	TAGGCTTTCTGTGATTCAGAGCGGCTGATAGGACGACACTCCGCGCAATTACAAGTGA	300
Db	504	TGGGGGTGTCTTGATTCAGAGCGGTTGGCTAGACAGATTCGGGCATTACAGATTGA	563
QY	301	TGCTCAGCGCGCGCCTCAACCGCGCAATTCAATTTCTCTCGGCAACATTCTCGCGGAA	360
Db	564	TGTCTAGAGAGAAAACTAACAGTTCGCGCAGGTTCTTAGCGGAAACCTGCTCGTGGGA	623
QY	361	TCAGCATCGGCTGGGGAGAGTGAACACAAAGCCCAACCAACTTGCATGACACAGCTCG	420
Db	624	TTAGTATTCGCTGTGGAGAGTGAACCAACAGCCCAACACTCTCGCTCTGACACAGCTTGG	683
QY	421	ACTATGACCCCTGATCTCGAGACATGCGGCTTGTGCAATTGCTGTCGCGGTTCTTCAAT	480
Db	684	ATTACGATCCGACCTCCAGCATATAGCCCTTCTGTGCTGCTCTTCCAAAGTTCTTCAAT	743
QY	481	CCATTAACCTCTCATTTNCTATGAGAGAGAGTTNGAGTTGATTNCAATTGCTANGTCTTGA	540
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QY	601	TGCAGACAAATCTGCTATTTGTTTTCGAGAGAAAGTCCAGATAGAGCTTGA-ACATPA	659
Db	864	CTCAGTGGTTATGTGCTTTTCTCGATGAGGAAGTGCCTGATGAGGTTCAAGAGATTT	923
QY	660	TGGGATCTCTGTGTTTGGACTTGGT-TCTCTTTTATGTGCTTGGCTGCCAAATTGGG	718
Db	924	TGGAAATAGGGGTGTTTGGGTTGGTATCCGCTCTTGGTCTTCTTCACTGGG	983
QY	719	CCTGATAGGGGATGTTTGGGCTTGCCTGCTGCTTGTGTTGNCMATCCAGACATTTCA	778
Db	984	-GTGAGAGATTAATGTTTGTGTGCTGACGCTTTTCTG-TTACGGGGAATCCAACTGTGA	1041
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AF031194			
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DEFINITION			
ACCESSION			
VERSION			
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SOURCE			
ORGANISM			
REFERENCE			
1 (bases 1 to 1788)			

AUTHORS	Delhalize, E., Hebb, D. M., Gardner, R. C. and Richards, K. D.
TITLE	Aluminum tolerance in yeast conferred by over-expression of wheat genes
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1788)
AUTHORS	Delhalize, E., Hebb, D. M., Gardner, R. C. and Richards, K. D.
TITLE	Direct Submission
JOURNAL	Submitted (23-OCT-1997) Plant Industry, CSIRO, Canberra, ACT 2601 Australia
FEATURES	Location/Qualifiers

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Query Match	Score	DB	Length
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Matches 543; Conservative 0; Mismatches 335; Indels 4; Gaps 3;

Qy	1	CGGCTCCCTCTCTCCCGGCTTTCAGCTCCAGCTTCCTTCGACACACGGCTC	60
Db	380	CTCTCGTGCGCCGCTCTCCGCGGCTTCTGTGTGGCGGCTACCGACTACATGTC	439
Qy	61	CGCGCGCTCTCTCGACTACCGCAAGCTCTTCTCGACTCTCCGCGCTCAACTCTTCA	120
Db	440	CCCCGCGCTCGGCGAGCTTCGGCGGCTCTCTCGGAGAGCTCTCTCCGCGGCGCTTTCG	499
Qy	121	ACCGCAAGGGCCACACACATTCATCTCTCTCTCCCTTATCTACCCCTTTTCTCTCT	180
Db	500	AGGCGCTCGGCGACACCCCAAGTTCCTGCTGTGTGCAATGTGAGTCTCTTCTGCATCG	559
Qy	181	CTGTCTGCGGCGCTCTCTCTCCGACAGACTTTGTGTCAAGTCTTTCGCTCATTTGA	240
Db	560	CCCTCTACTGCTCTCTCGCTCTCTCAGACACGGGGCCCAATGTTCGCGGCGGCTCA	619
Qy	241	TAGCTTTCTGTGAATTCAGAGCGGCTGATAGCCACAGACTCCGCGCATTAACAAGTGA	300
Db	620	TTGGCTTCACTGTGATTCAGATGGGCTGATTTGGCGCATGACTCGGCGACACCACAAATCA	679
Qy	301	TGCTAGCGCGCGGCGCTCAACCGCGCGAATTTCATGATTTCTCGGGCAACATTCCTCGCGGAA	360
Db	680	CCAGGACACCTTGCCCTTCAACCGCTCTCTGCAAGTGTCTCGGGAACTGCTCAACGGCC	739
Qy	361	TCAGACTGGCTGTGTGAAGTGAACACACACGCCCAACACATTTGATGCAACAGCTCG	420
Db	740	TCGGCATTCGCTGTGTGAAGTTCAACACACACACACACATCTCTCGAACAGCTCG	799
Qy	421	ACTATGACCTGATCTGACGACACACCGGCTTTGCAAGTTTGTGCGGCTTCTCAATT	480
Db	800	ACCATATACCTTACCTCAGACATTCGGCGCTTTCGGGTTTCCACCAAGCTTTCACA	859

QY	481	CCATTAACCTCATATNCATGAGGAGGAAGTNGAGTTGATTCATCTGATNGTCTTGA	540
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Db	980	TGCAGTCAATGCTGTCTCTGATCAACAAAAGAGGTCCGCAAGCGTGTGGCGAGATCG	1039
QY	660	TGGGATCCTGTGTTTTGGACTTGCTCTTTTAATGACTGCCCAATTTGGCC	719
Db	1040	CCGGTGTGCTGCGTTCTGAGTTTGGTAAACCCCTGTGTGTGCTTGTGCTCGCGAATTTGAT	1099
QY	720	CTGATAGGGGNAATGTTTNGCTGCTGTACTTGTGCTGTTGNNCNAATCCAGACACTTGAG	779
Db	1100	GGGAGAGGGTGGCTTTGTCTGTGCAACCTTTG-TGATCAGGGGATTCAGATGTGAG	1158
QY	780	TTTCTGTTGAATCACCTTGTGAAATTTATATGCGGGC--ACNAATGGGAATGACTGG	837
Db	1159	TTTCTGCCGAACCACTTCTCATACGCCGTTATGTGTGGCCACCAAGGGGAAACGACTGG	1218
QY	838	NTGANAATCAGACAAGGGGCTATTGGAATATCTTTGTCNC	879
Db	1219	TTTGAGAGGCAAAACCGCAGGCAACTTGATATCAAGTCTCC	1260

RESULT 4	
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LOCUS	1410 bp mRNA linear PLN 04-MAY-2003
DEFINITION	Pirimula farinosa fatty acid delta-6 desaturase mRNA, complete cds.
ACCESSION	AY234125
VERSION	AY234125.1 GI:30350276

SOURCE ORGANISM

11

REFERENCE
AUTHORS
1 (Pages 1 to 1410)
Sayanova, O. V., Beaudoin, F., Michaelson, L. V., Shewry, P. R. and Napier, J. A.

TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences(1)
JOURNAL FEBS Lett. 542 (1-3), 100-104 (2003)

PUBMED	12729906	
MEDLINE	22615586	
REFERENCE	2 (bases 1 to 1410)	

TITLE	AUTHORS
Direct Submission	Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and Napier, J.A.

JOURNAL Crop Performance & Improvement, Long Ashton
Submitted (10-FEB-2003)
Research Station, Long Ashton, Bristol BS41 9AF, UK
location/Qualifiers

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CDS     49. 1410
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Query Match	33.2%	Score 292.2	DB 8	Length 1410
Best Local Similarity	60.9%	Pred. 2.7e-58		
Matches 499, Conservative	0	Mismatches 319,	Indels 2,	Gaps 2,

QY 1 CGGCGTCCCTCTCTCCCGGCTTCTCCACTCCACCGTCTTTCGACCACACCGTCT 60
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61 CCGCGCCCTCTCGACTACCGCAGCTTTCTCGAGCTCTCGCGGCTCAACTCTTCA 120
 Db 263 CCACATGCCCGTCTCTCCCTCTCTCTCTACCAACTCCTTCTTCAAAAACCACTCCGCTCT 322
 QY

Db 323 CCCCCA C C C T C C T C A G A C T A C C G C A A C T C C T C G A C A A C T T C C A T A A A C A T G G C C T T T T C C 382

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Db 443 GCGTGA CTGAGT CCTT TGCAGCGACAGT GCGTGGT CCATT TGGCTAGCGGGCGGAGCAA 502

Qy	241	TAGGCTTTCGTGGATTCAAGACGGCGCTGGATAGGCACACTCCGGCATTAAACACTGA	300
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601 TGCAGCAATTCGTCTATTGTTTCGAGGNGAAGTCGAGATGAGCTTGA -ACATAA 659

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QY	660	TCGGGATCCTGTGTTTGGACTGCTCTCTTTAGTACNCTGCTCCAAATGGGC	719
Db	923	TCGACTGCGGTGTTTGGGTTTTCGCCCTTTACTTTCGTGTTACTTAATGGG	982

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[illegible]

RESULT 5

AF005096				
LOCUS	1856 bp	mRNA	linear	PLN 05-JAN-1999
DEFINITION	Rcinus communis desaturase/cytochrome b5 protein mRNA, complete			

cds.
ACCESSION AF005096

VERSION	AF005096.1	GI:4101625
KEYWORDS	Ricinus communis (castor bean)	
SOURCE	Ricinus communis	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid 1; Malpighiales; Euphorbiaceae; Ricinus.	
REFERENCE	1 (bases 1 to 1856) Sayanova,O., Smith,M.A., Lapinskas,P., Stobart,A.K., Dobson,G., Christie,W.W., Shewry,P.R. and Napier,J.A. Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta-desaturated fatty acids in transgenic tobacco Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)	
JOURNAL	97268723	
MEDLINE	9108131	
REFERENCE	2 (bases 1 to 1856) Napier,J.A. and Shewry,P.R.	
AUTHORS	Direct Submission	
TITLE	Submitted (22-MAY-1997) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK	
JOURNAL	Location/Qualifiers	
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Best Local Similarity	63.8%; Pred. No. 1.4e-55;	
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QY	186 TCGGCGCTCTTCTTCGACAGCATTTGTCGACGTCCTTCGCTGATTAAGGC 245	
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QY	426 GACCTGATTCGACGACATGCGGCTTTTGACAGTTTCTGCGGCTTCTTAATTCATA 485	
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 QY 121 ACCGCAAGGCGCACACAACCTCCATCTCTCTCTCTTATTTTCACTCTTCTCTCT 180
 DB 373 ATAAAAAGGTCAAGTCACTCTTATCAAGCTCAAGTCAAGTCAAGTCAAGTCAAG 432
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 QY 719 CCGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 778
 DB 972 CAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1030
 QY 779 GTTCTGTTGATCACTCTGCTGAAATTTATATGAGGAGGAGGAGGAGGAGGAGGAG 836
 DB 1031 GTTCTGTTTAAACATTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1090
 QY 837 GNT 839
 DB 1091 GTT 1093

RESULT 7
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 DEFINITION Brassica napus mRNA for delta-8 sphingolipid desaturase.
 ACCESSION AJ224160
 VERSION AJ224160.1 GI:3819707
 KEYWORDS delta-8 sphingolipid desaturase; fusion protein; sld1 gene.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
 1 Sperling, P., Zahring, U. and Heinz, B.
 A sphingolipid desaturase from higher plants. Identification of a new cytochrome b5 fusion protein

JOURNAL J. Biol. Chem. 273 (44), 28590-28596 (1998)
 MEDLINE 9903197
 PUBMED 9786850
 REFERENCE 2 (bases 1 to 1610)
 AUTHORS Sperling, P.
 TITLE Direct Submision
 JOURNAL Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18, D-22609 Hamburg, GERMANY
 COMMENT Related sequence: X87143
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 /db_xref="taxon:3708"
 /feature_type="ripening embryos"
 /dev_stage="18 to 35 DAF"
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 DSGHNVITKPCNKLVQLSGCTTGISIANWKTTHAHNLSNSLDDPDLOHPV
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 QY 61 CCGCGGCTCTCTCTCGACTACCGCAAGCTCTTCTCGACTCTCCGCGCTCAACTCTTCA 120
 DB 313 CCGACGCTGCGCGGACTACCGCTGTTAGCCGCGAGTTTCCAAAGCGGACTCTTCG 372
 QY 121 ACCGCAAGGCGCACACAACCTCCATCTCTCTCTCTTATTTTCACTCTTCTCTCT 180
 DB 373 ATAAAAAGGTCAAGTCACTCTTATCAAGCTCAAGTCAAGTCAAGTCAAGTCAAG 432
 QY 181 CTCTGCGCGCGCTCTCTCTCTCCGACAGCTTCTGTCAGTCTCTGCGCTCTCTCT 240
 DB 433 TTGTATACGCTGTTGTTGATGACGAGCATATGGCGCCCTTATATATCCGCGCTT 492
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 DB 493 TGGGCGCTTCTGTGATTCAGAGCGGCTGATAGGCGCAAGCTCCGCGCATTAACCTGA 552
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 QY 361 TCAGATCGGCTGTGAGTGGAGCAACCAAGCGCCCAATTCATGATGACAGCTCTG 420

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Qy      421  ACTATACCCGTAATTCGACACATGCCGCTCTTTCAGTTTCGCGGCTTCTCAAT 480
Db      673  ACCACGATCTGATCTCCACACATCCCTGTCTTACGGGCTCCACAGATTCCTTAAAGT 732
Qy      481  CCATTAACCTCTCATTCATGAGAGAAAGTTAGTTGATTCATTCATGCTTANGTCTTGA 540
Db      733  CGATGACGTACCTTTCTATGAGAGAAAGTTGACGTTTCGATTCACATGCTCGATTTCTTGA 792
Qy      541  TCTGCTACACGACACTTACTTTTACCCTGGTAATGTGTGTGTCAGAGGCTCACTTGATC 600
Db      793  TCAGTACCAACACTGCTGCTTTTATTCATCATGTCGTGGGAGAAATCAATCTCTTAA 852
Qy      601  TCGAGCAATCTGCAATTCCTTTTCGAGAGGAAAGCGACGATAGAG-CTTGAACATA 659
Db      853  TCCAAACGTTACTTGTGATTCCTCGAGACGTTACGTTCTGATTCGAGCCTTGAAACATAG 912
Qy      660  TGGGAGTCCCTGTGTTTGGACTTGG-TTCCTCTTTAGTACGCTTGCCCAATTTGG 718
Db      913  CTGGGATCTGTTTCTGACGCTGTTCTCTTTTATGATCTTCTTCAACCAACT-GG 971
Qy      719  CTTGATAGGGGAAATGTTTNGCTTGTGCTAGCTTGTGTGTCNATCCAGACATTC 778
Db      972  CAAGAGAGGATCACTTGTCTTTTAAGCATGGCGG-TCACGGCGATTCAGACAGTTCA 1030
Qy      779  GTTCTGCTGATCACTTCTGTAATAATTTATATGCGGCG--ACNANTGGGATGACTG 836
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Qy      837  GNT 839
Db      1091  GTT 1093

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RESULT 8
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 complete sequence.
 AC005397
 AC005397.3 GI:20197371
 HTG.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 110149)
 Rounsley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M.,
 Shen, M., Rongming, C.M., Fraser, C.M., Somerville, C.R. and Venter, J.C.
 Unpublished
 2 (bases 1 to 110149)
 Lin, X.
 JOURNAL Direct Submission
 REFERENCE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 3 (bases 1 to 110149)
 Town, C.D. and Kaul, S.
 JOURNAL Direct Submission
 COMMENT Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA, cdrom@tigr.org
 On Apr 18, 2002 this sequence version replaced gi:5598465.
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 /cultiVar="Columbia"
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Best Local Similarity 61.1%; Pred. No.1.6e-54;
Matches 472; Conservative 0; Mismatches 299; Indels 2; Gaps 2;

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QY 108 CTCACCTCTTCAACCGCAAGGCCACACACCTCATCTCTCTCTTATTCAC 167
DB 45717 CGCGGCTCTTCCACAAAAGGTCAAGACTCTTTCACACTCACTCACTGCGCGCGCTC 45658

QY 168 CTTTTCCT 227
DB 45657 ATCTCTCGCGCGCTCTCTACGCGCTTTTGGCGTGAACAGCACTTGGCTCACTCATC 45598

QY 228 TCCGCTGCAATGATAGCTCTTCTCTGATTCAGAGCGCGTGAATAGCAGACTCCGCG 287
DB 45597 TCGCGGCTTACTCGGCT 45538

QY 288 CATTACAGGTGATGCTCAGCGCGCGCTCAACCGCGCAATTCAGTTCTCTCGCAAC 347
DB 45537 CACTACAGGTGATGCTCAGCAACCAACCGGTGAACAACTAATCAGCTCTCTCTCGCAAC 45478

QY 348 ATTCCTCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407
DB 45477 TGTCTACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 45418

QY 408 TGCACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
DB 45417 TGTACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 45358

QY 468 CGGTTCTTCAATTCATTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 527
DB 45357 AATTCCTTCAATTCATTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 45298

QY 528 GCTANGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587
DB 45297 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 45238

QY 588 GTCACCTTATCTGACAGCAATTCGCTATTTGTTTCAGAGNGAAGATGAGATAGA 647
DB 45237 ATCAACCTCTTCAACCAATTCGATTTGCTATTTGCTGAAGCCAGCTCCAGATCGG 45178

QY 648 G-CTTGACATATATGAGGATCTTGTGTGTTGAGCTTGTCTCTTTAGTGTGCT 706
DB 45177 GCTTGAATATGAGCGGAGATTTTATGTTTCTGAGACATGTTCCCTCTTATGCTGCTC 45118

QY 707 TGCACATTTGGCTGATATGAGGATATGTTGAGCTTGTCTCTCTCTCTCTCTCTCT 766
DB 45117 CTTCGAAATTTGACAAAGATTCATCTTCTGCTGAGCTTCTGCGG-TCACGCGCAT 45059

QY 767 CCAGCATTCAGTTCTGTTGATATCATCTGCTGAAATTTATATGNCGGCG 819

RESULT 9	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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AP005554	Oryza sativa (japonica cultivar-group)	chromosome 9 clone					
LOCUS	OJ1118 A10, ***	SEQUENCING IN PROGRESS ***					
ACCESSION	AP005554	GI:21952922					
VERSION	HTG PHASE2.						
KEYWORDS	Oryza sativa (japonica cultivar-group)						
SOURCE	Oryza sativa (japonica cultivar-group)						
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.						
REFERENCE	1	Sasaki, T., Matsumoto, T., Hattori, M., Sasaki, Y., and Katayose, Y.					
AUTHORS	Oryza sativa nipponbare(GM3) genomic DNA, chromosome 9, BAC						
TITLE	clone:OJ1118 A10						
JOURNAL	Published only in Database (2002)						
REFERENCE	2 (bases 1 to 96312)						
AUTHORS	Sasaki, T., Matsumoto, T., Hattori, M., Sasaki, Y., and Katayose, Y.						
TITLE	Direct Submission						
JOURNAL	Submitted (23-JUL-2002) Takuji Sasaki, National Institute of Agricultural Sciences, Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki, 305-8602, Japan						
COMMENT	(E-mail: sasaki@nias.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)						
	The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.						
	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.						
	* NOTE: This is a 'working draft' sequence.						
	* This sequence will be replaced						
	* by the finished sequence as soon as it is available and						
	* the accession number will be preserved.						
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DB	88376 CGGCGCGCTCTCGGGAGGTCTCTGTGGCGCGCTCGAGCACTACAGCTTCCCGG 88433						
OY	67 CCTCTCCGACTACCGGACGCTCTTCTCGACCTCTCCGGCTCAACCTTTCAACCGCA 126						
DB	88436 CGTCCGCGCACTTCGCGGCTCTCTCGCGAGCTCTCTCCGGGGGCTGTTCGAACGG 88495						
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DB	88496 TGGGCGCCACCCCGAGAGTCAAGTCCCGGATGCTGCTCTCTCTGCGCGCCCTCT 88555						
OY	187 GCGGCGCTCTCTTCTCGACAGCACTTTCGACACGCTTTCCGGCTGATTAAGGCT 246						
DB	88556 ACTGCGTCTCTGCTGCGGAGCGCTGCGGCGCACTCTCTGCGGGGCGGCTCATGAGT 88615						

Oy		247	TTCCTCGGATTCAGAGCGGTGGATATGGGCACGACTCCGCCATTACAACGTGAATCCTCA	306
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Oy		307	GCGCGCCGCTCAACCGCGCAATTCAGAATTCCTCCGCGAAACATTCCTCGCGAATCAGCA	366
Dd		88676	ACGCGCGGCTCGAACCGGCTCTCCAGGTGTCTCCGGCAACTGCTCCACCGGCTTAGCA	88735
Oy		367	TCCGCTGTGTGAAGTGGAACCAACAGCCCCACACATTTGATATGCAACAGCTTCGACTATG	426
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Oy		427	ACCCGTATCTGAGCACATGCGGGTCTTTTGACAGTTTCGTCCGGGGTCTTCAATTCATAA	486
Dd		88796	ACCCGAGCTTCAGACATGCGGCTTTTGACGCTCTCTCTCAAGCTCTTC--GGCTCT	88855
Oy		487	CCTCTCAATTCATATGGAGAGAAATTTGAGTTGATTCATTTGCTANGTTCTTGATCTGCT	546
Dd		88855	GGTCTCACTTCTACAGCGGACCCCTGTGTGTGACCCCGGCTCCAGATTCTTGATCAGCT	88915
Oy		547	ACCAAGCACTTACTTTTATACCGGTAAATGTGTGTCCAGGGTCAACCTGTATCTGACA	606
Dd		88913	ACCAAGCATGGAGATTCACCCGGTCATGTGCTTCGCAAGGATTAACCTCTTATTCAGT	88972
Oy		607	CAATTCGCTATTTGTTTTGAGGAGAAAAGTGCAAGATTA-GAGCTTGAACATTAATGGGGA	665
Dd		88973	CGGCGGCTCTCTTGCTGTGAGCAGAGAAAGTGCACAGAGGGGGCTGAGATGCGGGG	89032
Oy		666	TCCTGTGTGTTTGGACTGTGGTTCCTCTTTAATGATCTTCGTCGCAATTTGGCCGTATA	725
Dd		89033	TCCGCGGGTCTCGGGTTTGGTACCCAATGGTGGTGTCTGCTTGCCCAATTTGGTGGAGA	89092
Oy		726	GGGNAATTTTNGAGCTTGTCTAGCTTTGCTTTGTGTCMAATCAGACATTCAGTTCTGG	785
Dd		89093	GGGTGGGCTTCGTGTGTCGACAGCTTGG-TGATTAACGGGAATTCAGATGTCAAGTCTCC	89152
Oy		786	TTGAATCACCTTCTCTAAAAATTATATGNCGGCG--ACNANTGGGAATGACTGANT	839
Dd		89152	CTGAACCACTTCTCTTCGAGGTGTATGTCCGGCCGCAAGGGGAATACATCGTT	89207
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LOCUS	AR200409	1702 bp	DNA	linear PAT 20-APR-2002
DEFINITION	Sequence 26 from patent US 6355861.			
ACCESSION	AR200409			
VERSION	AR200409.1	GI:20250483		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1702)			
AUTHORS	Thomas,T.L.			
JOURNAL	Production of gamma linoic acid by a .DEUTRA-6-desaturase			
FEATURES	Patent: US 6355861-A 26 12-VAR-2002;			
source	Location/Qualifiers			
	1..1702			
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ORIGIN	471 c	446 g		
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Best Local Similarity	59.6%; Pred. No. 5e-54;			
Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;				
Oy	18	CCCgCCTTTCACCTTCACCGCTCTTTCCGACACACACCGTCTCGCGCCTCTTCGAC	77	
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Oy	78	TACCGCAAGCTCTTCCGACGCTTCGCGGCTCAACCTTTCAACCGCAAGGGCCACACA	137	
Dd	327	TACCGAGGCTTTTGAACGAGATGTGCGGTGCGGAGATCTTGAAGAGAGGCCACAC	386	

Oy		138	ACCTGCATCCTCCCTCCCTTATTGTCAACCCTTTTCCTGCTCGTGAGGGAGCTC	197
Oy		138	ACCTGCATCCTCCCTCCCTTATTGTCAACCCTTTTCCTGCTCGTGAGGGAGCTC	197
Dd		387	ATCATGTGAGAGCTTGTGTGGCCTTCCGGTCATGATGGCGGCAATGCTTAAGGCCGTCTG	446
Oy		198	TTCCTCGACAGACACTTTCGTGACGACGTGCTTTCGCTGACATGATGAGCTTTCCTG	257
Dd		447	GCGTGGAGTCCGTGGAGATTACATGCTCTGCGGCGCACGTGCTGGGCTGTGTGAATC	506
Oy		258	CAGACCGGCTGGATGAGCCACGACTTCGGCCATTTCMAACGTGATGCTCAGCCGCGCTC	317
Dd		507	CAAGCCGGGTATGTGGGGCCATGACTCCGGCCATTACAGTGTATCCAAACCCGTGGATAC	566
Oy		318	AACCGCGAATTCAGATTCCTCGCGGCAACATTCGCGCGAATAGCATGGGCTG	377
Dd		567	AACAGATACGCAACTCATAGCAGGCAACATCTTAACCGGATACGATTCGCTGG	626
Oy		378	AAGTGAACAACAACGCCACCACATTCATGCAACAGCCTTCGATGATGACCTGATCTG	437
Dd		.627	AAGTGAACAACAAGCCACCACCTCGCTGCAACAGCCTTCGATGATGATGATGATGATG	686
Oy		438	CAGCAATGCGGGCTCTTTCGACGTTTGTGCGGGTCTTCAATTCATAACCTCTCATNC	497
Dd		687	CAGCAATGCGGGCTCTTTCGACGTTTGTGCGGGTCTTCAATTCATAACCTCTCATNC	497
Oy		498	TATGGAGAGAACTNGAGTTGATTCATNCAATGCTAGTCTTGTATCTGCTACAGACATTT	557
Dd		747	TATGGCCGAGTCTGAAAATTCGACGAGGCGAGCTTCTAGTAGCTACACGACATG	806
Oy		558	ACTTTTATCCGGTATGATGTTGTGCCAGAGTCACTTGTATCTGACACATTTCTGCTA	617
Dd		807	ACTTACTACCGGTATGATCTTGGCGAGTCAACCTTCTATCATCAAGCTTTTTATG	866
Oy		618	TTGTTTTCGAGNGAAGAAGTGCAGATGAGCT-TGAACTATATGAGGAGATCTTGTGTTT	676
Dd		867	CTCCCTCACAGGCGGAGCTCCCTGACGCGCTCTAACTTAATGAGTATGCGGTTTTTC	926
Oy		677	TGGATTGTTCTCTCTTTAGTGNCTTGCTGCTGCCAAATTTGGGCTGATAGGGANATGTTT	736
Dd		927	TGGAAGTGTGTTCCGCTCTTGTGATCTTGTCTCCGAACCTGGCCGTAACGTTTCGGTTC	986
Oy		727	GNGCTGTGAGCTTGTGCTGTTTGTGNCNAATCCAGACATTCAGTCTGGTGAATCACCT	796
Dd		987	GTCCTCATCAGCTTTGCG-GGTACGGCGATCCAGACGTCACGTTACAGCTAACCACTT	1045
Oy		797	TGCTGAAAAATTATATGNCGGGACACNANTGGG	828
Dd		1046	CTCGCGGACACATACGTGGGCCCCCAAGG	1077
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LOCUS	Echium gentianoides delta-6-desaturase (D6DS) gene, complete cds.			PLN 01-DEC-2001
DEFINITION	AY055117			
ACCESSION	AY055117			
VERSION	AY055117.1			
KEYWORDS	GI:17223794			
SOURCE				
ORGANISM	Echium gentianoides			
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	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Asteridae; Lamiales; Boraginaceae; Echium.			
REFERENCE	1 (bases 1 to 1478)			
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.			
TITLE	Cloning and Molecular Characterization of the D6-Desaturase from Echium: Functional Expression in Yeast and Tobacco			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1478)			
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-Sep-2001) Biochemistry, Universidad de Almeria,			
AUTHORS	Campus Universitario, La Canada s.n., Almeria 04120, Spain			

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BASE COUNT		364 a	258 c 365 g 491 t
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Query Match		28.9%	Score 254.2; DB 8; Length 1478;
Best Local Similarity		58.5%	Pred. No. 2.6e-49;
Matches		467; Conservative	0; Mismatches 329; Indels 2; Gaps 2
QY	24	TTCTCAACCTCCACCCGCTTTCGACACACACCGTCCTCCGCCCTCCGACATCCGC	83
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QY	84	AAGCTCTTCCGACCTCTCCGCCCTCAACTCTTCAAACGCAAGGGCCACACAACCTCC	143
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QY	204	GACAGCACTTTCGTGCAGCAGCTTTCGCGTCGATGATGAGGCTTTCCTGAGTTACAGC	263
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QY	324	GCAATTAGATTTCTCTCCGCAACATTTCCGCCGAATCAGCATTTGGCTGGTGAAGTGG	383
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QY	384	AACACCAACGGCCACACATTTGATGATGCAAGGCTCGACTATGACCTGATCTGCAGCAGC	443
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QY	504	AGGAAGTTTGAAGTTGATTAATGATGCTATGTTCTTGAATCTGCTACAGCACTTAATCTTT	563
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 DEFINITION complete cds.
 ACCESSION AY055118
 VERSION AY055118.1 GI:17223796
 KEYWORDS
 SOURCE Echium pitardii var. pitardii
 ORGANISM Echium pitardii var. pitardii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamiales; Boraginaceae; Echium.
 1 (bases 1 to 1450)
 Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Ruiz,J.R.
 Cloning and Molecular Characterization of the D6-Desaturase from
 Echium: Functional Expression in Yeast and Tobacco
 Unpublished
 2 (bases 1 to 1450)
 Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Ruiz,J.R.
 Direct Submission
 Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria,
 Campus Universitario, La Canada s.n., Almeria 04120, Spain
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 ORIGIN

Query Match 28.7%; Score 252.6; DB 8; Length 1450;
 Best Local Similarity 58.4%; Pred No. 6; Le-49;
 Matches 466; Conservative 0; Mismatches 330; Indels 2; Gaps 2;
 QY 24 TTCTCCACTCCCAACCGTCTTCCAGCAACCGTCTCGCGCTCTCCGACTACCGC 83
 Db 230 TTCTTCACTGGGTATTAATCTTAATAAGATTACTGTGTTGAGAGGTGTCCAAAGATTACAGG 289
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 QY 144 ATCCCTCCCTCCCTATATCTACCTTTTCTCTCTGTCGTGGGGCTCTCTTCC 203
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 LOCUS AR076814
 DEFINITION Sequence 1 from patent US 5959175.
 ACCESSION AR076814
 VERSION AR076814.1 GI:10003560
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1684)

AUTHORS Thomas, T.L., Nunberg, A.N. and Beremand, P.D.
TITLE Sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition

JOURNAL Patent: US 5959175-A 1 28-SEP-1999;

FEATURES Location/Qualifiers

source

1.1684

BASE COUNT 430 a 277 c 358 g 619 t

ORIGIN

Query Match 27.9%; Score 245.2; DB 6; Length 1684;

Best Local Similarity 57.7%; Pred. No. 3.5e-47;

Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

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265 TTTTTCACCTGGGATTTATCTTAAAGATTACTCTGTCTGAGGTTTAAAGATTATAG 324
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AR084177

LOCUS AR084177 1684 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 1 from patent US 5977436.

AR084177

AR084177.1 GI:10010948

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1684)

AUTHORS

TITLE

Olsepin 5' regulatory region for the modification of plant seed

lipid composition

Patent: US 5977436-A 1 02-NOV-1999;

Location/Qualifiers

source

1.1684

/organism="unknown"

BASE COUNT

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ORIGIN

Query Match 27.9%; Score 245.2; DB 6; Length 1684;

Best Local Similarity 57.7%; Pred. No. 3.5e-47;

Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCAACCGCTCTCCGCGCTCTCCGACTACCGC 83
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Qy	444	ATGCCGATCTTTGACGATTTGCTGGCGGTTCTTCAATTCATTAACCTTCATTTTCATGGG	503
Db	685	ATACCATTCCTGTTGTGTCTTCCAAATTTTTTGGTTCACATCCTCATTTCTATAG	744
Qy	504	AGGAATTTNAGTTGATTTNCAATTTGTATNGTTTATNCTTGAATCTGCATCCAGACATTTA	563
Db	745	AAAAGTTGACTTTTGACTCTTATTCAAAGATCTTTTGAATATTCACACATTTGACATTT	804
Qy	564	TACCCGGTATATGTTGTGTCAGAGGTCAACTGTATCTGCAGACAAATTCGCTATTTGTT	623
Db	805	TACCTTATATGTGTGTGCTGCTAGGCTCAATATGATATGACATCTCTCATATATGTTGTG	864
Qy	624	TCGAGNGAAAAGTGCAGATAGAGCT-TGAACATTAATGGGGATCTTGTGTTTGGACT	682
Db	865	ACCAAGAAATGTGTCTTATCGAGCTCAGGAACCTTGGAGATCCTATGTTCTCGATT	924
Qy	683	TGTTTCTCTTTTATGNTGNTCTTGCTGCAATATGGGCGTGA TAGGGGAATGTTNGCTT	742
Db	925	TGGTACCCGTTGCTTGTCTTGTGTTGCTTATATGGGGGTGAAGAAATATATTTGTTAT	984
Qy	743	GCTAGCTTCTGTTGTGNCNNATCCAGACATTCAGTTCTGTTGATATCACTTGCTGA	802
Db	985	GCAAGTTATACAGGACTG-GAATGCAACAAGTTCAATTTCTTGAACCACTTCTCTTC	1043
Qy	803	AAATTTATATGCGGCA--CNANTGGAAATGACTGNT--GANATTCAGCAAGGGCTC	858
Db	1044	AAGGTTTATTTGGAAGCCTAAAGGGAATTAATGTTTGAGAAACAACGATGGGAC	1103
Qy	859	ATTGGATATCTCTTGNCCT 880	
Db	1104	ACTTGACATTTCTTGCTCTCT 1125	

Search completed: December 31, 2003, 21:04:27
Job time : 2210.2 secs

PN WO200032790-A2.
 XX 08-JUN-2000.
 XX 02-DEC-1999; 99WO-US28589.
 XX 03-DEC-1998; 98US-0110784.
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
 XX WPI; 2000-412336/35.
 XX P-PSDB; AAY71553.
 DR Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 44-45; 57pp; English.
 XX The present sequence is a cDNA encoding sphingolipid desaturase
 CC derived from a contig of clones sfil.pk0012.05 and sfil.pk0031.d11
 CC isolated from soybean immature flower cDNA library, sfil.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as a primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 880 BP; 162 A; 267 C; 184 G; 251 T; 16 other;
 Query Match 98.2%; Score 864; DB 21; Length 880;
 Best Local Similarity 100.0%; Pred. No. 1e-208;
 Matches 880; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGCTCCCTCCCTCCGCGCTCTCCACCTCCGACGCTCTTCCGACCAACGCTCT 60
 DB 1 CGGCGCTCCCTCCCTCCGCGCTCTCCACCTCCGACGCTCTTCCGACCAACGCTCT 60
 QY 61 CGGCGCTCCCTCCCTCCGCGCTCTCCACCTCCGACGCTCTTCCGACCAACGCTCT 120
 DB 61 CGGCGCTCCCTCCCTCCGCGCTCTCCACCTCCGACGCTCTTCCGACCAACGCTCT 120
 QY 121 ACCGCAAGGGCCACACACCTCTCTCTCCCTTATCTCACCCTTTTCTCTCT 180
 DB 121 ACCGCAAGGGCCACACACCTCTCTCTCCCTTATCTCACCCTTTTCTCTCT 180
 QY 181 CTGCTCGCGCGCTCTCTCTCTCCGACGACCTTCCGACGCTCTTCCGACCAACGCTCT 240
 DB 181 CTGCTCGCGCGCTCTCTCTCTCCGACGACCTTCCGACGCTCTTCCGACCAACGCTCT 240
 QY 241 TAGGCTTTTCTCTGATTCAGAGCGCTGATAGGCAAGCACTCCGCGCATTAACAAGTGA 300
 DB 241 TAGGCTTTTCTCTGATTCAGAGCGCTGATAGGCAAGCACTCCGCGCATTAACAAGTGA 300
 QY 301 TGGCTTTTCTCTGATTCAGAGCGCTGATAGGCAAGCACTCTCCGCAACATTTCTGCGGAAA 360
 DB 301 TGGCTTTTCTCTGATTCAGAGCGCTGATAGGCAAGCACTCTCCGCAACATTTCTGCGGAAA 360
 QY 361 TCAGCATTCGCGTGTGAGTGAAGTGAACCAAGCCCAACCATTTGCAAGCAAGCTCG 420
 DB 361 TCAGCATTCGCGTGTGAGTGAAGTGAACCAAGCCCAACCATTTGCAAGCAAGCTCG 420
 QY 421 ACTATACCTCTGATTCAGAGCAATGCGGCTTTTGAAGTTTGTGCGGTTTCTCAAT 480
 DB 421 ACTATACCTCTGATTCAGAGCAATGCGGCTTTTGAAGTTTGTGCGGTTTCTCAAT 480
 QY 481 CCAATACCTCTGATTCAGAGCAAGTGAAGTTGATTCATTTGCTTANGTTCTTGA 540
 DB 481 CCAATACCTCTGATTCAGAGCAAGTGAAGTTGATTCATTTGCTTANGTTCTTGA 540

QY 541 TCTGTACAGACACTTACTTTTACCCGGTATGTTGTTCCAGGTCACCTTGTATC 600
 DB 541 TCTGTACAGACACTTACTTTTACCCGGTATGTTGTTCCAGGTCACCTTGTATC 600
 QY 601 TGCAGCAATTTCTGATTTGTTTTCAGAGGAAAAGTGCAGATAGAGCTTGAACATTAAT 660
 DB 601 TGCAGCAATTTCTGATTTGTTTTCAGAGGAAAAGTGCAGATAGAGCTTGAACATTAAT 660
 QY 661 GGGGATCCTTGTGTTTTCAGCTTGTCTCTTTAGTGNCTTGGCTGCAATTTGGGCC 720
 DB 661 GGGGATCCTTGTGTTTTCAGCTTGTCTCTTTAGTGNCTTGGCTGCAATTTGGGCC 720
 QY 721 TGATAGGGGATGTTGTTGCTGATGCTTGTGCTGTTTTCGATTCAGACATTCAGT 780
 DB 721 TGATAGGGGATGTTGTTGCTGATGCTTGTGCTGTTTTCGATTCAGACATTCAGT 780
 QY 781 TCTGTTGATCCTTGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 840
 DB 781 TCTGTTGATCCTTGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 840
 QY 841 ANAATCAGCAAGGGGCTATGATATCTCTGTCCT 880
 DB 841 ANAATCAGCAAGGGGCTATGATATCTCTGTCCT 880

RESULT 2
 AAD01352
 ID AAD01352 standard; cDNA; 1934 BP.
 AC AAD01352;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Soybean sphingolipid desaturase cDNA #2.
 XX
 KW Soybean; sphingolipid desaturase; membrane-bound desaturase;
 XX transgenic plant; fatty acid; ss.
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 305..1657
 FT /*tag a
 FT /product= "sphingolipid desaturase"
 XX
 PN WO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PR 03-DEC-1998; 98US-0110784.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
 XX WPI; 2000-412336/35.
 XX P-PSDB; AAY71554.
 DR Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 46; 57pp; English.
 XX The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone sfil.pk0017.b4.f15 isolated from soybean seedling cDNA
 CC library, sfil. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.

Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;

Query Match 53.1%; Score 467.6; DB 21; Length 1934;
Best Local Similarity 76.0%; Pred. No. 2.5e-108;
Matches 656; Conservative 0; Mismatches 199; Indels 8; Gaps 7;

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24 TTCTCCACCTCCACGCTCTTCCGACCAACCGCTCCGCGCCCTCCGACCTACCGC 83
Db TTTCTACCTGCTACCACTCAGTACTTCAAGCTCTGAGGTGTCGAAAGCTTACGAA 592
Qy AAGCTCTTCCGACCTCTCCGCTCAACCTTTCACCGGACGAGGACCAACACTCC 143
Db AAGCTTGATCTGAGTCTCAAAATTGGGCTTTTTCAGACCAAGGAGGATGCACTTA 652
Qy 144 ATCTCTCTCTCTTATCTCACCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTC 203
Db 653 TGCACCTTGCACTGCTGCTGTTATGTTCTCATTTGACTATGATGTTGAGGTGC 712
Qy 204 GACAGACTTGTGACGCTGCTTCCGCTGATGATAGGCTTCTCTGATTCAGAGC 263
Db 713 ACTAGTGTGTGGCTCTATTGGTTCAGGACATGCTTGAAGGTTGCTTGAATGAA 772
Qy 264 GCGTGTAGGCGCAGCTCCGCGCATTAACGATGCTCAGCGCGCTCAACCGC 323
Db 773 GCTTATGTGGCCATATTTCTGCGCACTATGTGTTATGACAAACAAATGTTCAAG 832
Qy 324 GCATTTGATTTCTCTCCGCAACATTTCTGCGGAAATGACATCGGCTGTGAAAGTG 383
Db 833 GTTGACACATCTCTCTGGAACCTGTTGACCGGATTAAGATTTCTTGAGAAAGTG 892
Qy 384 AACCAACAGCCCAACCAATGATGACAAACAGCTGATATACCTGATCTGCGACAC 443
Db 893 ACTCAAAATGCTCACCAATGCTGCAACAGCTTGACATGACCTTATCTGCGACAC 952
Qy 444 ATGCGGCTCTTTCAGATTCGTGCGGCTTCTCAATTTCCATACTCTGATTCATGAG 503
Db 953 ATGCGGCTCTTTCAGATTCGTGCGGCTTCTCAATTTCCATACTCTGATTCATGAG 1012
Qy 504 AGGAGTTGAGTTGATTCATTCATGCTGATGCTGATCTGATCTGATCTGATCTG 563
Db 1013 AGGAGTTGAGTTGATTCATTCATGCTGATGCTGATCTGATCTGATCTGATCTG 1072
Qy 564 TACCGGTAATGTGTGTGCGGAGGTCACCTGATCTGACAGCAATTTCTGATTTT 623
Db 1073 TACCGGTAATGTGTGTGCGGAGGTCACCTGATCTGACAGCAATTTCTGATTTT 1132
Qy 624 TCGAGNGAAGATGAGATAGAG-CTTGACATATGAGGAGTCTTGTGTTTGGACT 682
Db 1133 TCGAGGCGAAGATGAGATAGAGCTTGACATATGAGGAGTCTTGTGTTTGGACT 1192
Qy 683 TGGTT-CTCTTTTAACTGCTGCTGCGCAAAATGAGGCTGATAGGAGGATGTTNGCT 741
Db 1193 TGGTTCTCTTTTAACTGCTGCTGCGCAAAAT-GGCTGAGAGGATATGTTTGGCT 1251
Qy 742 TGTGACTTGTCTGTTTTCGCAATCAGACATTAATGATGATGATGATGATGATG 801
Db 1252 TGTGACTTGTCTGTTTTCGCAATCAGACATTAATGATGATGATGATGATGATG 1310
Qy 802 AAAATTATATGCGGGC--ACNANTGGGAATGACTG--NTGNANTCAGACAGGGGT- 857
Db 1311 CAATATATATGCTGGGCGACGAGTGGGATATGATGTTGAGAACAGACAGATGTA 1370
Qy 858 CATTGATATCTCTTGTGNCCT 880
Db 1371 CATTGATATCTCTTGTGCTCT 1393

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RESULT 3
AAD01353
ID AAD01353 standard; cDNA; 1972 BP.
XX

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AC AAD01353;
XX
DT 12-OCT-2000 (first entry)
XX
DE Wheat sphingolipid desaturase cDNA #1.
XX
KW Wheat; sphingolipid desaturase; membrane-bound desaturase;
XX transgenic plant; fatty acid; ss.
XX
OS Triticum aestivum.
XX
FH Key Location/Qualifiers
FT CDS 124..1533
FT /tag= a
FT /product= "sphingolipid desaturase"
XX
PN WO200032790-A2.
XX
PD 08-JUN-2000.
XX
PF 02-DEC-1999; 99MO-US28589.
XX
PR 03-DEC-1998; 98US-0110784.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
XX
XX WPI; 2000-412336/35.
XX DR P-PSDB; AAY71555.
XX
PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries
XX
PS Disclosure; Page 48-49; 57pp; English.
XX
CC The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone wrel.pk0004.c7: file isolated from wheat etiolated
CC seedling root cDNA library, wrel.
CC The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
XX
SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 other;

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Query Match 36.5%; Score 320.8; DB 21; Length 1972;
Best Local Similarity 61.8%; Pred. No. 3.5e-71;
Matches 545; Conservative 0; Mismatches 333; Indels 4; Gaps 3;

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1 CCGCCCTCCCTCTCTCCCGGCTTCTCCACTCCACGCTTTCCGACCAACCGTCT 60
Db 383 CTTCCGTGCGCGGCTCTCTCCCGGCTTCTGTGTGGCGGCTCTCCACTACACGCTC 442
Qy 61 CCGCCGCTCTCTCGACTACCGCAAGCTTTCTCGACCTTCCGCGCTCAACTCTTCA 120
Db 443 CCGCCGCTCTCGCACTTCCGCGCTCTCTCGCAAGCTCTCTCCGCGGCTCTTTCG 502
Qy 121 ACCGCAAGGCGCAACCACTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 503 AGCGGCTGCGCCACACCCCAAGTCTGCTGTCGCAATGTGGGTGCTCTTCTGATCG 562
Qy 181 CTGTCTGCGGCGTCTCTCTCTCTCCGACAGACTTGTGACGCTTTCGCTGATTA 240
Db 563 CCTTACTGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 622
Qy 241 TAGGCTTTCTGATTCAGAGCGGCTGATAGGCGACGCTCGGCGCAATTAACGTA 300
Db 623 TTGGCTTATCTGATTCAGTGGGCTGATTTGGCCATGACTCCGCGCACCAATCA 682

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QY 301 TGGTCAGCCGCGCCCTCAACCGCGCAATTCTCTCCGGCAACATTTCTCGCGGAA 360
DB 683 CAGGACACCCCGGGCTCAACCGCTCTCTGAGGTGGTCTCCGGGAATGCTCAACGCGC 742
QY 361 TCAGCATTCGGCTGTGGAGTGAACCAACGCGCCACCAATTCATGCAACAGCTCG 420
DB 743 TCGGCAATCGCTGTGGAGTGAACCAACGCGCCACCAATTCCTCTGCAACAGCTCG 802
QY 421 ACTATGACCCGTATTCGACAGCATTCGCGCTTTTGAGTTGGTGGCGGTTCTCAAT 480
DB 803 ACCATGACCCGCGACCTTCACAGCATTCGCGCTTTTGAGTTGGTGGCGGTTCTCAAC 862
QY 481 CCATTAACCTCTCAATTCATGAGAGAGTGAATGATTCATTCATGATTCATTCATTC 540
DB 863 ACCTTTGGTGGTGTGTGATGAGAGAGTGAATGATTCATTCATGATTCATTCATTC 922
QY 541 TCTGCTACCAAGCACTTACTTTTACCCTGTAATGTTGTGTGGCAGGTCACCTTGAT 600
DB 923 TCAGCTACCAAGCACTTACTTTTACCCTGTAATGTTGTGTGGCAGGTCACCTTGAT 982
QY 601 TGGAGCAATTCGCTATTCCTTTTTCGAGGAGAAAGCGAGATAG-AGCTTGAACATA 659
DB 983 TGGAGCAATTCGCTATTCCTTTTTCGAGGAGAAAGCGAGATAG-AGCTTGAACATA 1042
QY 660 TGGGATTCCTTGTGTTTGGACTTGTCTCTTTTATGATGCTTGTGCAATTCGAG 719
DB 1043 CCGGAGTGGAGGTTCTGGGTTTGGTACCCCTTCTGCTGTCTGTGCTGCGAATTCGT 1102
QY 720 CTGATAGGGGATGTTTGGCTTGTGATGCTTGTGCTGTTGTCATTCAGCAATTCAG 779
DB 1103 GGGAGAGGGTGTGTTTGTGCTTGTGCAAGCTTTG-TGATTCAGGGGATTCAGCAATTCAG 1161
QY 780 TTTGCTGATGATCAGCTTGTGCAAAATTTATATGNGGGG-ACNANTGGGAATGATG 837
DB 1162 TTTGCTGATGATCAGCTTGTGCAAAATTTATATGNGGGG-ACNANTGGGAATGATG 1221
QY 838 NTGANAATCAGACAGGGGTCTTGTGATCTCTTGTGNGCC 879
DB 1222 TTGAGAGGCAACAGGGGCGGCACTTGTATATCAAGTCTCC 1263

RESULT 4
AAD01350
ID AAD01350 standard; cDNA; 1764 BP.
XX
AC AAD01350;
XX
DT 12-OCT-2000 (first entry)
XX
DE Corn sphingolipid desaturase cDNA.
XX
KW Corn; sphingolipid desaturase; membrane-bound desaturase;
XX transgenic plant; fatty acid; ss.
XX
OS Zea mays.
XX
FH Key location/Qualifiers
FT CDS 89..1477
FT /tag= a
FT /product= "Sphingolipid desaturase"
PN MO200032790-A2.
PD 08-JUN-2000.
XX
XX 02-DEC-1999; 99MO-US28589.
XX
XX 03-DEC-1998; 98US-0110784.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
XX Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
XX

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DR WPI; 2000-412336/35.
DR P-PDB; AAY71552.
XX
PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries
XX
PS Claim 2; Page 41-42; 57pp; English.
XX
CC The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone cdelc.pX001.08:its isolated from corn developing
CC embryo cDNA library, cdelc. The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
XX
SQ Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 other;

Query Match 34.3%; Score 302; DB 21; Length 1764;
Best Local Similarity 61.6%; Pred. No. 1,9e-66;
Matches 519; Conservative 0; Mismatches 319; Indels 4; Gaps 3;

QY 1 CCGCTCCCTCTCTCTCCCGCTTCTCCACCTCCACCGCTTCTCCGACACCGCTCT 60
DB 327 CTTCCGCGCGCGCGCTCTCTCCCGCTTCTCTGTTGGCGCGCTCTCTGATACGCGCT 386
QY 61 CCGCGCTCTCTCTCTCCGACACCGAGCTTCTCTGACCTCTCCGCGCTCAACCTTTCA 120
DB 387 CCCCCCGTCCGCGCGCTACCGCGCTCTCTCCGCGAGCTATCTCCGCGCGCTCTTGG 446
QY 121 ACGGAGGAGGCAACAACCTCATCTCTCTCTCTTATTCACCTTTTCTCTCT 180
DB 447 AAGCGCTGCGCGCGCGCGCTACCGCGCTCTCTCCGCGAGCTATCTCCGCGCGCTCT 506
QY 447 AAGCGCTGCGCGCGCGCGCTACCGCGCTCTCTCTTATTCACCTTTTCTCTCT 506
DB 507 CGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 566
QY 241 TAGCTTTCTCTGATTCAGAGGCGGTGATAGGCGAGCTTCGCGCAATTCACAGTGA 300
DB 567 TTGGCTTCTCTGATTCAGAGGCGGTGATAGGCGAGCTTCGCGCAATTCACAGTGA 626
QY 301 TGGTCAGCCGCGCGCTCAACCGGCAATTCATTCCTCCGCGCAATTCGCGGAA 360
DB 627 CCGGCGATCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 686
QY 361 TCAGCATCGGCTGTGGAGTGAACCAACGCGCCACCAATTCATGCAACAGCTCG 420
DB 687 TCAGCATCGGCTGTGGAGTGAACCAACGCGCCACCAATTCATGCAACAGCTCG 746
QY 421 ACTATGACCCGTATTCGACAGCATTCGCGCTTGTGCAATTCGTCGCGGTCTTCAAT 480
DB 747 ACCATGACCCGCGACCTTCAGACATCCGCTCTTGTGCGCTCTCTCTCTCTCTCTCT 806
QY 481 CCATTAACCTCTCAATTCATGAGAGAGTGAATTCATTCATTCATTCATTCATTCAT 540
DB 807 ACATATGCTCTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 866
QY 541 TCTGCTACCAAGCACTTACTTTTACCCTGTAATGTTGTGTGGCAGGTCACCTTGAT 600
DB 867 TCAGCTACCAAGCACTTACTTTTACCCTGTAATGTTGTGTGGCAGGTCACCTTGAT 926
QY 601 TGGAGCAATTCGCTATTCCTTTTTCGAGGAGAAAGCGAGATAG-TAGACTTGAACATA 659
DB 927 CCGAGTCCGCGCTGTGTTCTCAACGAGAGGAGTGGCGAGCGGTTGTGATGATG 986
QY 660 TGGGATTCCTTGTGTTTGGACTTGTCTCTTTTATGATGCTTGTGCTGCAATTCG 719
DB 987 CCGGCGGTTCACCAATTCCTGAGTGTGATCCGCTGTGCTGCTCTCTCTCTCTCTCT 1046
QY 720 CTGATAGGGGATGTTTGGCTTGTGATGCTTGTGTCATTCAGCAATTCAG 779

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DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
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PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
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PR 06-JUL-1999; 99US-0142390.
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PR 12-JUL-1999; 99US-0142977.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149829.
PR 23-AUG-1999; 99US-0149802.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.

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PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160788.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

Query Match 31.5%; Score 277.2; DB 21; Length 1465;
 Best Local Similarity 61.1%; Pred. No. 3.4e-60;
 Matches 472; Conservative 0; Mismatches 299; Indels 2; Gaps 2;

```

QY 48 GACCAACACGCTCTCCGCCGCTCTCTCCGACTACCGAAGCTCTTCTCCGACTCTCCGCG 107
DB 365 GACCAACACGCTCTCCGCCGCTCTCTCCGACTACCGGCTTTCGCCGCCGACTCTCCCAA 424
QY 108 CTCAACCTCTTCAACCGCAAGGCGCACACACCTCATCTCTCTCTCTCTCTCTCTCTCT 167
DB 425 CCGCGGCTCTTTCGACAAAAGGTCAAGTCACTCTTTCACACTCACTGCGCGTCCGCTC 484
QY 168 CTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 227
DB 485 ATGCTCGCGCGGCTTCTTACGCGGCTTTCGCGTGTACAGAGATCTGGGCTCACTCATC 544
QY 228 TCCGCTGCATGTATAGCTTTCTCTGATTCAGAGGCGCTGATAGGCGACGACTCCGCGC 287
DB 545 TCCGCGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 604
QY 288 CATTACACGTGATGCTCAGCGCGCGCTCAACCGCGCAATTGATTCCTCCGCGCAC 347

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DB 605 CACTACACGCTGACGTCAACCAACCGGTGTAACAACATTCACGCTTCTCTCCGTAAC 664
QY 348 ATTCGCGCGGAATGAGATGCGGCTGTGTAGTGAACCAACAGCCACACATTTGA 407
DB 665 TGTCTACCGGATCTTCAATGCGCTGTGTGAATGAGCGACACAGCTTACCAATCGCT 724
QY 408 TGCAACAGCTTCGACTATGACCTGTATGCGAGACATGCGGCTTGTTCAGTTTCGTG 467
DB 725 TGTACACGCTTGAACGACGATCGGATCTTACACACATCCGATCTTCCGCTCTCTACA 784
QY 468 CGGTTCTTCAATTCCATAAAGCTTCTATTCATGATGAGAGAGAGTTGAGTTGATTTCAT 527
DB 785 AAATCTTCAATTCGATGACGCTCAAGTTCATGTCAGAGAAATTCAATTCGATCTCTCA 844
QY 528 GGTAGTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587
DB 845 GCTGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
QY 588 GTCAACTGTATCTGACAGCAATTCGCTATTTGTTGAGAGGAAAGTGCAGATAGA 647
DB 905 ATCAACCTCTTCATCCAAACATTCCTATTTGCTATTTGCTGAAAGCGACGTCACATCGG 964
QY 648 G-CTTGAACATPAGGGAGATCCCTGTGTTTGGAGCTTGCTCTCTTTAGTGTGCTGCC 706
DB 965 GCTTGAACATGCGCGGAATTTTGTGTTTGTGAGATGTTCCCTCTTGTGTCTGTTC 1024
QY 707 TGCCAAATTTGGGCGCTGATAGGGAGATGTTTGTGCTGATGTTGCTGTTTGTGTCNAT 766
DB 1025 CTTCGAATTTGGCAAGAGATTCATCTTCTGCTGAGATGCTGCCG-TCACGCGCAT 1083
QY 767 CCAGACATTCAGTCTGTTGATCACCTTGCTGAATTAATTAATTAATTAATTAATTAAT 819
DB 1084 TCACATGTTCAATGTTCTTTTAAACATTTGCGACAGATGTATACCGGTC 1136

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RESULT 7

ABK49503 standard; DNA; 1702 BP.

ABK49503;

15-JUL-2002 (first entry)

DNA encoding Evening primrose delta6-desaturase.

XX delaa6-desaturase; sunflower; soybean; maize; tobacco;
 KW peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
 KW chilling tolerance; gene; ds; evening primrose.

XX Oenothera biennis.

XX Key Location/Qualifiers

FT CDS 48..1406
 FT /*tag= a
 FT /product= "delta6-desaturase"

XX US635861-B1.

XX 12-MAR-2002.

XX 19-SEP-1997; 97US-0934254.

XX 13-OCT-1992; 92US-0959952.

XX 10-OCT-1991; 91US-0774475.

XX 08-JAN-1992; 92US-0817919.

XX 14-SEP-1994; 94US-0307382.

XX 28-JAN-1997; 97US-0789936.

XX (RHON) RHONE-POULENC AGROCHIMIE.
 XX Thomas TL;
 XX MPI; 2002-380944/41.

DR P-PSDB; AAU79851.
 XX Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linoleic acid to gamma linolenic acid useful for producing
 PT gamma linolenic acid in transgenic plant or bacteria
 XX
 PS Claim 2; Column 41-46; 53pp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increased
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC production low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This sequence encodes the evening primrose
 CC delta6 desaturase involved in the production of gamma linolenic acid.
 CC
 XX
 SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
 Query Match 31.2%; Score 274.2; DB 24; Length 1702;
 Best Local Similarity 59.6%; Pred. No. 2e-59;
 Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;
 18 CCGCGCTTCTCCACCTCCACCGTCTTCCGACACACCGTCCGCGCTCTCCGAC 77
 Db CCGCTTCTCCACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 267
 78 TACCGCAGCTCTTCTCCGACCTCTCCGCTCACTCTTCAACCGCAAGGCGCACACA 137
 Db TACCGGAGGCTTCTTGAACGAGATGCGCGGATCTTCAAGAAAGGCGCACAC 327
 138 ACCCTCATCT 197
 Db ATATATGTGACGTTCTGTCGCGCTTCCGCTATGATGCGGCAATCGTCTACGGGTC 387
 198 TTCTCCGACAGCACTTCTGTCAGCTTCTTCCGCTGTCATGTAGAGCTTCTCTG 257
 Db GCGTCCGAGTCCTGCGAGTTCATGCTGCGGCGCACTGCGGCTTCTGCTGTGATC 447
 258 CAGAGCGGCTGATAGGCGCACGCTCCGCTCACTTCAACGATGCTCAGCGCGCTC 317
 Db CAGCGCGCTGATGAGGCGCATGACTCCGCTATACGAGTGAAGCCGCTGATAC 507
 318 AACCGGCAATGAGATTTCTCCGCAATCTCGCGGATTCAGCATCGGCTGTG 377
 Db AACGAAATACGCAACTCATAGAGGCAATCTCTAAACGGAATCAGCATCGGTG 567
 378 AAGTGAACCAACAGCCGACCATTTGATGACAGAGCTCGATATGACCTGATCTG 437
 Db AAGTGAACCAACAGCCGACCATTTGATGACAGAGCTCGATATGACCTGATCTG 627
 438 CAGACATGCGGCTTCTTGAAGTTGCTCGCGGCTTCTTCAATTCATACCTCTCA 497
 Db CAGACATGCGGCTTCTTGAAGTTGCTCGCGGCTTCTTCAATTCATACCTCTCA 687
 498 TAGGGAGGAGTNGATTGATNTGATNTGATNTGATNTGATNTGATNTGATNTG 557
 Db TAGGGAGGAGTNTGATNTGATNTGATNTGATNTGATNTGATNTGATNTGATNTG 747
 558 ACTTTTACCCGTAATGTTGTTGACAGGTCATCTTGTATGTCAGAGAAATTTCTG 617
 Db ACTTACCTACCCGTAATGTTGTTGACAGGTCATCTTGTATGTCAGAGAAATTT 807
 618 TTGTTTTCAGAGGAAAGTGCAGATAGACT-TGAACATTAATGGGATCTTTGTTT 676
 Db CTCTCTACCAAGGCGCGAGCTCCGCTGACCGGCTCTAACTTAATGGGATCTTT 867
 677 TGACATTTGTTCTCTTTTATGATGCTGCTGCAATTTGGGCTGATAGGGAATCTT 736
 Db TGACATTTGTTCTCTTTTATGATGCTGCTGCAATTTGGGCTGATAGGGAATCT 927
 737 GAGCTTGCTAGCTTGTGTTGTGTCGATCTGCTCCGAAATGCGGCTTCTGAGTTC 986
 737 GAGCTTGCTAGCTTGTGTTGTGTCGATCTGCTCCGAAATGCGGCTTCTGAGTTC 986

Db 987 GTCCTCATGACGTTTGC-GGTACCGCGATTCAGACGCTCAGTTCACCTCAACCACTT 1045
 QY 797 TGCTGAATTTATATNGNGGCGACGACANTGG 828
 Db 1046 CTCGCGGACACATYACTGTGGCCCCCAAG 1077
 RESULT 8
 ABX15367
 ID ABX15367 standard; cDNA; 1702 BP.
 XX
 AC ABX15367;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Evening primrose delta-6-desaturase #1 cDNA.
 XX
 KM Delta-6-desaturase; gene; se; delta-12-desaturase; sunflower; soybean;
 KM maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KM octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 KM evening primrose.
 XX
 OS Oenothera biennis.
 XX
 FH Key Location/Qualifiers
 FT CDS 48..1406
 FT /*tag= a
 FT /product= "Evening primrose delta-6-desaturase #1"
 XX
 PN US2002108147-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001US-0029756.
 XX
 PR 13-OCT-1992; 92US-0959952.
 PR 19-SEP-1997; 97US-0934454.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JUN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 PA (THOM/) THOMAS T L.
 XX
 PI Thomas TL;
 XX
 DR WPI; 2003-066659/06.
 DR P-PSDB; ABG73416.
 XX
 PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant
 XX
 PS Claim 2; Fig 10; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding an evening primrose delta-6-desaturase polypeptide.
 CC
 XX
 SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;


```

Db      685 ATACCAATCTTGTGTGCTCTCCAAAGTTTGTGTTCACTCACTCTCATTTCTATAG 744
Qy      504 AGAAGTTNAGTTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 563
Db      745 AAAAGTTGACTTTTGTCTTTTATCAAGATCTTTTGTATGATCAACATTTGACATTTT 804
Qy      564 TACCCGTAATGTGTGTGTCAGAGGTCATCTGTATCTGACAGCAATTCGTATTTGTTT 623
Db      805 TACCTTATATGTGTGTGTGTCAGAGGTCATCTGTATCTGACAGCAATTCGTATTTGTTT 864
Qy      624 TCAGAGNAAAAGTGCAGATTAAGCT-TGAACATTAATGGGATCCTTGTGTTTGACT 682
Db      865 ACCAAGGAAATGTGTCCTATTCAGCTCAGAACTCTTGGAGATGCCATGTTCTGCATTT 924
Qy      683 TGGTTCCTCTTATAGTNCCTTGCCTGCAATTCGGCTTATGAGGATGTTGACCTT 742
Db      925 TGGTACCCGTTGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 984
Qy      743 GCTAGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 802
Db      985 GCAAGTTTATGATGACTG-CAATGCAACAAGTTTCTTCTTGAACACATTTCTTCTT 1043
Qy      803 AAATTTATATGCGGCA--CNATGGAATGACTGNT--GANAATCAGACAAGGGGTC 858
Db      1044 AAGTGTATATGTGAAAGGCTTAAGGGAATTAATGTTTGAAGAAACAAGATGGAG 1103
Qy      859 ATTGATATCTCTTGTGNCCT 880
Db      1104 ACTTGACATTTCTTGTCTCT 1125

```

RESULT 10

AAK24917 standard; cDNA; 1684 BP.

ID AAK24917;

XX 21-JUN-1999 (first entry)

XX Borage delta-6 desaturase cDNA.

XX Delta-6 desaturase; borage; oleosin; AtS21; promoter;
 XX transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 XX Gamma-linolenic acid; octadecatetraenoic acid; de.

XX Borage officinalis.

XX Key Location/Qualifiers

XX CDS 43..1389

XX MO9845461-A1.

XX 15-OCT-1998.

XX 09-APR-1998; 98MO-US07179.

XX 09-APR-1997; 97US-0831575.

XX (RHON) RHONE-POULENC AGROCHIMIE.

XX L4 Z, Thomas TL;

XX WPI; 1999-180333/15.

XX P-PSDB; AAW98130.

PT Nucleic acid containing oleosin 5'-regulatory region - useful for
 PT modulating fatty acid synthesis and lipid metabolism in plants,
 PT particularly to increase content of gamma-linolenic acid

XX Example 2; Page 59-61; 101bp; English.

CC The present sequence encodes borage delta-6 desaturase (see
 CC AAW98130), an enzyme that catalyses the conversion of linoleic acid
 CC to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was
 CC isolated from a borage membrane-bound polysomal cDNA library
 CC using a partial clone, obtained from an EST database search, as
 CC probe. The borage delta-6 desaturase nucleic acid can be
 CC operably linked to the seed-specific 5' regulatory region (see
 CC AAK24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed
 CC expression cassettes of the invention. Transgenic plants, e.g.,
 CC sunflower, soybean, maize, tobacco, cotton, peanut, oilseed
 CC rape or Arabidopsis are obtained that show increased levels of
 CC GLA or octadecatetraenoic acid. The levels of desirable fatty
 CC acids in oilseed crops can be manipulated to provide seed
 CC oils of use in human health and industrial applications.

XX Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;

Query Match 27.9%; Score 245.2; DB 20; Length 1684;

Best Local Similarity 57.7%; Pred. No. 4,4e-52;

Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

```

Qy      24 TTCTCCACCTCCACCGTCTTCCGACACACCGTCTCCGCGCTCTCCGACTACCGC 83
Db      265 TTTTTCACGCGGTATTATCTTAAAGTTACTCTGTTTGAAGTTTAAAGTTAAG 324
Qy      84 AAGCTTCTTCGACCTCTCCGCGCTCAACTCTTCAACCGGAGGCCACAACTCC 143
Db      325 AAGCTTGTGTGATGTTTCTAAATGGTTGTATGACAAATAAGTATATATGTTT 384
Qy      144 ATCTCTCTCTCCCTTATCTCACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 203
Db      385 GCAACTTGTGCTTATATGCAATGCTGTGTGATAGTGTATAGGGGTTTGTATTGT 444
Qy      204 GACAGCACTTGTGTGACGCTCTTCCGCTGATGATAGGCTTCTCGATTCAGAC 263
Db      445 GAGGCTTGTGTGATATGTTTCTGTGAGTGTGATGAGGTTTGTGATGACAT 504
Qy      264 GGCTGATAGGCGACGACTCCGCGCATTAACAGTATGCTGACGCCGCTCAACCGC 323
Db      505 GGTGTGATGACATGATGCTGCGCATTAATGATGATGATGATGATGATGATGATG 564
Qy      324 GCAATTCAGATTTCTCCGCAACATTTCTCCGCAATGACATGCGCTGTGGAAGTG 383
Db      565 TTATATGATATTTTCTCAAAATGCTTCTTCAAGATTAAGATTTGTTGGAATG 624
Qy      384 AACCAAGGCCACACATTCATGATGACAGCTGATGATGATGATGATGATGATGATG 443
Db      625 AACCATTAATGACATCAATGCTGTATATGATGATGATGATGATGATGATGATG 684
Qy      444 ATCCGCTCTTTCGATTCGTCGCGGCTTCTCAATTCATTAACCTCTGATTTGAG 503
Db      685 ATACCAATCTTGTGTGTCTTCAAGTTTGTGTTGTTGTTGTTGTTGTTGTTG 744
Qy      504 AGAAGTTNAGTTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTT 563
Db      745 AAAAGTTGACTTTTGTCTTATCAAGATTTCTTGTAAATTAATCAATGAGACATTT 804
Qy      564 TACCCGTAATGTGTGTGTCAGAGGTCATCTGTATCTGACAGCAATTCGTATTTGTT 623
Db      805 TACCTTATATGTGTGTGTCAGAGGTCATCTGTATCTGACAGCAATTCGTATTTGTTG 864
Qy      624 TCAGAGNAAAAGTGCAGATTAAGCT-TGAACATTAATGGGATCCTTGTGTTTGACT 682
Db      865 ACCAAGGAAATGTGTCCTATTCAGCTCAGAACTCTTGGAGATGCCATGTTCTGCATTT 924
Qy      683 TGGTTCCTCTTATAGTNCCTTGCCTGCAATTCGGCTTATGAGGATGTTTNGCTT 742
Db      925 TGGTACCCGTTGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 984
Qy      743 GCTAGCTTGTCTTGTGNCNATTCAGACATTCATTCATTCATTCATTCATTCATTCAT 802
Db      985 GCAAGTTTATGATGACTG-CAATGCAACAAGTTTCTTCTTGAACACATTTCTTCTT 1043

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QY 803 AATTATATGNCGGCA--CNANTGGAAATGACTGANT--GANAATCAGACAAGGGTC 858
 Db 1044 AAGTGTATTATGTTGAAAGCCTAAAGGAATATGTTGAGAACAAACGATGGAGC 1103
 QY 859 ATTGATATCTCTGTGNCCT 880
 Db 1104 ACTTGACATTTCTGTCTCT 1125

RESULT 11
 AAT30395
 ID AAT30395 standard; DNA; 1685 BP.
 AC AAT30395;
 XX
 DT 15-SEP-1996 (first entry)
 XX
 DE Borage delta-6-desaturase gene.
 XX
 KM Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KM polyunsaturated fatty acid; octadecatetraenoic acid;
 KM chilling resistance; oilseed; ss; ds.
 XX
 OS Borage officialis.
 XX
 FH Key Location/Qualifiers
 FT CDS 44..1390
 FT /tag= a
 XX
 PN W09621022-A2.
 XX
 PD 11-JUL-1996.
 XX
 PF 28-DEC-1995; 95WO-IB01167.
 XX
 PR 30-DEC-1994; 94US-0366779.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Freyssiuet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 DR WPI, 1996-333997/33.
 DR P-PSDB; AAR98455.
 XX
 PT Transgenic plants comprising the borage delta-6-desaturase gene
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 XX
 PS Claim 2; Page 51-52; 75PD; English.
 XX
 CC A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455),
 CC which catalyses the conversion of linoleic acid to gamma-linolenic
 CC acid (GLA). It was isolated from a borage membrane-bound polyosomal
 CC library using probes based on abundantly expressed seed storage
 CC protein cDNAs and with an isolated partial cDNA clone. The gene
 CC can be incorporated into a vector, pref. incorporating a
 CC tissue-specific promoter, for the expression of delta-6-desaturase
 CC in transgenic plants, esp. sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oilseed rape, resulting in increased GLA prodn.
 CC Alteration of plant lipids may also lead to improved chilling
 CC resistance.
 CC
 CC Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;
 SQ

Query Match 27.9%; Score 245.2; DB 17; Length 1685;
 Best Local Similarity 57.7%; Pred. No. 4.4e-52;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

QY 24 TTCTCAGCTCCGACGCTCTTCCGACGACGCTCTCGCGCCCTCTCCGACTACCGC 83
 Db 266 TTTTTCACCTGGGTATTATCTTAAAGATTAATCTGTTCTGAGGTTTCTAAAGATTATAG 325
 QY 84 AAGCTTCTCCGACCTCTCCGGCTCAACCTTCAACCGCAAGGCGACACAACTCTCC 143

Db 326 AAGCTGTGTGAGTTTCTTAAATGGGTTGTATGACAAAAGGCTATATATGTTT 385
 QY 144 ATCTCTCTCTCCCTTATCTACACCTTTTCTCTCTCTGTGCGGCTCCCTCTCC 203
 Db 386 GCAACTTGTGTCTTAAAGCAATGCTGTGTGATAGAGTGTATAGGGGTTTGT 445
 QY 204 GACAGCACTTGTGTCGACGCTTCCGCTGATGATGATGAGCTTCTGATTCAGAGC 263
 Db 446 GAGGTTTGTGTACATTTGTTTCTGTGGGTGTGATGGGTTTCTTGGATTGAGT 505
 QY 264 GGCCTGATAGGCGACGACTCCGGCCATTACAAAGTATGCTGAGCGCGCTCAACCGC 323
 Db 506 GGTGGATTGACATGATGCTGGGCTTATATGATGTCTGATTCAGAGCTTAATAG 565
 QY 324 GCATTCAGATCTCTCCGGCAACATTCGCGCGGAATAGCATCGGCTGTGAGAGTGG 383
 Db 566 TTTATGGGTATTTTGTGCGCAATGTCTTTCAGGAATAGTATGTTGTGGAATGG 625
 QY 384 AACCAACAGCCGACACATTCATGACACAGCTCGATATGACCTGATCGAGAC 443
 Db 626 AACCATATGACATACATTCCTCTGTATATAGCTTGAATATGACCTGATTTACAAT 685
 QY 444 ATGCGGCTTTGCAAGTTTCGTGCGGTTCTTCAATTCATACCTCTGATTCATGAG 503
 Db 686 ATACCATCTCTGTTGTGTCTTCAAGTTTGTGTTGCTGCTACCTCATTTCTATGAG 745
 QY 504 AGGAAGTTGAGTTGATTCATTCATGCTGATGTTCTGATCTGCTACGACATTTACTTT 563
 Db 746 AAAAGTTGACTTTGACTCTTATCAAGATCTTGTATGATTCATCACTTGACATTT 805
 QY 564 TACCGGTATGTTGTTGCCAGGTCACCTGTATCTGACAGACATTCGATTTGTT 623
 Db 806 TACCTATATATGTTGCTGATGCTCAATATATGATCAATCTCTCAATATGTTGTG 865
 QY 624 TCGAGGNGAAGTCCAGATAGACT-TGAATATATGGGATCTGTGTTTGGACT 682
 Db 866 ACCAAGAGAAATGTCTCATGAGCTCAGAACTCTTGATGCTGATGTTCTGAT 925
 QY 683 TGTTCCTCTTTAGTGTCTGCTGCAATTTGGGCTGATAGGGGATTTGNGCTT 742
 Db 926 TGTATCCGCTGCTGTTCTTCTTGTGCTTAATTTGGGGAATATATGTTTGTAT 985
 QY 743 GCTAGCTTGTCTGTTGNCNAATCCAGACATTCAGTTCTGTGAATCAGCTGCTGA 802
 Db 986 GCAAGTTATCTGATCTG-CAATGCAACAGTCAAGTCTCTTGAACACTTCTTTC 1044
 QY 803 AATTATATGNCGGCA--CNANTGGAAATGACTGANT--GANAATCAGACAAGGGTC 858
 Db 1045 AAGTGTATTATGTTGAAAGCCTAAAGGAATATGTTTGAAGAAACAAACGATGGAGC 1104
 QY 859 ATTGATATCTCTGTGNCCT 880
 Db 1105 ACTTGACATTTCTGTCTCT 1126

RESULT 12
 ABK49502
 ID ABK49502 standard; DNA; 1685 BP.
 AC ABK49502;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE DNA encoding Borage officialis delta6-desaturase.
 DE
 XX
 KM delta6-desaturase; sunflower; soybean; maize; tobacco;
 KM peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
 KM chilling tolerance; gene; ds; borage.
 XX
 OS Borage officialis.
 XX
 FH Key Location/Qualifiers

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FT CDS 44..1390
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XX 12-MAR-2002.
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XX 19-SEP-1997; 97US-0934254.
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XX 13-OCT-1992; 92US-0959952.
XX 10-OCT-1991; 91US-0774475.
XX 08-JAN-1992; 92US-0817919.
XX 14-SEP-1994; 94US-0307382.
XX 28-JAN-1997; 97US-0789936.
XX
XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX Thomas TL;
XX
XX MPI: 2002-380944/41.
XX P-PSDB; AAU79830.
XX
XX Novel nucleic acid encoding evening primrose delta6-desaturase which
XX converts linoleic acid to gamma linolenic acid useful for producing
XX gamma linolenic acid in transgenic plant or bacteria
XX
XX Example 9; Column 29-32; 53bp; English.
XX
XX The invention describes an isolated nucleic acid encoding an evening
XX primrose Delta6-desaturase. The nucleic acid and a vector expressing the
XX nucleic acid are useful for producing a plant such as sunflower, soybean,
XX maize, tobacco, peanut, carrot or oil seed rape plant, with increased
XX gamma linolenic acid (GLA) content, and also for inducing or increasing
XX production of GLA in a bacteria or plant deficient, lacking in or
XX producing low levels of GLA. The nucleic acid is also useful for inducing
XX chilling tolerance in plants. This sequence encodes the borage delta6
XX desaturase involved in the production of gamma linolenic acid.
XX
XX Sequence 1685 BP, 431 A, 277 C, 357 G, 620 T, 0 other;
XX
XX Query Match 27.9%; Score 245.2; DB 24; Length 1685;
XX Best Local Similarity 57.7%; Pred. No. 4,4e-52;
XX Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;
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XX 326 AAGCTTGTTGTTGATTTCTTAAATGGGTTTGATGACAAAAGGCTCATATTAGTTT 385
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XX 386 GCAACTTGTGCTTATAGCAATGCTGTTTGTATAGAGTTTATAGGGTTTGTTTGT 445
XX |||||
XX 204 GACAGCATTCTTGTGACGCTTTTCCGCTGCATTGATAGGCTTTCTTGATTCAGAGC 263
XX |||||
XX 446 GAGGGTGTGTTGTTGATATTGTTTCTGAGTGTGTTGAGTTTCTTGATTCAGAGT 505
XX |||||
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XX |||||
XX 506 GGTGATTTGAGATATATGCTGGGCATTTATAGTATGTTGATTTCAAGGCTTTAAG 565
XX |||||
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XX ID ABX15366 standard; cDNA; 1685 BP.
XX XX
XX ABX15366;
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XX 17-APR-2003 (first entry)
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XX Borage delta-6-desaturase #1 cDNA.
XX
XX Delta-6-desaturase; gene: ser; delta-12-desaturase; sunflower; soybean;
XX maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
XX octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
XX borage.
XX
XX Borage officinalis.
XX
XX Key Location/Qualifiers
XX CDS 44..1390
XX /*tag= a
XX /product= "Borage delta-6-desaturase #1"
XX /transl_except= (pos:1151..1153, aa:Ser)
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XX US2002108147-A1.
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XX 21-DEC-2001; 2001US-0029756.
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XX 13-OCT-1992; 92US-0959952.
XX 19-SEP-1997; 97US-0934254.
XX 10-OCT-1991; 91US-0774475.
XX 08-JAN-1992; 92US-0817919.
XX 14-SEP-1994; 94US-0307382.
XX 28-JAN-1997; 97US-0789936.
XX
XX (THOM) THOMAS T L.
XX
XX Thomas TL;
XX

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XX WPI: 2003-06659/06.
 DR P-PSDB; ABG73095.
 XX
 XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatrienoic acid production in plant
 XX
 XX Example 9; Fig 5A; 55pp; English.
 PS
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatrienoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatrienoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding a borage delta-6-desaturase polypeptide.
 XX
 SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

Query Match 27.9%; Score 245.2; DB 25; Length 1685;
 Best Local Similarity 57.7%; Pred. No. 4,4e-52;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTTTCCGACCAACCGTCTCCGCGCTCTCCGACTACCGC 83
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 386 GCACTTGTGTCTTATAGCAATGCTGTTGTATGAGTTTATGAGGTTTGTGTTTGT 445
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 506 GGTGATAGGACATGATGCTGGGCAATTATGATGATGCTGATTCAGAGCTTAATAG 565
 324 GCAATTCAGATTCTCTCCGCAACATTCGCGGGAATCAGATGGCTGTGAGAGTGG 383
 566 TTATATGGGATTTTGTGCAATTTGCTTCAAGATTAAGATTTGTTGGAATGG 625
 384 AACCAACAGCCACACATTCATGACACAGCTCGATAGACCTGATTCGACAGC 443
 626 AACCAATTAAGACATCAATGCTGTAATACCTGAAATAGACCTGATTTACAAAT 685
 444 ATGCGGCTTTTGCAGATTCTGCGGCTTCAATTCATTAACCTGATTTCTATGAG 503
 666 ATACATCTCTGTTGTGTCTTCAAGTTTGTGTTCTCAGCTCATCTTCTATAG 745
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 746 AAAAGGTTGACTTTGACTCTTATCAAGATCTTGTGAATTAATCAACATTTGACATTT 805
 564 TACCGGTAATGTTGTTGCGAGGCTGATTCGACAGACATTTCTGATTTGTT 623
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 624 TCAGAGNGAAGATGACAGATAGACT-TGAACATTAATGGGATCTTGTGTTGACT 682

Db 866 ACCAAGAAATGCTCCTATGAGCTGAGAACTCTTGAGATGCTGATTCGATT 925
 Qy TGGTCTCTTTTATGATGCTGCTGCCAAATGGGCGCTGATAGGAGNATGTTNGCTT 742
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 Db 986 GCAAGTTATCAGTACGCTG-GAATGCAACAAAGTTCAAGTTCTCTGAAACACTTCTTTC 1044
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RESULT 14

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 DT 21-JAN-2003 (first entry)
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 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.
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 KW Arabidopsis thaliana; plant; gene; stress; transgenic; de.
 XX
 OS Arabidopsis thaliana.
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 PN W0200216555-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US26685.
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 PR 24-AUG-2000; 2000US-227866P.
 XX
 PR 26-JUN-2001; 2001US-264647P.
 XX
 PR 22-JUN-2001; 2001US-300111P.
 XX

PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Krepe J, Wang X, Zhu T;
 XX

WPI: 2002-304127/34.

Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 PT
 PS Claim 6; SEQ ID NO 558; 577bp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stresses. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 SQ Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 other;

Query Match 27.7%; Score 244.2; DB 24; Length 1350;
 Best Local Similarity 57.2%; Pred. No. 7.3e-52;
 Matches 469; Conservative 0; Mismatches 349; Indels 2; Gaps 2;

QY 1 CGGCTCCCTCTCTCTCCCGCCTTCTCCACGCTCCGCTTTCCGACACACGCTCT 60
 DB 203 CGGCTTGCGACATCTGACATCTCTTCCCGTTACACATCAGAGATTTCCAACTCT 262
 QY 61 CGCGCGCTCTCCGACATCCGCAAGCTCTTCCGACCTCCGCGCTCAACTCTTCA 120
 DB 263 CGCAAGTCTACCGGATACCGGTGATGAGCTGCGAGTTTCGTAACCTGGTCTTG 322
 QY 121 ACCGCAAGGCGCACACAACTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 DB 323 AAAACAAGGTACAGTTACTCTTACACTTACCTCTGCGCGCATCTCTCTGAG 382
 QY 181 CTGTCTGCGGCT 240
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XX AAC51462;
 DT 18-OCT-2000 (first entry)
 XX Arabidopsis thaliana DNA fragment SEQ ID NO: 68612.
 DE Hybridisation assay; genetic mapping; gene expression control;
 XX protein identification; signal transduction pathway;
 KM

KM metabolic pathway; promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
 XX EP1033405-A2.
 PD 06-SEP-2000.
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 PF 25-FEB-2000; 2000EP-0301439.
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 XX 25-FEB-1999; 99US-0121825.
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PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151348.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.

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PR 10-SEP-1999; 99US-0153070.
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PR 22-OCT-1999; 99US-0160989.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 27.7%; Score 244.2; DB 21; Length 1650;
 Best Local Similarity 57.2%; Pred. No. 7,8e-52;
 Matches 469; Conservative 0; Mismatches 349; Indels 2; Gaps 2;

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QY 61 CCGCGCCTCTCTCGACCTTCTCCGACCTTCTCCGACCTTCTCCGCTCAACTCTTCA 120
DB 469 CCGAAGTCTCAGCGATTACCTCGTAGGCTGCGGAGTTTGTAATCGGCTCTTGG 528
QY 121 ACCGCAAGGCGCACCAACATCTTCCTCTCTCTCTTATTTCAACCTTTTCTCTCT 180
DB 529 AAAACAAAGGTACAGTTACTCTACACTCTAGCTTGCCTGCGCCGACATGTTCTCGAG 588
QY 181 CTGTCTCGGCGCTCTCTTCTCCGACAGACTTTGTGTGACGTGTTCCGCTGATTTCA 240
DB 589 TTCTCTACCGGTATTTGGCTGTACTCTCGTCTGCTTACCAATTCGCGCGGCTTC 648
QY 241 TAGGCTTCTCTGATTGAGACGGGCTGATAGGCGACACTCCGCGCATTTACAGTGA 300
DB 649 TGGGTCTCTCTGATCCAGAGCGCTTACATAGTTCACAGATTTCTGTACATTATCA 708
QY 301 TGCTAGCGCGCGCTCAACCGCGCAATTGAGATTTCTTCGCGCAACTTTCGCGGAA 360
DB 709 TGTGCAACAAATCTTATTAACAGATTGCTCAGCTTCTCTCGGTAACTGTCTCACCGGAA 768

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Oy	361	TCAGATCGCGTGGGAAAGTGGAAACCAACAGCCACCAATGGCATGCAACAGCCTCG	420
Db	769	TCTCAATGCGGTGGGAAATGGACTCAACAAATGCTACATCTAGCTTGTAAAGCCTCG	828
Oy	421	ACTATGACCCGTGATCTGGAGACATGCGCGTCTTTCAGTTTCGTGGCGGTTCTTCAAT	480
Db	829	ATTACGATCCAGATCTCAACACATCCGTCTTCGCGGTCCACCAAAATTTCTTCTCT	888
Oy	481	CCATTAACCTTCATTCATATGGAGGAAGTTNGAGTTTGATTTNCACTTGCTANGTCTTGA	540
Db	889	CATTGACCTCGAGATCTTACAGATGGAAATCTACGTTTGATTCAGTCCGAGATTCCTAG	948
Oy	541	TCTGCTACCAACACATTTACTTTTAAACCGGTAATGTGTGTGGCAGGGTCAACTGTATC	600
Db	949	TCAGTATCAACACCTTACTATTAATTCAGTTATGTGCTTTGGAAAGATCAATCTCTTCA	1008
Oy	601	TGCAGACATTTCTGCTATTTGTTTTCGAGAGGAAAGTGCAGAGATAGAC-TTGAACATPA	659
Db	1009	TTCAACGCTTTCCTGTGCTCTTCTCCAAACGTGAAGTACAGATGTGTCCTTTAAACTTCG	1068
Oy	660	TGGGATCTCTGTGTGTTTGACTTGGTCCCTCTTTAATGACTGCTCGCCAAATTTGGCG	719
Db	1069	CCGGAATTTAGTCTTCTTGAGACTTGTTCCACCTTTAGTCTCATGTCTACCAAACTGGC	1128
Oy	720	CTGATAGGGGNAATGTTGNGCTTGCTAGCTTTCGTGTTGTGNCNATCAGACACATTCAG	779
Db	1129	CTGAGAGATTCCTTCTTCGCTTTCACAAAGCTTCAACCG-TCACGGCGGCTTCAACACATTCAA	1187
Oy	780	TTCTGCTTGATCAACCTTGCGAAAAATTTAATAGCGGGC	819
Db	1188	TTCAAGCTTAACATTTGCTGCTGATGATCTTACGTTGGTCT	1227

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Search completed: December 31, 2003, 16:16:41
Job time : 170.985 secs
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: cdu@resgen.com web site:
 www.resgen.com

Seq primer: -40RP from Gibco
 High quality sequence stop: 434.
 Location/Qualifiers

FEATURES

source

1. 726
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1062-9581"
 /tissue_type="stem tissue of greenhouse grown plants"
 /dev_stage="1 month old"
 /lab_host="DH10B"
 /clone_lib="Gm-c1062"
 /note="Vector: pBluescript II SK+, Site 1: EcoRI, Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from stem tissue of 1 month old greenhouse grown plants
 for the cultivar Raiden. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with a XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA fragments were
 directionally cloned into the EcoRI-XhoI restriction site
 of the pBluescript vector. The ligated cDNA fragments were
 transformed into DH10B host cells (GibcoBRL). This library
 was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT

121 a 216 c 158 g 231 t

ORIGIN

Query Match 57.1%; Score 502.8; DB 14; Length 726;
 Best Local Similarity 82.8%; Pred. No. 1e-110;
 Matches 581; Conservative 0; Mismatches 120; Indels 1; Gaps 1;

Qy 57 GTCTCCGCGGCTCTCTCGACTACCGCAAGCTCTTCTCCGACCTCTCCGGCTCAACTTC 116
 Db 1 GTCTCCGCGGCTCTCTCGACTACCGCAAGCTCTTCTCCGACCTCTCCGGCTCAACTTC 60
 Qy 117 TTCAACCGCAAGGCGCACAACTCATCTCTCTCCCTTAATTCACCTTTTCT 176
 Db 61 TTCAACCGCAAGGCGCACAACTCATCTCTCTCCCTTAATTCACCTTTTCT 120
 Qy 177 CTCTCTGTGCGGCGCTCTCTCTCCGACGACATTCGTCGACGCTTTCCGCTGCA 236
 Db 121 CTCTCTGTGCGGCGCTCTCTCTCCGACGACATTCGTCGACGCTTTCCGCTGCA 180
 Qy 237 TTGATAGGCTTTCTCTGATTCAGAGCGGCTGATAGGCAAGCTCCGGCCATTACAC 296
 Db 181 TTGATAGGCTTTCTCTGATTCAGAGCGGCTGATAGGCAAGCTCCGGCCATTACAC 240
 Qy 297 GTATAGTCAGCGCGCGGCTCAACCGGCAATTCAGATTCTCCCGGCAATTCTCGCC 356
 Db 241 GTATAGTCAGCGCGGCTCAACCGGCAATTCAGATTCTCTCCGGCAATTCTCGCC 300
 Qy 357 GGAATCAGATCGGCTGTGGAAGTGAACCAACCCGACACCATTCGATGCAAGC 416
 Db 301 GGAATCAGATCGGCTGTGGAAGTGAACCAACCCGACACCATTCGATGCAAGC 360
 Qy 417 CTGACTATACCTCTGATTCGACGACATCGCGGCTTTGCGAGTTCTCTTC 476
 Db 361 CTGACTATACCTCTGATTCGACGACATTCGCGCTTCTCTGAGTTTCTTC 420
 Qy 477 AATTCCATACCTCTGATTCGAGAGAGATTGAGTTGATTCATTTGCTGAGTTTC 536
 Db 421 AATTCCATACCTCTGATTCGAGAGAGATTGAGTTGATTCATTTGCTGAGTTTC 480
 Qy 537 TTGATCTGACACGACTTACTTTTACCCGGTAATGTTGTCAGAGGCTCAATTG 596

Db 481 TTGTTAGTTACGACACTGACTTTTACCCCTGTGATGTTTCCGTAGGGTTAATCTG 540
 Qy 597 TATCTGACAGCAATTCGCTATTGTTTGGAGGNGAAGTGCAGATGAG-GCTTGAAC 655
 Db 541 TTGCGGAGCTTTTCTGTGTGTTCTTAAGAGAGGGGTGAGAACAGGCACTGAG 600
 Qy 656 ATATAGGAGATCTTGTGTTTGGAGTTGCTCTTTTATGATGCTTCGCAATT 715
 Db 601 CTTTGGGGTGTGTTGATTCCTGGGTTGTAACCTTTGTGTTTCTCTTCCCAAT 660
 Qy 716 GGGCTGATAGGGGAAATGTTGCTGCTGCTGCTGTT 757
 Db 661 TGGTGGAGAGGCTTTGTTGTTTCTGAGTTTCTGTT 702

RESULT 2
 A1748200 579 bp mRNA linear EST 30-NOV-2001
 LOCUS b949411.y1 Gm-c1011 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-c1011-238 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME B5.
 mRNA sequence.

ACCESSION A1748200
 VERSION A1748200.1 GI:5126464
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 579)
 Shoemaker R., Keim P., Vodkin L., Erpelting J., Corryell V., Khana
 A., Bolla B., Maria M., Hillier L., Kueba T., Martin J., Beck C.,
 Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers
 Y., Person B., Swaller T., Gibbons M., Page D., Harvey N., Schuck
 R., Ritzer E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann
 R., Waterston R. and Wilson R.
 Public Soybean EST Project

TITLE Unpublished
 JOURNAL Contact: Shoemaker R./Public Soybean EST Project
 COMMENT Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 Possible reversed clone: similarity on wrong strand This clone is
 available through: ResGen, Invitrogen Corp. 2130 South Memorial
 Parkway Huntville, AL 35801 For further information call: (800)
 533-4363 or contact via email: cdu@resgen.com
 Insert Length: 1134 Std Error: 0.00
 High quality sequence stop: 412.
 Location/Qualifiers

FEATURES

source

1. 579
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1011-238"
 /tissue_type="immature cotyledons of greenhouse grown
 plants"
 /lab_host="DH10B"
 /clone_lib="Gm-c1011"
 /note="Vector: pBluescript II SK+, Site 1: EcoRI, Site 2:
 XhoI; This cDNA library was constructed from mRNA isolated
 from immature cotyledons (100-200mg) of greenhouse grown
 plants. The cDNA library was prepared using the Life
 Technologies SuperScript cDNA library construction kit.
 Complementary DNA was synthesized from mRNA using a poly
 (dT) sequence with a Not I restriction site. Sal I
 linkers adapters were ligated to the blunt-ended cDNA
 fragments followed by NotI digestion. The cDNA fragments
 were directionally cloned into the NotI-Sal I restriction
 site of the pSPORT 1 vector. The ligated cDNA fragments

were transformed into E. coli Electromax DH10B host cells.
This library was constructed by Dr. Lila Vodkin and Dr.

BASE COUNT 119 a 126 c 143 g 187 t 4 others

Query Match 45.7%; Score 402.4; DB 9; Length 579;

Best Local Similarity 89.6%; Pred. No. 1.6e-86;
Matches 499; Conservative 0; Mismatches 50; Indels 8; Gaps 7;

ORIGIN

330 CAGATTCTCTCCGGCAACATTCCTGCGCGGAATCAGATCGGCTGTGGAAAGTGAACAC 389
16 CGATCTCTCTGGGAAGTCTTGAACCGGATTAAGCATTTGTTGGAAGTGAATCTCAC 75
390 AAGCCACACATTCGATGCAACACCTCGATAGCCCTGATGCGATGCAACGAC 449
76 AATGTCACACATTCGATGCAACACCTCGATAGCCCTGATGCGATGCAACGAC 449
450 GTCTTTGCAATTCGATGCAACACCTCGATAGCCCTGATGCGATGCAACGAC 509
136 GTCTTTGCAATTCGATGCAACACCTCGATAGCCCTGATGCGATGCAACGAC 195
510 TTGAGCTTTGATTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 569
196 TTGAGCTTTGATTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 255
570 GTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629
256 GTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
630 NGAAGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687
316 CGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 375
688 CCTTTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 747
376 CCTTTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
748 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 807
435 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
808 TATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863
494 TATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
864 ATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
554 ATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570

RESULT 3
BE347857 592 bp mRNA linear EST 04-DEC-2001
LOCUS sp06107.Y1 Gm-cl041 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl041-2102 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
EST. BE347857
VERSION BE347857
KEYWORDS BE347857.1 GI:9259710
SOURCE Glycine max (soybean)
ORGANISM Glycine max

REFERENCE
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schuck, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE Public Soybean EST Project
JOURNAL Unpublished
CONTACT Shoemaker R/Public Soybean EST Project
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Trace considered overall poor quality This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccr@resgen.com
Insert Length: 149 Std Error: 0.00
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1..592
/organism="Glycine max"
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl041-2102"
/issue_type="Senescing leaves, mature plant, greenhouse grown"
/lab_host="DH10B"
/clone_lib="Gm-cl041"
/note="Vector: pT733Pac (Pharmacia); Site 1: EcoRI; Site 2: HindIII. This library was constructed from mRNA isolated from senescing leaf tissue of mature greenhouse grown plants of the cultivar Williams. Complementary DNA was synthesized from mRNA using a 3' anchored poly(dT) primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and HindIII. The cDNA fragments were directionally cloned into the EcoRI-HindIII restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells. This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 132 a 124 c 139 g 197 t

Query Match 38.8%; Score 341.6; DB 10; Length 592;

Best Local Similarity 83.7%; Pred. No. 7.8e-72;
Matches 427; Conservative 0; Mismatches 79; Indels 4; Gaps 4;

ORIGIN

312 CGCTTCACCGCGCAATTCATCTCTCCGCAACATCTCGCGGATCGATCGCG 371
2 CGTCCCAACATGTTGCAACATCTCTCTGGAATGCTTACCGGATGACATGCT 61
372 TGATGAGTGGACACACAGCCACCATTCGATGCAACAGCTCGATGACCT 431
62 TGATGAGTGGACACATGATCTCAACATTCGATGCAACATCTTACCATGACCT 121
432 GATTCGACACATGCGGCTCTTTCAGTTTCGCGGCTTTCATTCATTCATCTCT 491
122 GATTCGACACATGCGGCTCTTTCAGTTTCGCGGCTTTCATTCATTCATCTCT 181
492 CATTCATGAGGAGAGATGATTCATTCATTCATTCATTCATTCATTCATTCAT 551
182 CATTCATGAGGAGAGATGATTCATTCATTCATTCATTCATTCATTCATTCAT 241
552 CACTTACTTTTACCCGTAATGATGATGATGATGATGATGATGATGATGATGAT 611
242 CACTTACTTTTACCCGTAATGATGATGATGATGATGATGATGATGATGATGAT 301
612 CTGCTATTTTTCAGAGGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 670
302 CTGCTATTTTTCAGAGGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 361
671 GGTGTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 729
362 GAGTTTGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 420
730 NAGTTTGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 789

BASE COUNT	36 a	186 c	74 g	113 t	5 others
ORIGIN					
Query Match	36.1%;	Score 318;	DB 12;	Length 414	

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1. 538
source
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"

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Db 807 ACATATGCTCTTCTTACCAACGACCCCTGGGCTTCATGCGCCTCGAAATTCCTCA 866
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 Db 867 TCAAGTACGACACTGACCTTCTACCCGGTAATGTGTGTCAGAGGTCAACTGTATC 926
 QY 601 TCGACAAATTCCTGCTATTTGTCAGAGGAAAGTCAAGA-TAGAGCTTGAAATTA 659
 Db 927 CGCAGTCCGCTGTGTCTTCACGGAAGAGGGTGGCCAGCGGTGCTTGAGATCG 986
 QY 660 TGGGATCTCTGTGTGTGACTGTCTCTTTTATGATGCTTGCTGCAATTTGGC 719
 Db 987 CGGAGGCTCGCAATCTCGGCTGTGATCCGCTGTGCTGTGCTGTCCCTCGAATTTGT 1046
 QY 720 CTGATAGGGGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779
 Db 1047 GGAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1105
 QY 780 TTTCTGTTGATGACCTTGTGTAATTTATGATGCGAGC-ACNANTGGGAATGACTGG 837
 Db 1106 TTTCTGCTGTAACACTTCTGCTGCGAGCTGATGTGCGGCGCACCAGGCAATGACTGG 1165
 QY 838 NT 839
 Db 1166 TT 1167

RESULT 7
 BH687867/c 823 bp DNA linear GSS 19-FEB-2002
 LOCUS BOHS094TR BO_2.3 KB Brassica oleracea genomic clone BOHS094,
 DEFINITION genomic survey sequence.
 ACCESSION BH687867
 VERSION BH687867.1 GI:18758304
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eustosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 823)
 REFERENCE Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other GSSs: BOHS094TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 FEATURES
 source location/Qualifiers
 1. 823
 /organism="Brassica oleracea"
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 /strain="TO100DH3"
 /db_xref="taxon:3712"
 /clone="BOHS094"
 /clone_1b="BO_2.3 KB"
 /note="Vector: pHD51, Site 1: BstXI, 2-3 kb sheared
 genomic DNA inserted into pHD51 using BstXI linkers"
 BASE COUNT 182 a 197 c 283 g 161 t
 ORIGIN
 Query Match 31.9%; Score 281; DB 28; Length 823;
 Best Local Similarity 63.6%; Pred. No. 3.8e-57;
 Matches 439; Conservative 0; Mismatches 250; Indels 1; Gaps 1;
 QY 1 CGCGCTCCCTCTCTCTCCCGCTTCTCCACCTCCACCGCTTTCGACACACCGCTCT 60

Db 705 CCCCTGGGACACCCCTCGACGCGCTTCTTCAACCGGCTACACATCGAGAGTACGAACTCT 646
 QY 61 CGCGCGCTCTCTCGACTACCGGAGCTCTCTCGAGCTCTCGGCTCTCACTCTTCA 120
 Db 645 CCGAGTCTCCCGGCTACCGGCTACCGGCTACCGGCTACCGGCTACCGGCTACCGGCT 586
 QY 121 ACCGAAAGGCGCACACACCTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 Db 585 AATCCAAAGGAGACAAACACTCTACACGCTATCTTCAATGCGGCTATGCGCGGCG 526
 QY 181 CTCTCTCGGCGCT 240
 Db 525 TCTCTACGCTGTTTGTGGGCTGCGACTCGATCTGCTCTACAGATCGCGCGCTTC 466
 QY 241 TAGGCTTCTCTGATTCAGAGGCTGATAGGCGGACAGCTCCGCGCAATTAAGTGA 300
 Db 465 TCGGACTCTCTGATTCAGAGGCTGATAGGCGGACAGCTCCGCGCAATTAAGTGA 406
 QY 301 TGTCAAGCGCGCTCTCAACCGGCAATTCAGATCTCTCTCTCTCTCTCTCTCTCTCT 360
 Db 405 TGTCAAGCAAGAGATTAACAGATGCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 346
 QY 361 TCAAGTCCGCTGTGGAAGTGAACCAACGCGGCAACCAATTCAGATTCAGAGCTCTG 420
 Db 345 TCTGATCGGCTGTGGAAGTGAACCAACGCGGCAACCAATTCAGATTCAGAGCTCTG 286
 QY 421 ACTATGACCTCTGATTCAGAGGCTGATAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 480
 Db 285 AATGACATCCGATTCAGAGGCTGATAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 226
 QY 481 CCATTAACCT 540
 Db 225 CGATGACGCTGATTCAGAGGCTGATAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 166
 QY 541 TCTGCTACGACACTTACTTTTACCCGGTAATGTGTGTCAGAGGTCAACTGTATC 600
 Db 165 TTAGTACACGACACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 106
 QY 601 TCGACAAATTCCTGCTATTTGTCAGAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAG 659
 Db 105 TCGACAGCTTCT 46
 QY 660 TGGGATCTCTGTGTGTGACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 689
 Db 45 CGGAGATCTTGTGTGTGACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 16

RESULT 8
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 LOCUS saj48e09.y1 Gm-cl072 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-cl072-2921 5' similar to FR:082348 082348 PUTATIVE CYTOCHROME
 B5., mRNA sequence.
 ACCESSION BM143768
 VERSION BM143768.1 GI:17453835
 KEYWORDS EST.
 ORGANISM Glycine max (soybean)
 SOURCE Glycine max
 REFERENCE Glycine max (soybean)
 AUTHORS Shoenaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoenaker R/Public Soybean EST Project

Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: cdu@resgen.com web site:
 www.resgen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 426.
 Location/Qualifiers

FEATURES

source

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 /issue_type="seedlings induced for symptoms of SDS
 (Sudden Death Syndrome) disease"
 /dev_stage="2-3 weeks old"
 /lab_host="DH10B"
 /clone_lib="Gm-c1072"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI, Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from 2-3 week old seedlings that were induced for symptoms
 of SDS (Sudden Death Syndrome) disease by the
 translocation of culture filtrate of Fusarium solani f.
 sp. Glycines (Plant Cell Report 18:375-380). Cultivar PI
 567374 is partially resistant to the disease SDS. Plant
 tissue (expanded leaves, folded leaves, and new shoots)
 were collected at 1, 6, 24, and 48 hrs. after inoculation
 and their mRNA pooled equally for cDNA construction. The
 library was prepared using the Stratagene pBluescript II
 SK(+) library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with an XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA insert is protected
 from XhoI digestion via methylation during first strand
 synthesis. The cDNA fragments were directionally cloned
 into the EcoRI-XhoI restriction site of the pBluescript
 vector. The ligated cDNA fragments were transformed into
 E. coli Electromax DH10B host cells. Plants were inoculated
 by Shuxian Li (Glen Hartman lab, University of Illinois).
 Library was constructed by Steve Clough (Illa Vodkin lab,
 University of Illinois)."

BASE COUNT 124 a 120 c 138 g 205 t 1 others
 ORIGIN

Query Match 31.4%; Score 276.4; DB 12; Length 588;
 Best Local Similarity 67.5%; Pred. No. 4.3e-56;
 Matches 396; Conservative 0; Mismatches 190; Indels 1; Gaps 1;

169 TTTTCTCTCTCTGCTGGCGGCTCTTCCGACAGCACTTCGAGCACTGCTT 228
 Db 2 TGTTCATTTGTTTATGATGATGATGATGATGATGATGATGATGATGATG 61
 229 CCGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 288
 Db 62 CTGCGCTTTTGTGGGCTTCTTGTGATGATGATGATGATGATGATGATGATG 121
 289 ATTACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 348
 Db 122 ACTATAGGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 181
 349 TTCTCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 408
 Db 182 GCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
 409 GCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 468
 Db 242 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 301

Qy 469 GGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 528
 Db 302 GGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 361
 Qy 529 CTATGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 588
 Db 362 CAGGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
 Qy 589 TCACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 648
 Db 422 TCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 481
 Qy 649 -CTGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 707
 Db 482 CTTTACATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 541
 Qy 708 GCCAATTTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 754
 Db 542 TACCAATTTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 588

RESULT 9
 CA935212 449 bp mRNA linear EST 30-DEC-2002
 LOCUS sau50d04.y1 Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-c1071-4376 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
 B5.1, mRNA sequence.
 ACCESSION CA935212 GI:27423692
 VERSION CA935212.1
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 449)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,
 R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,
 R., Materston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished

TITLE JOURNAL
 COMMENT Public Soybean R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: cdu@resgen.com web site:
 www.resgen.com
 Seq primer: -40RP from Gibco.
 Location/Qualifiers

FEATURES

source

1. 449
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1071-4376"
 /issue_type="immature pods (~2cm long) of greenhouse
 grown plants"
 /lab_host="DH10B"
 /clone_lib="Gm-c1071"
 /note="Vector: pSPORT1; Site 1: NotI, Site 2: SalI, The
 cDNA library was constructed from mRNA isolated from
 immature pods (approximately 2cm long) of greenhouse grown
 plants. The library was prepared using the Life
 Technologies superscript cDNA library construction kit."


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source
1. .783
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="pHOGA-15P24"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C
with 0.5 mg/ml oligogalacturonide (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="X10LR"
/clone_lib="HOGA"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-aseIst
helper phage and propagated in SOLR cells."

BASE COUNT      173 a      142 c      169 g      299 t
ORIGIN
Query Match      29.0%; Score 254.8; DB 10; Length 783;
Best Local Similarity 65.2%; Pred. No. 7.8e-51;
Matches 441; Conservative 0; Mismatches 226; Indels 9; Gaps 5;

207 AGCACTTGTGACGCGCTTCCCGCATGATGAGCTTTCTCGGATTGACAGCGGC 266
    |||
21 AGGTGTTGGGCTATTAAGTCTGATGATGTTGGTTGCTATGATGACAAAGTACT 80
    |||
267 TGGATAGGCGACACTCCGCGCATTAACAGTATGCTACCGCGCTCAACCGGCA 326
    |||
81 TATATTGCTATATTTCTGCTATTAAGAGTTATGCGATGGAATTATTAACAATTA 140
    |||
327 ATTCAATTTCTCCGCAACATTTCTCGGAAATGACATCGGCTGGTGAAGTGAC 386
    |||
141 GCACAATTTCTTGTGTAATTTATGATGATGATTAAGTATGCTGGTGAAGTACT 200
    |||
387 CACAAGGCCACACATGATGACAAAGCTGATGATGATGATGATGATGATGATG 446
    |||
201 CATTAAGCTCATATGATGCTGCAATGATGATGATGATGATGATGATGATGATG 260
    |||
447 CCGGCTTTGCACTTGTGCGCGCTTCTCAATTCATTAATCTCTCATTTGAGGAG 506
    |||
261 CCGTGTTCGCTGCTCATGCGATTTCTTGTTGATTAATCTTATTTCTATGATGA 320
    |||
507 AAGTNGAGTTGATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 566
    |||
321 CAGTTAAGTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 380
    |||
567 CCGGTAATGCTGCTGCGAGGTCATTTGATCTGACAGCAATTCGCTATTTGTTGG 626
    |||
381 CCGTCTTGTGTTGCAAGGCTTAATCTTACCTTCAACATTTTGTGCTTTGTTGG 440
    |||
627 ---AGGNGAAGATGAGATGAGCTT-GAACATTAATGAGGATCCCTGTTTGGACT 682
    |||
441 CCATCAAGAAATTTCTGATAGCTTTACAAATCATGAGTATCGGTGTTCTGAGCT 500
    |||
683 TGGTCTCTTTAGTATGCTGCTGCAATTTGGGCTGATAGGAGGATGTTGNCCTT 742
    |||
501 TGGTCCCTCTGCTATGATGATGCTGCAAGTTGGCAGAAAGGCTCATGTTGTTCTT 560
    |||
743 GCTAGCTTTGCTGTTGTCNCAATCCAGCAATTCAGTTGCTGTTGATTAACCTTGCTGA 802
    |||
561 GCTTGTGTTGTTGTTGTTTC-ATCCAAATCTTCAATTTGTTTGAACATTTGCTGTC 619
    |||
803 AAATTTATATGNGGCG--ACNANTGGAGTGAATGCTGANTGAMATGACAAG--GGGTC 858
    |||
620 AAACGCTATCTGGTTCACCGAGCGAATGATGTTGTTTCAAGAAACAGCTGGAAC 679
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859 ATTGATATCTCTTGT 874
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680 ATTGATATCATCTTGT 695
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RESULT 13
BG882077
LOCUS
DEFINITION
  BG882077 494 bp mRNA linear EST 29-NOV-2001
  sae95g06.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
  ID: Gm-cl065-3779 5' similar to TR:082348 082348 PUTATIVE
  CYTOCHROME B5. ; mRNA sequence.
ACCESSION
  BG882077
VERSION
  BG882077.1 GI:114259169
KEYWORDS
  SOURCE
  ORGANISM
    Glycine max (soybean)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
    ; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
    Glycine.
  1 (bases 1 to 494)
  Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
  ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
  Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
  ,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuck
  ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
  ,R., Waterston,R. and Wilson,R.
  Public Soybean EST Project
  Unpublished
  Contact: Shoemaker R./Public Soybean EST Project
  Public Soybean EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@wustl.wustl.edu
  This clone is available through: Resgen, Invitrogen Corp. 2130
  South Memorial Parkway Huntville, AL 35891 For further information
  call: (800)-533-4363 or contact via email: ccu@resgen.com
  Insert Length: 1782 Std Error: 0.00
  High quality sequence stop: 415.
  Location/Qualifiers
    1..494
      /organism="Glycine max"
      /mol_type="mRNA"
      /db_xref="taxon:3847"
      /clone="GENOME SYSTEMS CLONE ID: Gm-cl065-3779"
      /tissue_type="germinating shoots"
      /lab_host="DH10B"
      /clone_lib="Gm-cl065"
      /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
      XhoI; The cDNA library was constructed from mRNA isolated
      germinating shoots of the cultivar Williams. The seeds
      were allowed to germinate for 24 hours prior to being
      cold stressed for 2 days at 4C. Complementary DNA was
      synthesized from mRNA using a primer consisting of a
      poly(dT) sequence with a XhoI restriction site. EcoRI
      adapters were ligated to the blunt-ended cDNA fragments
      followed by XhoI digestion. The cDNA fragments were
      directionally cloned into the EcoRI-XhoI restriction site
      of the pBluescript vector. The ligated cDNA fragments were
      transformed into DH10B host cells (GibcoBRL). This library
      was constructed in the laboratory of Dr. Randy
      Shoemaker."

BASE COUNT      113 a      106 c      105 g      170 t
ORIGIN
Query Match      28.9%; Score 254.2; DB 12; Length 494;
Best Local Similarity 70.6%; Pred. No. 9.2e-51;
Matches 345; Conservative 0; Mismatches 143; Indels 1; Gaps 1;

306 AGCCGCGCTCAACCGCGCATTCATTTCTCCGCAACATTTCCCGGAAATCAGC 365
    |||
3 AGCCCTGGCTACAAATTTGGCAAAATCTTTGTTGGCAATTCATGATGATGATGATG 62
    |||
366 ATGGCTGTGTAAGTGAACCAACAGCCACACATTCATGATGATGATGATGATGAT 425
    |||

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Db 63 ATGTCATGCTGGAGTGAAGTCACTACATGCTACACATCTCATGACATAGTCTTGACTAT 122
Qy 426 GACCCGATCTGACAGACATGCCGCTTTTGACGTTTCGCGGGTCTTCAATTCATA 485
Db 123 GATTCGATCTCCAGACATACCTGCTTGGCCGCTGACACGCGTCTTCAATTCATA 182
Qy 486 ACCTCTCATCTCATGAGAGAAAGTGGATTGATTGATTCATGCTTATGTTCTGATCTGC 545
Db 183 AATCTGTTTCTTATGAAAGAAATGCTGTTGATTCTATCATAGTTTCTCATCAGC 242
Qy 546 TACACACACTTTACCTTTTACCCGCTAATGCTGTTGACGAGGCTCACTTGAATCTGAC 605
Db 243 TACACACACTTTACCTTTTACCCGCTAATGCTGTTGACGAGGCTCACTTGAATCTGAC 302
Qy 606 ACAATCTCTCATGTTTCTGAGAGNAAAAGTCCAGAGATGAG-CTTGAACATATGGGG 664
Db 303 ACTTGTGCTGCTGTTGCTCTAGAGAAAAGTCCAGATGAGCTTTTAACTAATGAGGG 362
Qy 665 ATCCCTGCTGTTTGAAGTCTGCTCTTCTTGTAGTGTGCTGCTGCAAAATGGGCTGAT 724
Db 363 ATCTCTGTTGTTGGGTTGGTTGCTCCTCTGTTGATCTCTTCACTACCAATGGGAGAA 422
Qy 725 AAGGAGATGTTGAGCTTCTGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 784
Db 423 AAGGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 482
Qy 785 GTTGAACTCA 793
Db 483 TTTGAACCA 491

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RESULT 14

CB829088 585 bp mRNA linear EST 16-MAY-2003
 LjNEST93hr Lotus japonicus nodule library 5 and 7 week-old Lotus japonicus cDNA 5', mRNA sequence.

CB829088
 CB829088.1 GI:29969635

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

122 a 124 c 141 g 198 t
 BASE COUNT
 ORIGIN

Query Match 28.6%; Score 251.8; DB 14; Length 585;
 Best Local Similarity 64.3%; Pred. No. 3,7e-50;
 Matches 373; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

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Qy 75 GACTACCGCAAGCTTCTCTCGACCTCTCGCGCTCAACCTTTCACCGCAAGGCCAC 134
Db 5 GATTACAGAAACCTGTGACCGAGTTTGTCAAAATGGGGCTTTTGTAGAAAGAAAGCAT 64
Qy 135 ACAACCTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 194
Db 65 GTACACCTTATACACCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 124
Qy 195 CTTCTCTCGACAGCACTTGTGTCAGCGTCTTTCGCGTCAATGATAGGCTTCTCTG 254
Db 125 CTCAGATGCAAGAGCTGTGGCTATTTGGCTCTGCAATGTTCTGGGTTTCTTGG 184
Qy 255 ATTCAGAGCGGCTGTATAGGCCAGACTCCGCGCTTCAACAGTATGCTCAGCCGCGC 314
Db 185 ATGACAGAGCACTTATGTGGGTATGATTCTGGTCACTATGAGGTTATGTCAGTCCG 244
Qy 315 CTCACCGCGCAATTCATCTCTCGGCAATTCCTCGCGAATCAGCATCGGCTG 374
Db 245 TACAACAAATTAGCCCAAGTTTGTGTGGAAATTGTATGACTGGGATAGCATTTGCT 304
Qy 375 TGGAGTGGAAACCAACAGCCACCAATTCGATGCAACAGCTCGACTATGACCTGAT 434
Db 305 TGGAAATGACTCACAAAGCTCATCATCATCTTCAACAGCTTGAATATATCTGAT 364
Qy 435 CTGACAGCATGCGCGCTCTTGCATTTCTGCGGTTCTTCAATTCATTAACCTCTCAT 494
Db 365 CTGACAGCATGCGCGCTCTTGCATTTCTGCGGTTCTTCAATTCATTAACCTCTCAT 424
Qy 495 TNCATGAGAGAGATGAGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 554
Db 425 TTCTATGAGAGAGAGATGAGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 484
Qy 555 TTTACTTTTAAACCGGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 614
Db 485 TGGACATTTTAAACCGGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 544
Qy 615 CTATGTTTTCAGAGGAAAGTGCAGATAGAGCTTGA 654
Db 545 CTCTGTTTTCAGAGGCGTAAAGTCCCATAGATAGAGCTTTGA 584

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RESULT 15

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF003445 673 bp mRNA linear EST 06-OCT-2000
 EST431943 KVI Medicago truncatula cDNA clone pKVI-5L4, mRNA
 sequence.
 BF003445
 BF003445.1 GI:10703720
 EST.
 Medicago truncatula (barrel medic)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 673)
 Vandenoosh, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,
 Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
 Frazer, C.M.
 ESTs from roots of Medicago truncatula 24 hours after inoculation
 with Sinorhizobium meliloti
 Unpublished
 Contact: Vandenoosh K
 Department of Plant Biology
 University of Minnesota
 220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
 Tel: 612 624 2755
 Fax: 612 625 1738

Email: kvandenb@cds.umn.edu
Texas A&M University name: T67255e TIGR sequence name: MTAPE27K
More information is available at: <http://chrysis.tamu.edu/medicago>
Seq primer: Skmod (CTA gaa CTA gtc gat CC).
Location/Qualifiers

FEATURES

Source

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1. 673
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="PKV1-5L4"
/tissue_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XLOLR"
/clone_idb="KV1"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
```

BASE COUNT

139 a 119 c 136 g 279 t

ORIGIN

Query Match

28.1%; Score 247.4; DB 10; Length 673;

Best Local Similarity 64.5%; Pred. No. 4.5e-49; Indels 5; Gaps 3;

Matches 409; Conservative 0; Mismatches 220; Indels 5; Gaps 3;

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QY 172 TTCTCTCTCTGCTGCGGCGCTCTCTCCGACAGCACTTCGTCAGCTGCTTCG 231
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Db 40 TTGCTATGTTGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 99
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QY 232 CTGCAATTGATAGCTTTCTCTGATTCAGAGCGGCTGATAGGCGCAGCTCCGCCATT 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 100 GTATGTTGTTGGTTGCTATGATGCAAGTACTTATTTGTCATGATTCGTCATT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 292 ACAACGTGATGCTCAGCGCGCGCTCAACGGCGCAATTCCTCCGCGCAACATTC 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 ATGAGGTTTTTTTGTAGTGAAGTTATACAAATTAGCAAAATCTTGTGTAATTGTA 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 352 TCGCCGGATCAGCATCGCTGTGTGAAGTGAACCAAGCCCAACACATTGTCATGCA 411
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Db 220 TGACTGATTAAGATATGCTTGTGGAATGAGCTCATTAATGTCATATATGTTGCA 279
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QY 412 ACAGCTCTGACTATGACCTGATTCGACACATGCGGCTTTGCAGTTTCGTGCGGT 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 ATAGCTTTGATTAATGATCTGATTTGACAGATATCCCTGTTTGTGCTCATCGCAT 339
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QY 472 TCTTCAATTCATTAACCTCTATTCATAGGAGAGTNGAGTTGATTNCAATTCCTA 531
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Db 340 TCTTGTGATTAATTAATCTTAATTAATTAATTAATTAATTAATTAATTAATTA 399
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QY 532 NGTCTTGATCTGCTACAGCACTTTACTTTTACCCGTAATGTTGTCAGAGGTCA 591
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Db 400 GGTTCCTTACAGTATACAGATATACCTTTTACCTGCTGTTGTTGCAAGCTTA 459
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QY 592 ACTTGATCTGACAGCAATTCGCTATGTTTTCG--AGAGAAAAGTCAAGATAGAG 648
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 ACTTGATCTTCAAAACATTTTGTCTTGTGTTTTCGATCAGAAATGTTCTGATAGG 519
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 649 CTT-GAACAATAAGGGATCTCTGTTGTTGGAATGTTGCTTCTTAACTGCTTGCCT 707
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 TTTACAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
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QY 708 GCCAAATTTGGCTGATAGAGGATGTTGATGTTGCTAGCTTGTGTTGTTGTTGTTG 767
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 TCCCAAGTTGGCCGAAAGGCTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 638
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 768 CAGCAATTCAGTTCTGTTGAATCACCTTGCCTG 801
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 639 CAACATCTCAATCTGTTGAACCATTTGCGCTG 672
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```

Search completed: December 31, 2003, 23:59:21
Job time : 1345.13 secs

Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;

18 CCGGCTTTCACCTCCCAACCGCTTTCCGACACACCGTCCGCGCTCCCTCCGAC 77
 267 CCGCTCTTACCGGCTTCTACTACTCAAGACTTCAAGTCTGAGATCTCAAGAC 326
 78 TACCGCAAGCTCTTTCGACCTTCCGCGCTCAACCTTCAACCGCAAGGCGACACA 137
 327 TACCGGAGCTTTTGAACGAGATGTCCGGATCTTCCAGAGAAAGGCGACAC 366
 138 ACCTCATCTCTCTCTTATTTTCACCTTTTCTCTCTCTCTCTCTCTCTCTCT 197
 387 ATCATGTGACGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 446
 198 TTCTCCGACGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 257
 447 GCGTCCGAGTCCGCTCGGAGTTCACTGCTCTGCGCGCTCTGCTGCTGCTGATC 506
 258 CAGAGCGCTGATAGGCGCACGACTCCGCGCATTAACAGTGTCTCAGCGCGCTC 317
 507 CAGCGCGGATGTGGGCGCATGACTCGGCGCATTAACAGTGTGTCAACCGGTGATC 566
 318 AACCGCGCAATTAGATTCTCTCGGCAATCTCTCGGCAATCTGAGATCGGCTGTG 377
 567 AACGAGATCAGCAACTCATAGCAGGCAACATCTTAACCGAAATCAGCATCGGCTGTG 626
 378 AAGTGAACCAACCGCGCACATGTGACAGCAACGCTCTGACCTTGAACCTGATCTG 437
 627 AAGTGAACCAACCGCGCACATGTGACAGCAACGCTCTGACCTTGAACCTGATCTG 686
 438 CAGCAGATCCCGGATTTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 497
 687 CAGCAGATCCCGGATTTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 746
 498 TATGGAGAGATTGAGATTGATTCATTTGATTTGATTTGATTTGATTTGATTTG 557
 747 TATGGAGAGATTGAGATTGATTCATTTGATTTGATTTGATTTGATTTGATTTG 806
 558 ACTTTTACCGGCAATGATTTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 617
 807 ACTTACTACCGGCAATGATTTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 866
 618 TTGTTTTCGAGGAAAGTGCAGATAGAGCT-TGAACATTAATGGGGATCTCTGTGTT 676
 867 CTCTCACCAGGCGGCGACGCTCTGACCGGCTCTTAATGATTTGATTTGATTTG 926
 677 TGAGCTGTGCTCTCTTTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736
 927 TGAGCTGTGCTCTCTTTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 986
 737 GAGCTGTGCTCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
 987 GTCTCATCAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045
 797 TGCTGAATTTTATGTCGCGCAACNANTGGG 828
 1046 CTCGCGGACACATACGTGGGCCCCCGCAAG 1077

RESULT 2
 US-08-831-570-1
 ; Sequence 1, Application US/08831570
 ; Patent No. 5959175
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Numburg, Andrew N.
 ; APPLICANT: Beremand, Phillip D.
 ; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
 ; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza
 City: Garden City
 STATE: New York
 COUNTRY: USA
 ZIP: 11530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/831,570
 FILING DATE: 09-APR-1997

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Digilio, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10545
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 743-4366

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1684 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43..1387

US-08-831-570-1

Query Match 27.9%; Score 245.2; DB 2; Length 1684;
 Best Local Similarity 57.7%; Pred. No. 1.1e-53;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCGACCGCTCTTTCGACACACGCTCTCGCGCGCTCTCCGCTACCGC 83
 265 TTTTTCACCTGGGATTAATCTTAAGATTAATCTCTGTTTCTGAGGTTTCTAAGATTATAG 324
 84 AAGCTCTTCTCCGACCTCTCCGCTCAACCTTTCACCGCAAGGCGCACCAACCTCC 143
 325 AAGCTGTGTTGATTTGATTTCTAATGATTTGATTTGATTTGATTTGATTTGATTTG 384
 144 ATCTCTCTCTCTTATTTCTACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 203
 385 GCAACTTTGCTTTATAGCAATGCTGTTGCTATGATGATGATGATGATGATGATGATG 444
 204 GACAGCACTTGTGTGACGCTTTCGCTGATGATGATGATGATGATGATGATGATGATG 263
 445 GAGGGTGTGTTGATGATTTGTTTGTGCTGTTGATGATGATGATGATGATGATGATG 504
 264 GCGTGTATAGGCGCACGACTCCGCGCATTAACGATGATGATGATGATGATGATGATG 323
 505 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 564
 324 GCAATTCAATTTCTCTCGGCAACATTTCTGCGGGAATAGCATGCGCTGTGTGAAGTGG 383
 565 TTATGAGTATTTTCTGCAAAATGCTCTTTCAGAGATTAAGATTTGTTGTGAAGTGG 624
 384 AACCAAGCGCGCACATTTGATGATGATGATGATGATGATGATGATGATGATGATG 443
 625 AACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684
 444 ATGCGGCTTTTGCATTTGCTGCGGCTTCTCAATTTCAATTAACCTCTCATTTNCTATGG 503
 685 ATACCATTTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 744
 504 AGGAGTTGAGTTGATTTNCAATGCTGATGATGATGATGATGATGATGATGATGATGAT 563
 745 AAAAGTTGACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804

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QY 564 TACCGGTAATGTGTGTGGCAGGTCAATTGTATCTGACAGCAATCTGTATTTT 623
DB 805 TACCTATTATGTGTCTGTAGCTCAATGTATGTACAACTCTCATTAATGTTGTTG 864
QY 624 TCGAGGAAAGATGCAAGATAGACT-TGACATATAGGGGATCTTGTGTTGGACT 682
DB 865 ACCAAGAAATGTCTCATGAGCTCAAGAACTCTGGGATGCTTAGGTTCTGATTT 924
QY 683 TGGTTCCTTTAGTGTGTGCTGCTCAATTTGGGCTGATAGGGGAAATGTTGACTT 742
DB 925 TGGTACCGGTGCTTGTCTTCTTGTCTTAAATTTGGGCTGAAGAAATTAATGTTGATTT 984
QY 743 GCTAGCTTTGCTGTTGTGNCNATCCAGACATTCAGTTCTGTGTAATCACTTGTCTGA 802
DB 985 GCAAGTTTATCACTGACTG-GAATGCAACAAGTTCACTTCTCTGAACCACTTCTTTC 1043
QY 803 AAATTTATATGNCGGCA--CNANTGGAAATGACTGANT--GANAATCAGACAAGGGGTC 858
DB 1044 AAGTGTATTATGTTGAAAGCTTAAAGGGAATATATGTTTGAGAAACAACGATGGGAC 1103
QY 859 ATTGATATCTCTTGTGNCCT 880
DB 1104 ACTGACATTTCTTGTCTCT 1125

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RESULT 3

US-08-831-575-1

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; Sequence 1, Application US/08831575
; Patent No. 5977436

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; GENERAL INFORMATION:

```

```

; APPLICANT: Thomas, Terry L.

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; APPLICANT: Li, Zhongsen

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; TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE

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; NUMBER OF SEQUENCES: 33

```

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; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

```

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; STREET: 400 Garden City Plaza

```

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; CITY: Garden City

```

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; STATE: New York

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```

; COUNTRY: U.S.A.

```

```

; ZIP: 11530

```

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; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patent in Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/831,575

```

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; FILING DATE: 09-APR-1997

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; CLASSIFICATION: 800

```

```

; ATTORNEY/AGENT INFORMATION:

```

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; NAME: Digiligo, Frank S.

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; REGISTRATION NUMBER: 31,346

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; REFERENCE/DOCKET NUMBER: 10203

```

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; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (516) 742-4343

```

```

; TELEFAX: (516) 742-4366

```

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; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS: 1:

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; LENGTH: 1684 base pairs

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; TYPE: nucleic acid

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; STRANDEDNESS: double

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; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)

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; FEATURE:

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; NAME/KEY: CDS

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; LOCATION: 43..1387

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; US-08-831-575-1

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QY 24 TTCTCAACCTCCACCGTCTTCCGACACACCGTCTCCGCCCTCCGACTACCGC 83
DB 265 TTTTTCATCGGGTATTAATCTTAAAGATTAATCTGTTCTTGAGGTTTCTAAAGATTAAG 324
QY 84 AAGCTCTTCTCCGACCTCTCCGCGCTCAACCTTTCAACCGGAGGGCACAACCTCC 143
DB 325 AAGCTTGTTGAGTTTCTTAAATAGGTTTGTATGACAAATAAGGTCATATTAATGTTT 384
QY 144 ATCTCTCTCTCTTATTTCTACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 203
DB 385 GCACCTTGTGCTTATATGCAATGCTGTTGCTATGAGTTTATAGGGGTTTGTGTTTGT 444
QY 204 GACAGACCTTGTGAGAGCTGCTTCCGCTGCATGATGATGAGCTTCTCTGATTCAGAC 263
DB 445 GAGGTTGTTTGTATCATTTGTTTCTGAGGTTTGTATGAGGTTTCTTGTGATTCAGAT 504
QY 264 GCGTGAATAGCCACAGACTCCGCGCATTAACAAGTATGCTCAGCCGCGCTCAACCGC 323
DB 505 GGTGGAATGACATGATGCTGGCATTAATATGATGCTGATGATCAAGGCTTAATAAG 564
QY 324 GCAATTCAGATTTCTCCGCAACATTTCTCCGGAATCAGATGCGCTGTGAAAGTGG 383
DB 565 TTTATGGGTATTTTGTCTGCAATTTGCTTTCAGGAATTAATGTTGTTGTTGGAATGG 624
QY 384 AACCAACAGCCACACATTCGATGCAACAGCTCGATATGACCTGATCGAGCAC 443
DB 625 AACCAATATGACATCAATTCCTGTAATGACCTTGAATATGACCTGATTAATCAATAT 684
QY 444 ATGCGGCTTTTTCAGATTTGCTGCGGTTCTTCAATTCATTAACCTCTCATTTGATGG 503
DB 685 ATACATTCCTGTTGTTGTTCTTCAAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 744
QY 504 AGAAGTTNAGTTGATTTNCAATGCTANGTTCTGATCTGCTACAGACATTTACTTTT 563
DB 745 AAAAGTTGACTTTGACTCTTATCAAGATTTCTTGTAGTTATCAACATTTGACATTT 804
QY 564 TACCGGTAATGTGTGTGCGAGGTCACTGTATATCGACACAAATTCGATTTGTTT 623
DB 805 TACCTATTATGTGTGTGCTAGCTCAATATGATATGCAATCTCTCAATTAATGTTTGG 864
QY 624 TCGAGGAAAGATGCAAGATAGACT-TGAACATATAGGGGATCTTGTGTTGAGACT 682
DB 865 ACCAAGAAATGTGTCTCATGAGCTCAGAACTTGTGGATGCTTAGTGTCTTCGATTT 924
QY 683 TGGTTCCTTTTAAAGTGTGCTTCCCAATTTGGGCTGATAGGGGAAATGTTGACTT 742
DB 925 TGGTACCGGTGCTTGTCTTCTTGTGCTTAAATTTGGGCTGAAGAAATTAATGTTGATTT 984
QY 743 GCTAGCTTTGCTGTTGTGNCNATCCAGACATTCAGTTCTGTGTAATCACTTGTCTGA 802
DB 985 GCAAGTTTATCAGTACTG-GAATGCAACAAGTTTCACTTCTTGAAACCACTTCTTTC 1043
QY 803 AAATTTATATGNCGGCA--CNANTGGAAATGACTGANT--GANAATCAGACAAGGGGTC 858
DB 1044 AAGTGTATTATGTTGAAAGCTTAAAGGGAATATATGTTTGAGAAACAACGATGGGAC 1103
QY 859 ATTGATATCTCTTGTGNCCT 880
DB 1104 ACTGACATTTCTTGTCTCT 1125

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RESULT 4

US-08-366-779-4

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; Sequence 4, Application US/08366779
; Patent No. 5614393

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; GENERAL INFORMATION:

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```

; APPLICANT: Thomas, Terry L.

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; APPLICANT: Reddy, Avutu S.

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; APPLICANT: Nuccio, Michael

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; APPLICANT: Freysinet, Georges L.

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; APPLICANT: Nunberg, Andrew N.

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; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

```

```

Query Match 27.9%; Score 245.2; DB 2; Length 1684;
Best Local Similarity 57.7%; Pred. No. 1,le-53;
Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

```


TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,779
 FILING DATE: 30-DEC-1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXX
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1685 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-366-779-4

Query Match 27.9%; Score 245.2; DB 1; Length 1685;
 Best Local Similarity 57.7%; Pred. No. 1,1e-53;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCACACCGCTCCGCGCTCTCCGACTACCGC 83
 Db TTTTCTACTGGGTAATTAAGATTACTGTCTTCTGAGTTTCTTAAGATTATAGG 325
 QY . 84 AAGCTCTTCCGACCTCTCCGCGCTCAACCTCTTCAACGCAAGGCGCACAACTCC 143
 Db . 326 AAGCTTGTGTTAGTTTCTTAAATGGGTTGTATGACAAAAAGGTCATATATGTTT 385
 QY 144 ATCTCTCTCCCTTATCTCACCCCTTTTCCTCTCTCTCTGCGCGCTCTCTCTCC 203
 Db 386 GCACTTTGCTTATAGCAATGCTGTTGCTATGAGTGTATATGGGGTTTGTGTTGT 445
 QY 204 GACAGCACTTTCGCGACGTCGCTTCCGCTGCAATGATAGGCTTCTCTGATTCAGAC 263
 Db 446 GAGGCTGTTTGGTACATTTGTTTCTGGGTGTTGATGGGGTTTCTTGGATTCAAGT 505
 QY 264 GGCTGATAGGCGCAGCTCCGCGCATTAACAAGTGAATGACGCGCGCGCTCAACGC 323
 Db 506 GGTGATTTGACATGATGCTGGGCAATTAATGTAAGTCTGATTTCAAGGCTTAATAG 565
 QY 324 GCAATTCAGATTCTCTCCGCGCAATTCCTCCGCAATCAGCATCGCTGGTGAAGTGG 383
 Db 566 TTTATGGGTAATTTTGTGCGAAATGTCTTTCAGGAATAGATATGTTGGTGAATGG 625
 QY 384 AACCAAGCGCCACCACTTGCATGCAACAGCTCGATGATGACCTGATTCGACAC 443
 Db 626 AACCATATGACATCACTGCTGTAATAGCTTGAATATGACCTGATTTTCAATAT 685
 QY 444 ATGCGGCTTGTGAGTTTGTGCGGTTCTTCAATCCAAATCCTCATTTCTATGGG 503
 Db 686 ATACCATTTCTTGTGTCTTCCAAATTTTGTGCTACCTCACTTCATTTCTATAGG 745
 QY 504 AGGAAGTTNAGTTGATTCAATGCTATGTTCTTGAATGCTGCTACGACACTTACTTTT 563

Db 746 AAAAGTTGACTTTTGACTCTTTATCAAGATTCTTTGTAAGTTATCAACATTGGACATTT 805
 QY 564 TACCGGTAATGTTGTTGCGAGGTCACCTTGATCTGACAGCAATTCGATTTGTTT 623
 Db 806 TACCTATTAATGTTGCTGTAAGCTCAATATGATGTAATCTTCAATATGTTGTTG 865
 QY 624 TCGAGNGAAAAGTCAGATNAGCT-TGAACATATGGGATCCTTGTGTTTGGACT 682
 Db 866 ACCAAGAAAATGTCATGAGCTCAGAGCACTCTTGGATGCTAGGTTCTGATTT 925
 QY 683 TGGTCTCTTTTATGATGCTTGCCTCCAAATTTGGCCCTGATAGGGAATGTTGACTT 742
 Db 926 TGGTACCGCTTGTGTTTCTTGTGTTGCTTAATTTGGGGTGAAGAATTTATGTTAT 985
 QY 743 GCTAGCTTGTGTTTGCNATCCAGCAATTCAGTTCTGTTGATATCACTTCTGA 802
 Db 986 GCAAGTTATCACTGACTG-GAATGCAACAAGTTCACTTCTTCAACCACTTCTCTTC 1044
 QY 803 AATTTATATGNCGGCA--CNANTGGAAATGACTGGNT--GANAATCAGACAAGGGGTC 858
 Db 1045 AAGTTTATGTTGAAAGCGTAAAGGGAATATGTTTGAAGAAACAACGATGGGAC 1104
 QY 859 ATTGATATCTCTTGTGNCCT 880
 Db 1105 ACTTGACATTTCTTGTCTCTCT 1126

RESULT 5
 US-08-789-936-4
 Sequence 4, Application US/08789936
 Patent No. 5789220
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freysinet, Georges L.
 APPLICANT: Nuberg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,936
 FILING DATE: 28-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/366,779
 FILING DATE: 30-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXX
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1685 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-789-936-4

Query Match 27.9%; Score 245.2; DB 1; Length 1685;

Best Local Similarity 57.7%; Pred. No. 1.1e-53; Mismatches 359; Indels 6; Gaps 4;

Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCAACAGCTCCGCGCTCTCCGACTACCGC 83
266 TTTTTCACGCGGATTAATCTTAAGATTAATCTCTGAGTTCTTAAGTTATAG 325

84 AAGCTCTTCTCCGACCTCTCCGCTCAACCTTCAACGCGAAGGCCACACACCTCC 143
326 AAGCTGTGTGAGTTTCTTAATAAGGTTGTATAGCAAAAAGATGATATATAGTT 385

144 ATCTCTCTCTCTTATCTCAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
386 GCAATTTGTGCTTATAGCAATGCTGTTGCTATAGATGTTATGAGGTTTGT 445

204 GACAGCACTTTCGTGACGCTTTCGCTGCAATGATAGGCTTCTCTGATTCAGAG 263
446 GAGGCTGTTTGTATCAATTTTCTGCTGCTGTTTATGAGGCTTCTTGAATTCAGAT 505

264 GGGTGTATAGGCCACGACCTCCGCAATTAACAGTATGCTCAAGCCGCTCAACCCG 323
506 GGTGTGATGACATGATGCTGGCATTAATAGTAGTGTCTGATTCAGAGCTTAATAG 565

324 GCAATTCAGATTTCTCCGCAACATTTCTGCGGATCAGCATCGGCTGTGGAAGTGG 383
566 TTATGCGTATTTTCTGCAATTTCTTTCAGGATTAAGTATGTTGTGTGGAATGG 625

384 AACCAACAGCCGACCAATTTGATGCAACAGCTGATGACCTGATTCGAGCAGC 443
626 AACCATTAATGACATACATGCTGATTAATGCTGGAATGACCTGATTAACATAT 685

444 ATGCGGCTCTTTCGACATTTCTGCGGCTTCTCAATTCATTAACCTCTGATTTGAGG 503
686 ATACCATTCCTGTTGTGCTTCTTCAAGTTTGTGTTCACTCACTCTCATTTCTATGAG 745

504 AGGAAGTTGAGTTGATTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 563
746 AAAAGCTTGAATTTGATCTTATCAAGATTTCTTGAATGATTAACATTTGACATTT 805

564 TACCGGATATGCTGCTGACGCTCACTGATTAATGCTGATTAATGCTGATTT 623
806 TACCTATTAATGCTGCTGACGCTCACTGATTAATGCTGATTAATGCTGATTT 865

624 TCGAGNCAAAAGTGCAGATAGAGCT-TGAACATATAGGAGATCTTGTGTTTGGACT 682
866 ACCAAGAAATGTGCTGATGAGCTCAAGACTCTTGGAGCTTGTGTTCTGATTT 925

683 TGGTCTCTTCTTATGCTGCTGCTGCAATTTGAGCTGATAGGAGATTTGAGCTT 742
926 TGGTATCCCTGCTGCTTCTTCTTGTGCTTATTTGGGATGAAGATTAATGTTTAT 985

743 GCTAGCTTGTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 802
986 GCAAGTTTATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044

803 AAATTAATAGNCGGCA--CNANTGGAGATGATGAGT--GANAAATGCAACAAGGAGT 858
1045 AAGTGTATGTTGGAAGGCTTAAGGAGATTAATGTTGAGAAACAAAGGATGGAG 1104

859 ATTGATATCTCTTGTGNCCT 880
1105 ACTTGACATTTCTGCTCTCT 1126

RESULT 6
US-08-934-254-4
; Sequence 4, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934.254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-934-254-4

Query Match 27.9%; Score 245.2; DB 4; Length 1685;

Best Local Similarity 57.7%; Pred. No. 1.1e-53; Mismatches 359; Indels 6; Gaps 4;

Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCAACAGCTCCGCGCTCTCCGACTACCGC 83
266 TTTTTCACGCGGATTAATCTTAAGATTAATCTCTGAGTTTCTTAAGATTAATAG 325

84 AAGCTCTTCTCCGACCTCTCCGCTCAACCTTCAACGCGAAGGCCACACACCTCC 143
326 AAGCTGTGTGAGTTTCTTAATAAGGTTGTATAGCAAAAAGATGATATATAGTT 385

144 ATCTCTCTCTCTTATCTCAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
386 GCAATTTGTGCTTATAGCAATGCTGTTGCTATAGATGTTATGAGGTTTGT 445

204 GACAGCACTTTCGTGACGCTTTCGCTGCAATGATAGGCTTCTCTGATTCAGAG 263
446 GAGGCTGTTTGTATCAATTTTCTGCTGCTGTTTATGAGGCTTCTTGAATTCAGAT 505

264 GGGTGTATAGGCCACGACCTCCGCAATTAACAGTATGCTCAAGCCGCTCAACCCG 323
506 GGTGTGATGACATGATGCTGGCATTAATAGTAGTGTCTGATTAAGGCTTAATAG 565

324 GCAATTCAGATTTCTCCGCAACATTTCTGCGGATCAGCATCGGCTGTGGAAGTGG 383
566 TTATGCGTATTTTCTGCAATTTCTTTCAGGATTAAGTATGTTGTGTGGAATGG 625

384 AACCAACAGCCGACCAATTTGATGCAACAGCTGATGACCTGATTCGAGCAGC 443
626 AACCATTAATGACATACATGCTGATTAATGCTGGAATGACCTGATTAACATAT 685

444 ATGCGGCTCTTTCGACATTTCTGCGGCTTCTCAATTCATTAACCTCTGATTTGAGG 503
686 ATACCATTCCTGTTGTGCTTCTTCAAGTTTGTGTTCACTCACTCTCATTTCTATGAG 745

QY	AGGAAGTNGAGTTGATTNCATTCCTNAGTCTTGATCTGTACAGACATTACTT	563
Db	AAAGGTGACTTTTGACTCTTTATCAAGATTCTTGTAAAGTTATCAACATTGGACATT	805
QY	TACCCGGTAATGTGTGTGCCAGGGTCAACTTGATCTGCAGACAACTCTGCTATTGTT	623
Db	TACCTTATTAATGTGTGTCTAGGCTCAATATGTATGATCAATCTCTCAATATGTGTTG	865
QY	TCGAGAGNAAAAGTCAGAGATGAGCT-TGAACATTAATGGGGATCTTGTGTTTGGACT	682
Db	ACCAAGAAATATGTCTCTATCGAGCTCAGGAACCTTGGGATGGCTATGTGTTCTCGATT	925
QY	TGGTTCCTCTTTAGTACCTGCCGCCAAATTGGGCGCGATGAGGGNATGTTTNGCCT	742
Db	TGTTACCCGTGTCTTGTCTTGTTCCTTAATTTGGGGTGAAGAATTTATGTTTGTATT	985
QY	GCTAGCTTGTGCTGTTTGTNCCNATCCAGACATTCAGTCTTGATGAATCACTTGCTGA	802
Db	GCAAGTTTATCAGTACTG-GAATGCAACAATTTCAAGTCTCTCTGAACCACTTCTCTTC	104
QY	AAATTATATGNCGGGCA--CNATGGGAATGACTGAGT--GANAATCAGACAGGGGTC	858
Db	AAGTGTATTATGTGGAAAGCCTAAGGGGAATATATGTTGTGAAGAAACAACGATGGGAC	1104
QY	ATTGATATCTCTTGNCCT	880
Db	ACTTGACATTTCTTGTCTCTCT	1126

RESULT 7
 US-08-232-463-14
 Sequence 14, Application US/08232463
 Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 City: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

;
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
US-08-232-463-14

Query Match 9.6%; Score 84.8; DB 1; Length 7218;
Best Local Similarity 2.2%; Pred. No. 2.8e-12;
Matches 8; Conservative 246; Mismatches 118; Indels 0; Gaps 0.

Qy	1	CCGGCTCCCTCTCTCTCCCGGCTTTCACCTCCACCGCTTTCGACACACCGCTCT	60
		:: ::	
Db	1078	YY	1137
Qy	61	CCGGCGCTCTCCGACTACCGCAGACTCTTTCGACCTCTCCGCGCTCAACTCTTCA	120
		:: ::	
Db	1138	YYY	1197
Qy	121	ACCGCAGGGCACAACAACCTCACTCCTCTCTCCCTATTCACCTTTTCTCTCT	180
		:: ::	
Db	1198	YYY	1257
Qy	181	CTGATCGGGGCTCTCTCTTCGACAGCACTTTCGTCAGCTGTTCCGCTGATGA	240
		:: ::	
Db	1258	YYY	1317
Qy	241	TAGGCTTCTCTGATTCAGAGCGGCTGATAGGCAAGCACTCCGCCATTACAAGTGA	300
		:: ::	
Db	1318	YYY	1377
Qy	301	TGCTCAGCCGCGGCTCAACCGCGCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGA	360
		:: ::	
Db	1378	YYGTA	1437
Qy	361	TCAGATCGGCT	372
		:: ::	
Db	1438	CCAAATCTTCT	1449

```

RESULT 8
US-09-249-585A-4
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

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Query Match	8.2%	Score 72	DB 4	Length 1926
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Matches 183; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

OY	1	CGGGCTCCCTCTCTCTCCCGCGCTTTCGACCTCCGACCGCTTTCGACGACACACCGCTT	60
Db	567	CGGTCCTCCCGCTCTCCCGCTCTGCGCTCTCCCGCTCTGCTCTCCCGCTCTCC	626
OY	61	CGGGCGGCTCTCTCGACCTACCGGAAGCTCTTCTCGACCTTCCGCGCTTCAACCTCTTCA	120
Db	627	CGGTCCTCCCGCTCTGCTCTCTCCCGCTCTGCGCTCTCTCCCGCTCTCCCGCTCTCC	686
OY	121	ACCGGACGCGACACACACTGCATCTCTCTCTGCTCCCTTATTCTACCTTTTCTCTCTCT	180

APPLICANT: KLINGER, KATHERINE W
 APPLICANT: LANDES, GREGORY M
 APPLICANT: BURN, TIMOTHY C
 APPLICANT: CONNORS, TIMOTHY D
 APPLICANT: DACKOMSKI, WILLIAM
 APPLICANT: GERMINO, GREGORY
 APPLICANT: QIAN, FENG
 TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENZYME CORPORATION
 STREET: ONE MOUNTAIN ROAD
 CITY: FRAMINGHAM
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 01701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/658,136
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: LASSEN, ELIZABETH
 REGISTRATION NUMBER: 31,845
 REFERENCE/DOCKET NUMBER: GEN4-17.8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 508-872-8400
 TELEFAX: 508-872-5415
 INFORMATION FOR SEQ. ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53577 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-658-136-1

Query Match 6.4%; Score 56.2; DB 3; Length 53577;
 Best Local Similarity 53.4%; Pred. No. 0.00012;
 Matches 118; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
 QY 1 CCGCTCCCTCTCTCTCCCGCTTCCACCTCCACCGCTTTTCCGACACACCGTCT 60
 DB 34634 CCGCTCCCTCTCTCTCCCGCTTCCACCTCCACCGCTTTTCCGACACACCGTCT 60
 QY 61 CCGCGCGCTCTCCGACCTACCGGACGCTCTTCCGACGCTCCGGGCTCAACCTCTCA 120
 DB 34694 TCCCGCTCCCGCTCTCTCTCTCCCGCTTCCCGCTCCCGCTCTCTCTCTCTCTCC 34753
 QY 121 ACCGCAAGGCGCACACACCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 DB 34754 ATCCCT 34813
 QY 181 CTGTCTGGCGGCT 221
 DB 34814 CT 34854

RESULT 12
 US-08-458-568A-11
 ; Sequence 11, Application US/08458568A
 ; Patent No. 5821339
 ; GENERAL INFORMATION:
 ; APPLICANT: Schaffer, Patricia A.
 ; APPLICANT: Yeh, Lily
 ; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339r1s
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,568A
 FILING DATE: 02-JUNE-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/065,146
 FILING DATE: 05-MAY-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Leary Ph.D., Kathryn R.
 REGISTRATION NUMBER: 36,317
 REFERENCE/DOCKET NUMBER: DFCI-0029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3439
 TELEFAX: (215) 568-3100
 INFORMATION FOR SEQ. ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12001 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Herpes simplex virus
 STRAIN: Herpes Simplex Virus Type 1
 US-08-458-568A-11

Query Match 6.2%; Score 54.4; DB 1; Length 12001;
 Best Local Similarity 52.2%; Pred. No. 0.00021;
 Matches 121; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
 QY 1 CCGCTCCCTCTCTCTCTCCCGCTTCTCCACCTCCACCGCTTTTCCGACACACCGTCT 60
 DB 1247 CCGCTCCCTCTCTCTCTCCCGCTTCTCCACCTCCACCGCTTTTCCGACACACCGTCT 60
 QY 61 CCGCGCGCTCTCCGACCTACCGGACGCTCTTCCGACGCTCCGGGCTCAACCTCTCA 120
 DB 1307 CCGCT 1366
 QY 121 ACCGCAAGGCGCACACACCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 DB 1367 CCGGCT 1426
 QY 181 CTGTCTGGCGGCT 232
 DB 1427 CCGGCT 1478

RESULT 13
 US-08-834-655-1
 ; Sequence 1, Application US/08834655
 ; Patent No. 5968809
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNITZON, DEBORAH
 ; APPLICANT: MURKERT, PRADIP
 ; APPLICANT: HUANG, YONG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-363-574-1

Query Match 6.0%; Score 53; DB 3; Length 1617;
Best Local Similarity 51.0%; Pred. No. 0.00023;

Matches 125; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY	210	ACTTTGCTGACGCTCTTCCGCTGCAATTAAGGCTTTCTTGATTCAGACGGCTGG	269
DB	518	ACCCTGCCAACGCTCTCGCTGCTTTGGCTTGTCTGCGCAGCAGTGGATGG	577
QY	270	ATAGGCCAGACTCCGGCCATTCAACGTGATGCTCAGCCGCGCTCAACGGCAATT	329
DB	578	TTGGCTCAGCACTTTTTCATCAACAGTCTTCCAGGACCGTTTCTGGGGTGAATCTTTTC	637
QY	330	CAGATTCTCCGCAACATTTCTGCCGGAATCAGCATCGCTGTGAGTGAAGTGAACAC	389
DB	638	GGCGCTTCTTGGAGAGTGTCTGCCAGGCTTCTGCTCGTGTGAGGAAGACAAGCAC	697
QY	390	AAGCCCACTGCAATTTGATGCAACAGCTTGACTATGACCTGATCTGCAGCATGCGG	449
DB	698	AACACTCACCACCGCCGCCCAACGTCACGCGAGGATCCGACATTTGACCCCACTT	757
QY	450	GTCTT 454	
DB	758	CTGTT 762	

Search completed: January 1, 2004, 00:05:26
Job time : 45.6671 secs

LENGTH: 1702 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 48..1406
 NAME/KEY: CDS
 LOCATION: 48..1406
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 us-10-029-756-26

Query Match 31.2%; Score 274.2; DB 14; Length 1702;
 Best Local Similarity 59.6%; Pred. No. 3.2e-74;
 Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;

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18  CCCGCTTCTCCACCTCCACCGCTTCCGACACACACGCTCCGCGCTCTCCGAC 77
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22  |||||
23  |||||
24  |||||
25  |||||
26  CCGCTCTTCCACCGGCTCTACTACTACCTGAGACTTGCAGATCTCCAGAGAC 326
27  |||||
28  |||||
29  |||||
30  |||||
31  |||||
32  |||||
33  |||||
34  78  TACCGAGCTCTTCTCCGACTCTCCGCGCTCAACCTCTTCAACGCAAGGCGCACACA 137
35  |||||
36  |||||
37  |||||
38  327  TACCGAGGCTTTGAAAGAGATGCGCGGCTCCGGGATCTTCGAGAAAGAGGCGCACAC 386
39  |||||
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41  |||||
42  138  ACCTCATCTCTCTCCCTTATCTACCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 197
43  |||||
44  |||||
45  |||||
46  387  ATCATGTGACGCTTCTGCGCGCTGCGGTATATGCGGCAATGCTATAGCGGCTGCTG 446
47  |||||
48  |||||
49  |||||
50  198  TTCTCCGACAGCACTTTCGTCAGAGCTTTCGCGTGCATTTGATGAGCTTCTCTGAT 257
51  |||||
52  |||||
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54  447  GCGTCCGAGTCCGTCGAGATTCATCTCTGCGGCGCACTGCTGGCTTCTGTGTATC 506
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56  |||||
57  |||||
58  258  CAGAGCGGCTGATGAGCCACGACTCCGCGCATTAACAGTATCTCAGCGCGCTC 317
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62  507  CAGCGCGGCTATGCGGCTATGACTCGCGCATTAACAGTATGCAACCGGTGATAC 566
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66  318  AACCGGCAATTGATCTCTCCGCAATTTCTCGCGGATTCAGATCGGCTGTG 377
67  |||||
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70  567  AACAGATTCAGCACTATGAGAGGACATCTTAACCGGAATCAGCATCGGCTGTG 626
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74  378  AAGTGAACCAACAGCCCACTATGATGATGCAACAGCTCTGACTATGACCTGATCTG 437
75  |||||
76  |||||
77  |||||
78  627  AAGTGAACCAACAGCCCACTATGATGATGCAACAGCTCTGACTATGACCTGATCTG 686
79  |||||
80  |||||
81  |||||
82  438  CAGCAATGCGGCTTGTGAGTTGCTGCGGCTTCAATTCAATCACTCTCATTTNC 497
83  |||||
84  |||||
85  |||||
86  687  CAGCAATGCGGCTTGTGAGTTGCTGCGGCTTCAATTCAATCACTCTCATTTNC 497
87  |||||
88  |||||
89  |||||
90  498  TATGGAGAGAGTTGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 557
91  |||||
92  |||||
93  |||||
94  747  TATGGAGAGAGTTGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 806
95  |||||
96  |||||
97  |||||
98  558  ACTTTTAAACCGGTAATGTTGTTGCAAGGATCACTTATCTGACAGCAATTTCTGCTA 617
99  |||||
100  |||||
101  |||||
102  807  ACTTACTACCGGCTATGATCTTCCGCGGATCACTCTTCACTCAAGACTTTTATTTG 866
103  |||||
104  |||||
105  |||||
106  618  TTGTTTGAAGGAAAGTGAAGATGAGCT-TGAACATTAATGGGATCTTGTGTTT 676
107  |||||
108  |||||
109  |||||
110  867  CTCTCAACAGGCGGCGATCCCTGACCGGCTCTAACTTAATAGGATTCGCGTTTTC 926
111  |||||
112  |||||
113  |||||
114  677  TGAATTTGTTCTCTTTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736
115  |||||
116  |||||
117  |||||
118  927  TGAACGTTGTTTCCGCTCTTCTGATCTTCTCCGAACTGAGCTGAACTGAGCTTTC 986
119  |||||
120  |||||
121  |||||
122  737  GAGCTTGTGCTTGTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 796
123  |||||
124  |||||
125  |||||
126  987  GTCTCTATCAAGCTTTTGC-TGTTCAAGGCTGATCAGACGTTCAAGCTTCAAGCTT 1045
127  |||||
128  |||||
129  |||||
130  797  TGTGAAATTTTATGTCGAGGCAACNANTGG 828
131  |||||
132  |||||
133  |||||
134  1046  CTCGCGGACACATACGTGTGGCCCCCAAGG 1077

```

RESULT 2
 us-10-029-756-4
 Sequence 4, Application US/10029756
 Publication No. US20020108147A1
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/029,756
 FILING DATE: 21-Dec-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/934,254
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXWVU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1685 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 us-10-029-756-4

Query Match 27.9%; Score 245.2; DB 14; Length 1685;
 Best Local Similarity 57.7%; Pred. No. 3.2e-65;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

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24  TTCTCCACCTCCACCGCTTTCGACCAACCGCTCCGCGCTCTCCGACTACCGC 83
25  |||||
26  |||||
27  |||||
28  266  TTTTACAGGGATATATCTAAAGATTAATCTGTTCTGAGGTTTCTAAAGATTAAG 325
29  |||||
30  |||||
31  |||||
32  84  AAGCTTCTCCGACTCTCCGCGCTCAACCTTTCAACCGCAAGGCGCAACAACTCC 143
33  |||||
34  |||||
35  |||||
36  326  AACCTTGTTGAGTTTCTAAATGCGTTGTATGACAAAAAAGGTATATATGTTT 385
37  |||||
38  |||||
39  |||||
40  144  ATCTCTCTCCCTTATTTCAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
41  |||||
42  |||||
43  |||||
44  386  GCAACTTGTGCTTTATAGCAATGCTGTTTGTCTATAGTGTATTAAGGGTTTGTGTT 445
45  |||||
46  |||||
47  |||||
48  204  GACAGCACTTGTGACAGTCTTTCGCTGCAATGATAGGCTTTCTGATTCAGAC 263
49  |||||
50  |||||
51  |||||
52  446  GAGGAGTTTGTGTAATTTGTTTCTGGGTGTTTATGAGGTTTCTTTGATTCAGAG 505
53  |||||
54  |||||
55  |||||
56  264  GCGTGATAGGCGCAACATTCGCGCACTTACACGTATGCTACGCGCGCTCAACCG 323
57  |||||
58  |||||
59  |||||
60  506  GGTGTGATGACATATGCTGGGCAATTTATGATGATGATGATGATGATGATGATG 565
61  |||||
62  |||||
63  |||||
64  324  GCAATTCAATTTCTCTCCGCAACATTTCTGCGGCAATGACATCGGCTGTGGAAGTG 383

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Db 566 TTATATGTAATTTCTGCAAAATGCTTTTCAGAGATATGATGTTGGTGAATG 625
 Qy 384 AACCAAGCCCAACCAATTCATGCAACAGCTGATGATGACCTGATCGCAAC 443
 Db 626 AACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 685
 Qy 444 ATGCCGATCTTTCATGATGATGATGATGATGATGATGATGATGATGATG 503
 Db 686 ATACATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 745
 Qy 504 AGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
 Db 746 AAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 805
 Qy 564 TACCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 623
 Db 806 TACCGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
 Qy 624 TCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 682
 Db 866 AACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 925
 Qy 683 TGGTCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATG 742
 Db 926 TGGTACCGTCTGATGATGATGATGATGATGATGATGATGATGATG 985
 Qy 743 GCGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 802
 Db 986 GCGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1044
 Qy 803 AATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 858
 Db 1045 AAGTCTTTCATGATGATGATGATGATGATGATGATGATGATGATG 1104
 Qy 859 ATTGATATCTCTGATGATGATGATGATGATGATGATGATGATGATG 880
 Db 1105 ACTTGATCTCTGATGATGATGATGATGATGATGATGATGATGATG 1126

RESULT 3
 US-09-938-842A-558
 ; Sequence 558, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krepes, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 558
 ; LENGTH: 1350
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-558

Query Match 27.7%; Score 244.2; DB 10; Length 1350;
 Best Local Similarity 57.2%; Pred. No. 5,9e-65;
 Matches 469; Conservative 0; Mismatches 349; Indels 2; Gaps 2;

Db 203 CCGCTTGGACCATCTCGACATCTCTTCACCGGTTACACATGAGATTTCCAGTCT 262
 Qy 61 CGCGGCTCTCTCGACATACCGCAAGCTCTTCGAGCTCTCGGCTCAACCTCTCA 120
 Db 263 CCGAGTCTACCGCAATACCGTCTGATGCTGCGGAGTTTGTAACCTGCTCTTG 322
 Qy 121 ACCGAGGAGCCACAACTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 Db 323 AAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 382
 Qy 181 CTGTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 Db 383 TTCTCTACCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 442
 Qy 241 TGGGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 300
 Db 443 TGGGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 502
 Qy 301 TGGTACGCGCGCTCTCAACCGGCAATTCAGATTCTCTCCGCAACATTCCTGCGGAA 360
 Db 503 TGTGCAACAAATCTTATACAGATTCGCTCAGCTCTCTCCGTAATCTCTCAGCGAA 562
 Qy 361 TCGATCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 563 TCTCAATCGCGTGGGAAATGAGCTCAAAATGCTCATCATCTGATGATGATGATG 622
 Qy 421 ACTATGACCGTATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 623 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 682
 Qy 481 CCATTAACCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
 Db 683 CATGACCTCGAGATCTTACAGATCGGAATCAAGCTGATGATGATGATGATG 742
 Qy 541 TCTGTACCAAGCATTTTATACCGGATATGATGATGATGATGATGATGATG 600
 Db 743 TCGCTATCAACATCTTACTTATATCAAGTATGATGATGATGATGATGATG 802
 Qy 601 TCGAGACATTTCTGATGATGATGATGATGATGATGATGATGATGATG 659
 Db 803 TTCAAACGTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 862
 Qy 660 TGGGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 719
 Db 863 CCGGATCTTACTCTCTGATGATGATGATGATGATGATGATGATGATGATG 922
 Qy 720 CTGATAGGAGATGATGATGATGATGATGATGATGATGATGATGATG 779
 Db 923 CTGAGAGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 981
 Qy 780 TTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 819
 Db 982 TTCACGCTTAAACATTTGCTGATGATGATGATGATGATGATGATGATGATG 1021

RESULT 4
 US-09-878-574-9255
 ; Sequence 9255, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rose, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 9255
 ; LENGTH: 263

TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701102270H1
US-09-878-574-9255

Query Match 15.0%; Score 132.4; DB 10; Length 263;
Best Local Similarity 72.0%; Pred. No. 1.3e-30;
Matches 183; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

QY 315 CTGACCGCGCAATTCAGATTCTCCGGCAACATTCGCCCGAATCAGCATCGCTGG 374
DB 11 CTGACCGCGCTCAGCAAAATCTTTGGCAATTCAGTACGAGATGAGCAATGATG 70
QY 375 TGGAGTGGAGCAACGCGCCCAATTCAGTACGAGATGAGCAATTCAGTACGAGAT 434
DB 71 TGGAGTGGAGCTACAAATGCTCAACATTCAGTACGAGATGAGCAATTCAGTACG 130
QY 435 CTGACGACATGCGCGCTTTGAGATTGCGCGGTTCTTCAATTCATACCTCTCAT 494
DB 131 -TCCAGCAATACCTGCTTTCGCGGTGCGACAGGTTCTTCAATTCATACCTCTGT 189
QY 495 TNCATGGAGAGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTG 554
DB 190 TTCTATGGAAGGAATGTTGTTGATTGATTGATTGATTGATTGATTGATTGATTG 249
QY 555 TTTACTTTTACCC 568
DB 250 TTCACTTCTACCC 263

RESULT 5

US-10-369-493-27824
Sequence 27824, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianning
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27824
LENGTH: 1098
TYPE: DNA
ORGANISM: Neurospora crassa
US-10-369-493-27824

Query Match 12.7%; Score 111.6; DB 12; Length 1098;
Best Local Similarity 53.2%; Pred. No. 8.2e-24;
Matches 231; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

QY 167 CTTTCT 226
DB 96 CCGCTATACCT 155
QY 227 TTCCTGCTGATTTAGGCTTTCTCTGATTTAGGCTTTCTCTGATTTAGGCTTTCTCTG 286
DB 156 TAGTGGCTTCT 215
QY 287 CCAATCAAGATGATGCTGACGCGCCCTCAACCGCGCAATTCAGATTCTCTCCGCAA 346
DB 216 AACATGGGATACGACCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 275
QY 347 CATCTCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 406
DB 276 CTTCATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 335

QY 407 ATGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 466
DB 336 CACCAACAGCTCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 395
QY 467 GCGCTCTCTCAATTCATTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 526
DB 396 TGGTTCTTCAATTAATCTGCGGTCATGATGATGATGATGATGATGATGATGATGAT 455
QY 527 TGGTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 586
DB 456 TGGCAATTTCTGCT 515
QY 587 GGTCACTGTATC 600
DB 516 CTTGAACCTCTACCC 529

RESULT 6

US-09-770-444-39
Sequence 39, Application US/09770444
Patent No. US2002023280A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Joern
APPLICANT: An, Yong-Olang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krieger, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39
LENGTH: 476
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or G
US-09-770-444-39

Query Match 12.6%; Score 111.2; DB 9; Length 476;
Best Local Similarity 54.4%; Pred. No. 6.9e-24;
Matches 221; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 1 CCGCT 60
DB 70 CCGCTTGGACATCTCTGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 129
QY 61 CCGCGCT 120
DB 130 CCGAAGTCTCAGCGATTAACCGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 189

```

QY 121 ACCGAGAGGCGCACACACCTCCATCTCTCCCTTAATTCACCCCTTTTCTCTCT 180
DB 190 AAAAAAGAGTACGTTACTCTCTACACTAGCTTCGCGCGGCAATGTTCTCGAG 249
QY 181 CTGTCTGCGGCTCTCTCTCTCCGACAGCACTTGTGACGCTTTTCCGTCGATGA 240
DB 250 TTCTCTACAGTGTGTTTGGCTTGACTCCGCTCTCCCTACCAAAATCGCGCGCTTC 309
QY 241 TAGGCTTTCTGATTCAGAGCGGCTGATAGAGCAGACCTCCGCGCAATTAACAGTGA 300
DB 310 TCGGTTCTCTGATTCAGAGCGGCTTACATAGGTACAGTTCTGTCAATACGTTATCA 369
QY 301 TCTCAGCGCGCGCTCAACCGCGCAATTCAGATTCTCTCCGCAATTTCTCGCGGAA 360
DB 370 TGTGCAACAATCTTATTAACAAGTTGGCTCAGCTTCTCTNNGGTAACTGTCTACCGGA 429
QY 361 TCAGCATCGGCTGTGTGGAAGTGAACCAACCGCCACCAACATTCG 406
DB 430 TCTCAATCCGCTGTGGAATGAGTCAACAATGCTCATCATAGC 475

```

RESULT 7

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US-09-923-876-5116
; Sequence 5116, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 5116
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
US-09-923-876-5116

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Query Match 10.6%; Score 93; DB 9; Length 265;
Best Local Similarity 60.7%; Pred. No. 2.3e-18;
Matches 147; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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QY 402 ATTGATGCAACAGCTGCACTATGACCCCTGATCTGCAGACATGCGGCTTTGCAATT 461
DB 1 ATGCGCTGCAACAGCTGCACTATGACCCGACCTCAAGACATGCGCTTTCGTTGTC 60
QY 462 TGTGCGGCTTCTCAATTCATACCTCTCATTTCTATGAGGAGAGTTGAGTTGAT 521
DB 61 TCCCCCAACCTGTTCGCAACATATGCTCTACTTCTACAGGAGACCTCGGCTTCGAC 120
QY 522 TNCATTGCTAGTTCTTGTATCTGCTACAGCACTTACTTTTACCGGGTAATGTGTT 581
DB 121 GCCGCTCGAAATTTCTCTACGCTACAGCACTGAGCTTCTTACCGGGTAATGTGATC 180
QY 582 GCCAGGTCAACTTGTATCTGACAGCAATTTGCTATTTGTTTGAAGAAAGTGAC 641
DB 181 GCCAGATTAATCTTGTGCGGAGTGGCTGTCTTGTCTCTGACGAGAAAGGCGGCG 240
QY 642 GA 643
DB 241 CA 242

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RESULT 8

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US-09-923-876-5116
; Sequence 5116, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 5116
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
US-09-923-876-5116

```

```

Query Match 10.6%; Score 93; DB 12; Length 265;
Best Local Similarity 60.7%; Pred. No. 2.3e-18;
Matches 147; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

```

```

QY 402 ATTGATGCAACAGCTGCACTATGACCCCTGATCTGCAGACATGCGGCTTTGCAATT 461
DB 1 ATGCGCTGCAACAGCTGCACTATGACCCGACCTCAAGACATGCGCTTTCGTTGTC 60
QY 462 TGTGCGGCTTCTCAATTCATACCTCTCATTTCTATGAGGAGAGTTGAGTTGAT 521
DB 61 TCCCCCAACCTGTTCGCAACATATGCTCTACTTCTACAGGAGACCTCGGCTTCGAC 120
QY 522 TNCATTGCTAGTTCTTGTATCTGCTACAGCACTTACTTTTACCGGGTAATGTGTT 581
DB 121 GCCGCTCGAAATTTCTCTACGCTACAGCACTGAGCTTCTTACCGGGTAATGTGATC 180
QY 582 GCCAGGTCAACTTGTATCTGACAGCAATTTGCTATTTGTTTGAAGAAAGTGAC 641
DB 181 GCCAGATTAATCTTGTGCGGAGTGGCTGTCTTGTCTCTGACGAGAAAGGCGGCG 240
QY 642 GA 643
DB 241 CA 242

```

RESULT 9

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US-10-156-761-2285
; Sequence 2285, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109

```

SEQ ID NO 2285
 LENGTH: 1095
 TYPE: DNA
 ORGANISM: Streptomyces avermectilis
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1095)
 US-10-156-761-2285

Query Match 8.4%; Score 74.2; DB 15; Length 1095;
 Best Local Similarity 49.9%; Pred. No. 3.4e-12;
 Matches 187; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 59 CTCGCGCGCTCTCCGACTACGCAAGCTCTTCTCCGACCTCCGCGCTCAACCTTT 118
 DB 54 CACCGGGCTTCGGCCACGTTCCGCCGACCTGCTCAAGCGGCAAGGCGCTTCT 113
 QY 119 CAACCGCAAGGGCCACACCACTTCATCTCTCTCTTATTTCTCAACCTTTTCTCT 178
 DB 114 CGACCTGATCCCGCTACTACATAGGCGGCTGGCGCTGACACGCGCTGCTGCT 173
 QY 179 CTCTGTCGGGGGCTCTCTTCTCCGACGACCTTTGTGACAGTCTTCCGCTGAT 238
 DB 174 CGGGTTCGCGCGCTTCTTCCGCTGGGCGACTGCTGTGACGCTGTGCGCTGTG 233
 QY 239 GATAGGCTTCTCTGATTCAGAGCGGCTGATAGGCGGACGCTCCGCGCATTAACA 298
 DB 234 GATGGGCTGTGGCGGCTGATGTCGCTTCTGATGTGACGAGCGCGGCAAGGCT 233
 QY 299 GATGCTCAGCGCGGCTCAACCGCGCAATTCTCTCGGCAACCTTCTCGCGG 358
 DB 294 GTTCGCGAGCAAGAGGCGCGCTCCGCGTCCGATCTTCCAGCGCAACCTCTGCA 353
 QY 359 AATCAGATCGGCTGTGGAAGTGAACCAAGCCGACCATTCATGCAAGGCT 418
 DB 354 GGTGAGCTTGGGTGGGTGATCAACCAACCGGCGACCAAGCAACCAAGCT 413
 QY 419 CGACTATGACCTGA 433
 DB 414 GGACATGACCCGA 428

RESULT 10
 US-10-156-761-1/c
 ; Sequence 1, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; PRIOR FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1
 ; LENGTH: 9025608
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermectilis
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (4187715)
 ; OTHER INFORMATION: a, c, g, other or unknown
 US-10-156-761-1

Query Match 8.4%; Score 74.2; DB 15; Length 9025608;
 Best Local Similarity 49.9%; Pred. No. 4.8e-10;
 Matches 187; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 59 CTCGCGCGCTCTCCGACTACGCAAGCTCTTCTCCGACCTCCGCGCTCAACCTTT 118
 DB 2801106 CACCGGGCTTCGGCCACGTTCCGCCGACCTGCTCAAGCGGCAAGGCGCTTCT 2801047
 QY 119 CAACCGCAAGGGCCACACCACTTCATCTCTCTCTTATTTCTCAACCTTTTCTCT 178
 DB 2801046 CGACCTGATCCCGCTACTACATAGGCGGCTGGGCTGGAACACCAAGCTGCT 2800987
 QY 179 CTCTGTCGGGGGCTCTCTTCTCCGACGACCTTTGTGACAGTCTTCCGCTGAT 238
 DB 2800986 CGGGTTCGCGCGCTTCTTCCGCTGGGCGACTGTGTGGAGCTGTGTGGCTGTG 2800927
 QY 239 GATAGGCTTCTCTGATTCAGAGCGGCTGATAGGCGGACGACTCCGCGCATTAACA 298
 DB 2800926 GATGGGCTGTGGGGGTGATGTCGCTTCAITGTGACGAGCGCGGCAAGGCT 2800867
 QY 299 GATGCTCAGCGCGGCTCAACCGCGCAATTCTCTCGGCAACCTTCTCGCGG 358
 DB 2800866 GTTCGCGAGCAAGAGGCGCGCTCCGCGTCCGATCTTCCAGCGCAACCTGCT 2800807
 QY 359 AATCAGATCGGCTGTGGAAGTGAACCAAGCCGACCATTCATGCAAGGCT 418
 DB 2800806 GGTGAGCTTGGGTGGGTGATCAACCAACCGGCGACCAAGCAACCAAGCT 2800747
 QY 419 CGACTATGACCTGA 433
 DB 2800746 GGACATGACCCGA 2800732

RESULT 11
 US-10-156-761-1580
 ; Sequence 1580, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; PRIOR FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1580
 ; LENGTH: 1059
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermectilis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1059)
 US-10-156-761-1580

Query Match 8.2%; Score 72.2; DB 15; Length 1059;
 Best Local Similarity 55.9%; Pred. No. 1.4e-11;
 Matches 137; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 189 GGGCTCTCTCTCCGACGACCTTCCGACAGTCTTCCGCTGATTCATGAGCTTT 248
 DB 184 GGGCTCTCTCTGATGATGATCTCTGAGGCTCTCTCTGCGCGGCTGCTGCTG 243
 QY 249 CTCTGATTCAGAGCGGCTGATAGGCGACGACTCCGCGCATTAACAAGTGTCTGAG 308

```

Db      244 CTCTCCACGCGACCGCGTTTCATAGTCAAGACCGCGTCTCATCCGACATCAACGCGGAC 303
Qy      309 CGCGCGCTCAACCGCGCAATTGATTTCTCTCGGCAACATTTGGCGGAAATCAGCATC 368
Db      304 AAGTCCGTACGCGCTCTCATGAGATTCACGCGCACTTTCTCGCATGAGCTTAT 363
Qy      369 GCGTGTGGAAGTGAACCAACGCGCCACACATTGACATGCAACAGCCTTGAATGAC 428
Db      364 GCGTGTGGAACGACAGCAACGCGTCAACGCGCAACCCGCAACATCGCAAGAGAC 423
Qy      429 CCTGA 433
Db      424 CCCGA 428

```

RESULT 12

```

US-10-184-644-332/c
; Sequence 332, Application US/10184644
; Publication No. US2003004930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 332
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-332

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Query Match 7.7%; Score 67.6; DB 15; Length 520;

Best Local Similarity 25.9%; Pred. No. 2.6e-10; Mismatches 174; Indels 0; Gaps 0;

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Qy      2 CGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 61
Db      406 CCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 347
Qy      62 CGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
Db      346 CATC.SC.SC..CTYC.SCTSC..CMTG.DCBTC..C.BC..C..C.HCMTC..CT.C.. 287
Qy      122 CGGCAAGGCGCACACACTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 181
Db      286 C.YC.HCMSC.TC..CKBCTHCKYCHMSC..C.HCM.CMACA.CM.C..CCHCMSCM. 227
Qy      182 TGTCTGCGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241
Db      226 C..C.ACATC.MC.TC..C..CT.CMBG..C..CS.CATCHYKCTMTCTM.T..C..C.T 167
Qy      242 AGCGTTTCTGTGATTCAGAGCGGTGATGAGCGGACGACTCGGCGCATTTACAGCTGAT 301
Db      166 C.KCKTQMDG..C.TC..CM.Y.KC.N.A.NHBY...D.DSBVMA..T..B..YSTC.T 107
Qy      302 GCTCAGCGCGCGCTCA 318
Db      106 .D.C.DTS...S.S.SH 90

```

RESULT 13

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US-10-184-634-332/c
; Sequence 332, Application US/10184634
; Publication No. US2003006868A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 332
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-332

```

Query Match 7.7%; Score 67.6; DB 15; Length 520;

Best Local Similarity 25.9%; Pred. No. 2.6e-10; Mismatches 174; Indels 0; Gaps 0;

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Qy      2 CGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 61
Db      406 CCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 347
Qy      62 CGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
Db      346 CATC.SC.SC..CTYC.SCTSC..CMTG.DCBTC..C.BC..C..C.HCMTC..CT.C.. 287
Qy      122 CGGCAAGGCGCACACACTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 181
Db      286 C.YC.HCMSC.TC..CKBCTHCKYCHMSC..C.HCM.CMACA.CM.C..CCHCMSCM. 227
Qy      182 TGTCTGCGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241
Db      226 C..C.ACATC.MC.TC..C..CT.CMBG..C..CS.CATCHYKCTMTCTM.T..C..C.T 167
Qy      242 AGCGTTTCTGTGATTCAGAGCGGTGATGAGCGGACGACTCGGCGCATTTACAGCTGAT 301
Db      166 C.KCKTQMDG..C.TC..CM.Y.KC.N.A.NHBY...D.DSBVMA..T..B..YSTC.T 107
Qy      302 GCTCAGCGCGCGCTCA 318
Db      106 .D.C.DTS...S.S.SH 90

```

RESULT 14

```

US-10-101-487-74/c
; Sequence 74, Application US/10101487
; Publication No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUISF, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGNER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077119/0329
; CURRENT APPLICATION NUMBER: US/10/101,487

```

CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 720
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: oligonucleotide
NAME/KEY: CDS
LOCATION: (2)..(718)
US-10-101-487-74

Query Match 7.5%; Score 65.6; DB 14; Length 720;
Best Local Similarity 48.6%; Pred. No. 1.3e-09;
Matches 179; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 5 CTCCCTCTCTCTCCGCTTCTCCACCTCCACCGCTTTCGACGACACCGCTTCGGC 64
DB 719 CTTCCT 660
QY 65 CGCTCTCTCGACTACGCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 124
DB 659 CTTCT 600
QY 125 CAAGGCGCACACCT 184
DB 599 CTTCCT 540
QY 185 CTGCGGCGTCT 244
DB 539 CTTCT 480
QY 245 CTTCCTCTGATTCAGAGCGGCTGATGAGGCGACGACCTCTCTCTCTCTCTCTCT 304
DB 479 CTTCCT 420
QY 305 CAGCGCGCGCTCTCAACGCGCAATTCAGATTCCTCTCTCTCTCTCTCTCTCTCT 364
DB 419 CTTCT 360
QY 365 CATCGGCT 372
DB 359 CTTCCTCT 352

RESULT 15
US-10-101-487-76
Sequence 76, Application US/10101487
Publication No. US20020169125A1
GENERAL INFORMATION:
APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LORQUIST, ALAN
APPLICANT: PIETZ, GREGORY E.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 76
LENGTH: 720
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
US-10-101-487-76

Query Match 7.5%; Score 65.6; DB 14; Length 720;
Best Local Similarity 48.6%; Pred. No. 1.3e-09;
Matches 179; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 5 CTCCCTCTCTCTCCGCTTCTCCACCTCCACCGCTTTCGACGACACCGCTTCGGC 64
DB 6 CTTCCT 65
QY 65 CGCTCTCTCGACTACGCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 124
DB 66 CTTCT 125
QY 125 CAAGGCGCACACCT 184
DB 126 CTTCCT 185
QY 185 CTGCGGCGTCT 244
DB 186 CTTCT 245
QY 245 CTTCCTCTGATTCAGAGCGGCTGATGAGGCGACGACCTCTCTCTCTCTCTCTCT 304
DB 246 CTTCCT 305
QY 305 CAGCGCGCGCTCTCAACGCGCAATTCAGATTCCTCTCTCTCTCTCTCTCTCTCT 364
DB 306 CTTCT 365
QY 365 CATCGGCT 372
DB 366 CTTCCTCT 373

Search completed: January 1, 2004, 05:19:32
Job time: 238.488 sec


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FT      /note= "Encoded by TG"
FT      Misc-difference 227..228
FT      /note= "Encoded by TTGTAGTNCCTTGCCTGCCAATATGGGCC
FT      TGTATAGGAGGATGTGTCG"
FT      Misc-difference 252
FT      /label= "Unknown
FT      /note= "Encoded by GNC"
XX      WO200032790-A2.
XX      08-JUN-2000.
XX      02-DEC-1999; 99WO-US28589.
XX      03-DEC-1998; 98US-0110784.
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX      Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
XX      WPI; 2000-412336/35.
XX      N-PSDB; AAD01351.
XX      DR
XX      PS Claim 10; Page 45-46; 57pp; English.
XX      CC The present sequence is a sphingolipid desaturase
XX      CC derived from a contig of clones sfil.pK0012.c5 and sfil.pK0031.d11
XX      CC isolated from soybean immature flower cDNA library, sfil.
XX      CC The present sequence is useful for producing
XX      CC transgenic plants having altered levels of sphingolipid desaturase which
XX      CC in turn would alter the fatty acid composition. The enzyme is also useful
XX      CC for producing polyclonal or monoclonal antibodies. The polynucleotide
XX      CC is useful as primer or probe for screening cDNA libraries to
XX      CC isolate desired full-length cDNA clones.
SQ      Sequence 253 AA;
Query Match 99.1%; Score 1306; DB 21; Length 253;
Best Local Similarity 100.0%; Pred. No. 3,7e-137;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 LPAFSTSHRLSDHTVSAASDYSKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 60
DB      1 LPAFSTSHRLSDHTVSAASDYSKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 60
QY      61 LFSDFSTFVHLSAALIGFLMIQSGWIGHDSGHYVWLSRRLNRAIQIILSGNIIAGISIGW 120
DB      61 LFSDFSTFVHLSAALIGFLMIQSGWIGHDSGHYVWLSRRLNRAIQIILSGNIIAGISIGW 120
QY      121 WKNNNNAHHIACNSLDYDPLQHPVFAVSRRFNSITSHXGKKEFDXIAKFLICYQH 180
DB      121 WKNNNNAHHIACNSLDYDPLQHPVFAVSRRFNSITSHXGKKEFDXIAKFLICYQH 180
QY      181 FTFYPVWCVARVNLVYQITILLFSRXKYODRALNIGILVFWTWFLFLALLFVPIQHIO 240
DB      181 FTFYPVWCVARVNLVYQITILLFSRXKYODRALNIGILVFWTWFLFLALLFVPIQHIO 240
QY      241 FWINHLAENLYXG 253
DB      241 FWINHLAENLYXG 253

```

```

XX      XX
XX      DE soybean sphingolipid desaturase #2.
XX      KW Soybean; sphingolipid desaturase; membrane-bound desaturase;
XX      KW transgenic plant; fatty acid.
XX      OS Glycine max.
XX      PN WO200032790-A2.
XX      PD 08-JUN-2000.
XX      PF 02-DEC-1999; 99WO-US28589.
XX      PR 03-DEC-1998; 98US-0110784.
XX      PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX      PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
XX      DR WPI; 2000-412336/35.
XX      DR N-PSDB; AAD01352.
XX      PS Claim 10; Page 47-48; 57pp; English.
XX      CC The present sequence is a sphingolipid desaturase
XX      CC from clone sfil.pK0017.b4.f15 isolated from soybean seedling cDNA
XX      CC library, sfil. The present sequence is useful for producing
XX      CC transgenic plants having altered levels of sphingolipid desaturase which
XX      CC in turn would alter the fatty acid composition. The enzyme is also useful
XX      CC for producing polyclonal or monoclonal antibodies. The polynucleotide
XX      CC is useful as primer or probe for screening cDNA libraries to
XX      CC isolate desired full-length cDNA clones.
SQ      Sequence 450 AA;
Query Match 68.2%; Score 899.5; DB 21; Length 450;
Best Local Similarity 65.3%; Pred. No. 1.6e-91;
Matches 175; Conservative 20; Mismatches 58; Indels 15; Gaps 2;
QY      1 LPAFSTSHRLSDHTVSAASDYSKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 60
DB      74 LKRFETGTHSDPKVSEVSKDYRKLSSEFSKGLFDTKGHVISTLAIVAAMFLIVLGV 133
QY      61 LFSDFSTFVHLSAALIGFLMIQSGWIGHDSGHYVWLSRRLNRAIQIILSGNIIAGISIGW 120
DB      134 LRCTSVMAHLGSGMLGLMGSAYVGHDSGHVVTWTTGPNKVAQIILSGNCLTGISIAM 193
QY      121 WKNNNNAHHIACNSLDYDPLQHPVFAVSRRFNSITSHXGKKEFDXIAKFLICYQH 180
DB      194 WKMTNNAHHIACNSLDHDPDQHPVFAVSRRFNSITSHFYGRKLEFDIFIAFLICYQH 253
QY      181 FTFYPVWCVARVNLVYQITILLFSRXKYODRALNIGILVFWTWFLFLALLFVPIQHIO 240
DB      254 FTFYPVWCVARVNLVYQITILLFSRXKYODRALNIGILVFWTWFLFLALLFVPIQHIO 240
QY      227 FLALFLV-PIQHIOFWNLHLENLYXG 253
DB      314 FVLASPAVCSIQHIOFCLNHFANVYVG 341

```

RESULT 2
 ID AAY71554 standard; Protein; 450 AA.
 AC AAY71554;
 XX
 DT 12-OCT-2000 (first entry)

RESULT 3
 ID AAG29290 standard; Protein; 449 AA.
 AC AAG29290;
 XX
 DT 17-OCT-2000 (first entry)

PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155569.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161820.
PR 28-OCT-1999; 99US-0161822.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match Best Local Similarity 59.9%; Score 789.5; DB 21; Length 449;

Matches 147; Conservative 38; Mismatches 68; Indels 15; Gaps 2;

QY 1 LPAFSTSHRLSDHTVASAASDYKRLFSALNLFNRKGGHTTSILSLITLTFPLSVCGV 60
DB 73 LKLNHGCVHRDHNHVDVSRDYRLAERFSKRGLPFKKGHTVLTCTCGVMAAVLYGV 132
QY 61 LFSDSFVAVLSAALIGFLMIGSGWIGHSGHYNWMLSRRLRAIOTISGNIAIGISIGW 120
DB 133 LACTSIWAHLISAVLLGLMIGSAYVGHSGHVTSTKPCNGLDILSGNCTLGISIAM 192
QY 121 WKMNHAHHIACNSLDYDPDLOHMPVFAVSRFNSITSXHXGKKXEPXIAFELICYOH 180
DB 193 WKMTNHAHHIACNSLDHDPDLOHPIPAVSTKFNSTSFYGRKLTDPDLAFLISYOH 252
QY 181 FTFYPMCAVAVNLVYQTLILLFSRXKVDRAINIGILVFWTFLLAL----- 232
DB 253 WFFYPMCAVAVNLVYQTLILLFSRXKVDRAINIGILVFWTFLLVSLPBMQGRPI 312
QY 233 --FV-----PIOHIOFWLNHLAENLYXG 253
DB 313 FVFSFAVTAIOHVOFCNLNHPADVYTG 340

RESULT 4
ID AAG07392 standard; Protein; 449 AA.
XX
AC AAG07392;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4528.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-012825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 15-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.

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PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144331.
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PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
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PR 23-JUL-1999; 99US-0145224.
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PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR 13-AUG-1999; 99US-0148565.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.

PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
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PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159330.
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PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 59.2%; Score 780.5; DB 21; Length 449;
Best Local Similarity 54.8%; Pred. No. 3, 1e-78;
Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVGAASDQRYKLFSDLSALNLFNRKHTTSLILSLITLFPISVCVLFSS 65
| : : | | | | | : : : | | | | | : : : | |
DB 78 TGYHTRDPQVSEVSVDYRMALEFRKLG.FENKGVTLTYLAFVAMFLRVLYGVLACTS 137
| : : | | | | | : : : | | | | | : : : | |
QY 66 TFVHLSAALIGFLTIGSCWIGDSGHYVWMLSRRLNRAIOLSGNLAGISIGMMKMH 125
| : : | | | | | : : : | | | | | : : : | |
DB 138 VFAHQIAALGLGLTIQSAVYIGDSGHYVWMLSRRLNRAIOLSGNLAGISIGMMKMH 197
| : : | | | | | : : : | | | | | : : : | |
QY 126 NAHHLIACNSLDYDPLQHPVFAVSRRFNSITSHXGKXEPDIXAFELICYOHTFPY 185
| | | : | | | | | : | | | : | | | : | | | : |
DB 198 NAHHLIACNSLDYDPLQHPVFAVSRRFNSITSHXGKXEPDIXAFELICYOHTFPY 257
| | | : | | | | | : | | | : | | | : | | | : |

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QY 186 VMCVARVNLVLTITLLFSRXKVDRAINMGILVFWTWFLPLALL-----FV---- 234
DB 258 VMCFGINLFIQIFLLFSKREVPDRALNFAGLVFWTWFLPLVSCLPMPKPEFFVFPNG 317
QY 235 ---PIQHIQFWLNHLAENLYXG 253
DB 318 FVTALQHIQFTLNHFADVYVG 340

RESULT 5
AA51333
ID AA51333 standard; Protein; 449 AA.
XX
AC AA51333;
XX
DT 27-APR-2000 (first entry)
XX
DE B. napus sld1 protein.
XX
KM Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KM pharmaceutical; food; chemical raw material.
XX
OS Brassica napus.
XX
PN DE19828850-A1.
XX
PD 30-DEC-1999.
XX
PF 27-JUN-1998; 98DE-1028850.
XX
PR 27-JUN-1998; 98DE-1028850.
PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
PI Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
DR WPI; 2000-127549/12.
XX
DR N-PSDB; AAZ44832.
XX
PT New sphingolipid desaturase that selectively introduces double bond
XX into sphingolipide and capnoids -
XX
PS Claim 8; Fig 2; 62pp; German.
XX
CC This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents the Brassica napus sphingolipid
CC desaturase sld1 protein described in the method of the invention.
XX
SQ Sequence 449 AA;

Query Match 59.2%; Score 780.5; DB 21; Length 449;
Best Local Similarity 54.0%; Pred. No. 3,1e-78;
Matches 141; Conservative 44; Mismatches 61; Indels 15; Gaps 2;
QY 8 HRLSDHTVASASDVKRLPDSLSALNLPFRKHTTISLILTLPLPLSGVLPFSDSRF 67

DB 80 YHKXDHVDSVSDRYRRLAABFSKGLPDKGHVTLVTLTCVAAMAAVAVYGACTSTW 139
QY 68 VHTLSAALIGFLMIGSGMIGHDSGRNVMLSRLNRAIQILSGNIIAGISIGMKKNHNA 127
DB 140 AHLISAVLLGLMIGSAYVGHDSGHVNVSTRCNKLVOILSGNCTGISIAWKKWTHNA 199
QY 128 HHACNSLDYDDPDLQMPVFAVSSRPFNSITSHXGKKEFPDXIAXFLCYOHFTFPVW 187
DB 200 HHISCNSLDHPDLOHITPVLAIVSNKFEKMTSRFYGRKLTDPDLARFLISYOHMSFPYPLW 259
QY 188 CVARVNLVLTITLLFSRXKVDRAINMGILVFWTWFLPLLA-----LLFV----- 234
DB 260 CVGRINLFIQITLLFSRRYVDPDRALNIGILVFWTWFLPLVSLPNNQERIIFFVLSMA 319
QY 235 ---PIQHIQFWLNHLAENLYXG 253
DB 320 VTAIQHVQCLNHFADVYTG 340

RESULT 6
AAG07391
ID AAG07391 standard; Protein; 517 AA.
XX
AC AAG07391;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4527.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131443.
PR 30-APR-1999; 99US-0132048.
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PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 11-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140891.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 26-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145818.
PR 27-JUL-1999; 99US-0145819.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.

PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 59.2%; Score 780.5; DB 21; Length 517;
Best Local Similarity 54.8%; Pred. No. 3,6e-78;
Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVSAASDYRKLFDLSALNLPNRKHTTSLTSLTLTLPVSGVLFSDS 65
DB 146 TGHYIDFOVSEVSRIRMAAFRKLGLFENKGHVTLTYLAVAAFLRYLGVLACTS 205
QY 66 TFWVLSAALIGLMTQSGWIGDSGHVYMLSRRLRAIOILSGNLIAGISIGWKMKN 125
DB 206 VFHNGQAALLGLMLQSAVITGDSGHVYIMSNKSYNRFQQLSGNCLTGISIAMKMTW 265
QY 126 NAHHIHCNSLDYDPDIQHPVFAVSSRFNSITSHYGRKKEPDIXAFICYQHTFYP 195
DB 266 NAHHIHCNSLDYDPDIQHPVFAVSTFFSLSRFPDRKLTFDPVAFIVSYQHFTYYP 325
QY 186 VMCVARVNLVLTOTLLFSRXXVODRALNTMGILVFWTWFLFLALL-----FV--- 234
DB 326 VMCFGRIINFIQFLFLFSKREVPDRALNPAIGLVEFWTFPLVSCLPNMPERFPVFTG 385
QY 235 ----PIQHIQFWMNLHAENLYXG 253
DB 386 FVTVALQHIQFTLNHFADVYVG 408

RESULT 7
AAG53861
ID AAG53861 standard; Protein; 449 AA.

AC AAG53861;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68613.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX -06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134270.
PR 18-MAY-1999; 99US-0134768.
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PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135553.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
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PR 14-JUN-1999; 99US-0139119.
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PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
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PR 16-JUL-1999; 99US-0144086.
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PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 03-AUG-1999; 99US-0146389.
 PR 04-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148341.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158332.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
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 PR 13-OCT-1999; 99US-0159295.
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 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
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PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 59.1%; Score 778.5; DB 21; Length 449;
 Best Local Similarity 54.8%; Pred. No. 5, 1e-78;
 Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVSAASDYLKFDLSALNLFNRKHTTSLILSLTLFPLSVGVLFSDS 65
 DB 78 TGYHIDFQVSEVSRYRMAALEFRKLGFEKKGHTLVTLAVFAAMFGLVGLACTS 137
 QY 66 TPVHVLSAALLIGFLWQSGMIGHDSCHYVNLRLRAIQLISGNTLAGISGMKMH 125
 DB 138 VFAHQIAAALLGLWIOSAYIGHDSCHYVIMNSKSYRPAQLSGNLTGISIAMMKTH 197
 QY 126 NAHIIACSLDYPDLOHMPVFAVSRRFNSITSHXGKXERDIXAFILCYOHTFYP 185
 DB 198 NAHIIACSLDYPDLOHMPVFAVSRRFNSITSHXGKXERDIXAFILCYOHTFYP 257
 QY 186 VMCVARVNLQTLILLFSRXKVDRLNIMGLVFWTLFLALL-----FY--- 234
 DB 258 VMCFGRIINFLOTFLILFSKREVPDRALNPAQILVFWTLPPLVSLCPMMPERFFVETS 317
 QY 235 ----PIQHIQFWNLHAEVLYXG 253
 DB 318 FVTALQHIQFTLNHPADVVYG 340

RESULT 8
 AA51334
 ID AA51334 standard; Protein; 449 AA.
 XX
 AC AA51334;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE A. thaliana sld1 protein.
 XX
 KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Arabidopsis thaliana.
 XX
 PN DE19628850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 XX 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GBS ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E, Zaehneringer U, Schmidt H, Sperling P;
 XX WPI, 2000-127549/12.
 DR N-PSDB; AA244833.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 into sphingolipide and capnoids -

XX Claim 8; Fig 4; 62pp; German.

CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents the Arabidopsis thaliana sphingolipid
 CC desaturase sld1 protein described in the method of the invention.

XX Sequence 449 AA;

Query Match 59.1%; Score 778.5; DB 21; Length 449;
 Best Local Similarity 54.8%; Pred. No. 5, 1e-78;
 Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLDHYVAASSDYRKLPSDLNALNFRKGGHTTSLLSLILTFPLSCVGLFSDS 65
 DB 78 TGVHIDFQVSEVSRVRRMAAEFRKLGLENKGHTLTYTLAFVAAVGLVGVACTS 137
 QY 66 TGVHIDFQVSEVSRVRRMAAEFRKLGLENKGHTLTYTLAFVAAVGLVGVACTS 137
 DB 138 VFNHQAALALIGLWIGWIGSGHYVMSRRLNRAIQILSGNLAGISIGWKMKNH 125
 QY 126 NAAHIAACNSLDYDPPDLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYQHFTYP 185
 DB 198 NAAHIAACNSLDYDPPDLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYQHFTYP 185
 QY 186 VMCVAARVNLVLTOTILLFSKXKQDRALNIMGLVFWTWLFLALL-----PV--- 234
 DB 258 VMCVEGINFETIQFLLFSKREVPDRALNIMGLVFWTWLFLALL-----PV--- 234
 QY 235 -----PIQHQFMNLHAEMLYXG 253
 DB 318 FTVTALQHQFTLNHRAADYVVG 340

RESULT 9

AAU79851
 ID AAU79851 standard; Protein; 452 AA.

AC AAU79851;

DT 15-JUL-2002 (first entry)

DE Evening primrose delta6-desaturase.

KW delta6-desaturase; sunflower; soybean; maize; tobacco;
 KW peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KW chilling tolerance; evening primrose.

OS Oenothera biennis.

PN US6355861-B1.

PD 12-MAR-2002.

PF 19-SEP-1997; 97US-0934254.

PR 13-OCT-1992; 92US-0959952.

PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.

PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.

PA (RHON) RHONE-POULENC AGROCHIMIE.

PT Thomas TL;

DR WPI; 2002-380944/41.

DR N-PSDB; ABK49503.

PT Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linoleic acid to gamma-linolenic acid useful for producing
 CC gamma-linolenic acid in transgenic plant or bacteria

PS Claim 3; Column 45-48; 53pp; English.

CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma-linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This is the amino acid sequence of the
 CC evening primrose delta6 desaturase involved in the production of gamma
 CC linoleic acid.

SO Sequence 452 AA;

Query Match 57.2%; Score 753.5; DB 23; Length 452;
 Best Local Similarity 53.2%; Pred. No. 3, 2e-75;
 Matches 142; Conservative 37; Mismatches 73; Indels 15; Gaps 2;

QY 2 PAFSTHRLSDHYVAASSDYRKLPSDLNALNFRKGGHTTSLLSLILTFPLSCVGL 61
 DB 74 PLFTGYTYKDFEVSISIKDYRRLNEMERSGIFERKGGHIMTWFGVAVMMAIYGV 133
 QY 62 FSDSTGVHIDFQVSEVSRVRRMAAEFRKLGLENKGHTLTYTLAFVAAVGLVGV 121
 DB 134 ASSEVGVHMLCGALLDLMLQAAYVGHDSGHVMTREGRNRTQILAGNILGISIAW 193
 QY 122 KMNHNAHIAACNSLDYDPPDLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYQH 181
 DB 194 KMNHNAHIAACNSLDYDPPDLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYQH 181
 QY 182 TFPVNCVARNVNLVLTOTILLFSKXKQDRALNIMGLVFWTWLFLALL-----PV--- 227
 DB 254 TFPVNCVARNVNLVLTOTILLFSKXKQDRALNIMGLVFWTWLFLALL-----PV--- 227
 QY 228 -LTLALFVPIQHQFMNLHAEMLYXG 253
 DB 314 VLISFAVTALQHQFTLNHRAADYVVG 340

RESULT 10

ABG73416
 ID ABG73416 standard; Protein; 452 AA.

AC ABG73416;

DT 16-APR-2003 (first entry)

DE Evening primrose delta-6-desaturase #1.

KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
 KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KW octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;

KW evening primrose.

OS Oenothera biennis.

PN US2002108147-A1.

PD 08-AUG-2002.
 XX
 PF 21-DEC-2001, 2001US-0029756.
 XX
 PR 13-OCT-1992, 92US-0959952.
 PR 19-SEP-1997, 97US-0934454.
 PR 10-OCT-1991, 91US-0774475.
 PR 08-JAN-1992, 92US-0817919.
 PR 14-SEP-1994, 94US-0307382.
 PR 26-JAN-1997, 97US-0789936.
 XX
 PA (THOM/) THOMAS T L.
 XX
 PI Thomas TL;
 XX
 DR WPI: 2003-066659/06.
 DR N-PSDB; ABX15367.
 XX
 XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant
 XX
 PS Claim 3, Fig 10; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC an evening primrose delta-6-desaturase polypeptide.
 CC
 SQ Sequence 452 AA;
 Query Match 57.2%; Score 753.5; DB 24; Length 452;
 Best Local Similarity 53.2%; Pred. No. 3.2e-75;
 Matches 142; Conservative 37; Mismatches 73; Indels 15; Gaps 2;
 QY 2 PAFSTSHRLSDHTVSAASSDYRKLPSDLSALNLFNRKHTTSLLSLITLPLPVSQGV 61
 DB 74 PLFTGYLYLKDFEVSSEISKDYRLNEMSGIFFEKKGHIMWTFVGAVMMALVYGV 133
 QY 62 FSDSTFVHLVSAALIGFLWISGMIHDSGHVVMLSRRLNRAIQISGNIAGISIGW 121
 DB 134 ASESVCVHMLCGALDLMLIQAAYVGHDSGHVQVMPTRGVNRTQLIAGNILLGISIAW 193
 QY 122 KNNHNAHIAACNSLDYDPDLQHPVPAVSRFPNSITSHYGRKXKFPDIAFLICYQHF 181
 DB 194 KHTHNAHIAACNSLDYDPDLQHPVPAVSRFPNSITSHYGRKXKFPDIAFLICYQHF 253
 QY 182 TTYPVNCAVAVNLVLTQTLILFSRXKVQDPAALNMGILVFTWTF-LF----- 227
 DB 254 TTYPVNCAVAVNLVLTQTLILFSRXKVQDPAALNMGILVFTWTF-LF----- 313
 QY 228 -LLALLFVPIQIHFQFNLHAEULYXG 253
 DB 314 VLISFAVTAIQHVFQTLNHFSGDTYVG 340

XX
 DE Sphingolipid desaturase protein.
 XX
 KW Sphingolipid desaturase, sld1, sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Unidentified.
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS ERMERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E. Zaehrerger U, Schmidt H, Sperling P;
 XX
 DR WPI: 2000-127549/12.
 DR N-PSDB; AA244851.
 XX
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipid and capnoids -
 XX
 PS Disclosure, Fig 15; 62pp; German.
 XX
 CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a sphingolipid desaturase protein
 CC described in the method of the invention.
 CC
 SQ Sequence 458 AA;
 Query Match 56.7%; Score 747.5; DB 21; Length 458;
 Best Local Similarity 52.8%; Pred. No. 1.5e-74;
 Matches 140; Conservative 40; Mismatches 66; Indels 19; Gaps 4;
 QY 6 TSHRLSDHTVSAASSDYRKLPSDLSALNLFNRKHTTSLLSLITLPLPVSQGV 63
 DB 87 TGYHLKDYQVSDISIDYRKLASEFAKGFEEKGH--GVYSLCFVSLLSACVYGVLS 144
 QY 64 DSTFVHLSAALIGFLWISGMIHDSGHVVMLSRRLNRAIQISGNIAGISIGW 123
 DB 145 GSFVHMLSGALIGLAAQIAYLGHDAHYQMAATRGKMKPGIFRGICITGISTIAW 204
 QY 124 NENAHIAACNSLDYDPDLQHPVPAVSRFPNSITSHYGRKXKFPDIAFLICYQHF 183
 DB 205 TNNAHIAACNSLDYDPDLQHPVPAVSRFPNSITSHYGRKXKFPDIAFLICYQHF 264
 QY 184 YPVNCAVAVNLVLTQTLILFSRXKVQDPAALNMGILVFTWTF-LF-----PV- 234
 DB 265 YPIMCAVAVNLVLTQTLILFSRXKVQDPAALNMGILVFTWTF-LF-----PV- 324
 QY 235 -----PIQIHFQFNLHAEULYXG 253

DB 325 VSECVTGTGHIQIPLTNHFGSDVYVG 349

RESULT 12

AA607393

ID AA607393 standard; Protein; 353 AA.

XX

AC AA607393;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 4529.

XX

KM Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126284.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

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PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

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PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144684.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

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PR 22-JUL-1999; 99US-0145192.

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PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

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PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

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PR 05-AUG-1999; 99US-0147360.

PR 06-AUG-1999; 99US-0147303.

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PR 09-AUG-1999; 99US-0147493.

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PR 12-AUG-1999; 99US-0148341.

PR 13-AUG-1999; 99US-0148565.

PR 13-AUG-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.

PR 17-AUG-1999; 99US-0149375.

PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161820.
PR 28-OCT-1999; 99US-0161822.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.

Query Match 56.2%; Score 741; DB 21; Length 353;
Best Local Similarity 55.2%; Pred. No. 5.7e-74;
Matches 138; Conservative 35; Mismatches 55; Indels 22; Gaps 3;

QY 19 SSDYRKLFDLSALNLFNRKHTTSLILSLTLFPLSCGVLFSDSTFVHVSALLIGF 78
DB 2 AAEFRK-----IGFENKKGHTLYTLAFVAMFRLVLYGVLAQTSVFHQIAAALLGL 54
QY 79 LNIQSGWIGHDSGHVVMISRLNRAIQIISGNTLAGISIGWKKNNNAHHIACNSLDYD 138
DB 55 LNIQSAVIGHDSGHVYIMNSKYNRPAQLISGNCITGISIAWKKWTHNAHHIACNSLDYD 114
QY 139 PDLQHMVPFAVSSRFNSITSHXGKRKXEPDXIAFLICQHTFPVWCVARVNLXLQT 198

DB 115 PDLQHMVPFAVSTKFPSSILTSRFDYDKLFFDVARFLVSQFTYYPVWCGRINLIQFT 174
QY 199 ILLFSRKVQDRAINIMIGIIVFWTWFLFLALL-----FV-----PIQHQFPL 243
DB 175 FLLFSKREVPDRALNFAGILVFWTWFLVSCLPNWPBPFVFTGTVTALQHQFTL 234
QY 244 NHLAENTLYXG 253
DB 235 NHFADVYVG 244
RESULT 13
AAG53862
ID AAG53862 standard; Protein; 353 AA.
AC AAG53862;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68614.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
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PR 25-MAY-1999; 99US-0136021.
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 PR 05-AUG-1999; 99US-0147192.
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PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
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 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
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 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151308.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 56.1%; Score 739; DB 21; Length 353;
 Best Local Similarity 55.2%; Pred. No. 9, 6e-74;
 Matches 138; Conservative 35; Mismatches 55; Indels 22; Gaps 3;

```

QY 19 SSDYKRLFDLALNLFNRKHTTSLILSLTLFPLSVCGVLPDSSTFVHVLAAALIGF 78
DB 2 AAFFRK-----LGLFENKGGHTVLTFLAFVAMFLGVLYGLACTSVFAHQIAAALLGL 54
QY 79 LMIQSGWIGHDSGHVNMLSRLNRAIQILSGNITLAGISIGWKKNNNAHNAHNAHNAH 138
DB 55 LMIQSYVIGHDSGHVYIMSNKSYNRFAPOLISGNCILGISIAMWKNHNAHNAHNAHNAH 114
QY 139 PDLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICQHPFTFYPVACVAVNLXLQT 198
DB 115 PDLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICQHPFTFYPVACVAVNLXLQT 174
QY 199 LILFSSRXVQDRALNIMGLVFWTWFLPLADL-----FV-----PIQIQFWL 243
DB 175 FLLFSSKRVDPDALNFAGLVFWTWFWPLLVSCLPWMPBRFFVFTSFTVTLQHQFTL 234
QY 244 NMLAENLYXG 253
DB 235 NHFAADVYVG 244

RESULT 14
AAR98455
ID AAR98455 standard; Protein; 448 AA.
AC AAR98455;
XX
XX
DT 15-SEP-1996 (first entry)
XX
DE Borage delta-6-desaturase.
XX
XX Delta-6-desaturase: gamma-linolenic acid; transgenic plant; borage;
KM polyunsaturated fatty acid; octadecatetraenoic acid;
KW chilling resistance; oilseed.
XX
XX Borage officinalis.
OS
XX
XX Key Location/Qualifiers
FH Region 156..163
FT /label= lipid_box
FT Region 196..200
FT /label= Metal_box-1
FT Region 372..377
FT /label= Metal_box-2
XX
XX WO9621022-A2.
XX
XX 11-JUL-1996.
XX
XX 28-DEC-1995; 95MO-IB01167.
XX
XX 30-DEC-1994; 94US-0366779.
XX
XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX Freyssinet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
XX WPI; 1996-333997/33.
XX DR N-PSDB; AAT30395.
XX
XX Transgenic plants comprising the borage delta-6-desaturase gene -
PT show increased production of gamma linolenic acid and having
PT increased resistance to chilling
XX
XX Claim 3; Page 52-53; 75pp; English.
XX
XX Borage delta-6-desaturase (AAR98455) catalyses the conversion of
CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
CC deduced from that of the delta-6-desaturase gene (AAT30395) isolated
CC from a borage membrane-bound polysomal library. The sequence is
CC distinct from that of Synchocystis delta-6-desaturase (AAR98456).
CC Expression of the desaturase in transgenic plants, esp. sunflower,
CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in

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CC increased GLA prodn. Alteration of the plant membrane lipids as a
CC result of expression of the desaturase may also result in increased
CC resistance to chilling.
XX
SQ Sequence 448 AA;
Query Match 55.4%; Score 730.5; DB 17; Length 448;
Best Local Similarity 48.9%; Pred. No. 1,1e-72;
Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
QY 1 LPAFSTSHRLSPHTVSAASDDYKRLFSDLSALNLFNRKHTTSLILSLTLFPLSVCGV 60
DB 72 LKFFFTGYLXKQYSVSEVSKDYKLVFEFSKMGIDKCHIMFATLCFIAMLFAMSVYGV 131
QY 61 LPDSSTFVHVLAAALIGPMTQSGWIGHDSGHVNMLSRLNRAIQILSGNITLAGISIGW 120
DB 132 LFCBGVLVHLFSGCLMFLMIQSGWIGHDSGHVNMVSDSRLNKFIPANCLSGISIGW 191
QY 121 WKNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 180
DB 192 WKNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 251
QY 181 FTFYPVACVAVNLXLQITLILFSSRXVQDRALNIMGLVFWTW-----L 226
DB 252 WTFYPTMCAARLNMVQSLIMLTGRNVSYRAQELGLVSIWPLVSLPMMGERIM 311
QY 227 FLLALLFVP-IOHQFWLNLAEENLYXG 253
DB 312 FVIAISLSTVGMOOVQFSLNHFSSVYVG 339

RESULT 15
AAM67471
ID AAM67471 standard; Protein; 448 AA.
AC AAM67471;
XX
XX
XX 02-MAR-1999 (first entry)
DT
XX
DE Borage delta-6 desaturase protein.
XX
XX Upstream region; regulatory region; sunflower; albumin; seed; expression;
KM lipid metabolism; delta-6 desaturase; transgenic plant.
XX
XX Borage officinalis.
OS
XX
XX Key Location/Qualifiers
FH Region 40..44
FT /note= "cytochrome b5 haem-binding motif"
FT Domain 156..163
FT /note= "His-rich metal binding motif"
FT Domain 196..200
FT /note= "His-rich metal binding motif"
FT Domain 373..377
FT /note= "His-rich metal binding motif"
XX
XX WO945460-A1.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98MO-US07178.
XX
XX 09-APR-1997; 97US-0831570.
XX
XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX Beremand PD, Nunberg AN, Thomas TL;
XX WPI; 1998-583201/49.
XX DR N-PSDB; AAV34398.
XX
XX New sunflower albumin 5' regulatory region - useful for directing
PT altered lipid metabolism in plant seeds

```


C/Species: Mucor rouxi
 C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
 C/Accession: J07556
 R/Biochem: K.; Mannonitrar, R.; Tanticharoen, M.; Cheevadhanarak, S.
 A/Title: Deltac6-desaturase of Mucor rouxi with high similarity to plant deltac6-desaturase
 A/Reference number: J07556, M01D: 20563795, PMID:1112411
 A/Accession: J07556
 A/Molecule type: DNA
 A/Residues: 1-523 <LMO>
 A/Cross-references: GB:AF290983
 A/Experimental source: strain ATCC 24905
 C/Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformation
 C/Keywords: oxidoreductase; transformation

Query Match 28.6%; Score 377.5; DB 2; Length 523;
 Best Local Similarity 32.5%; Pred. No. 2.1e-28;
 Matches 81; Conservative 46; Mismatches 87; Indels 35; Gaps 5;

QY 22 YRLTFLDLSALNLFN-----RKG--HTSLSLSLTLPLPVSQVLFSDSTFVHVL 72
 DB 167 YRLTFLDLSALNLFN-----RKG--HTSLSLSLTLPLPVSQVLFSDSTFVHVL 72
 QY 73 AALIGFLWISQGWIGHDSGHYVNLSSRLNRAIQILSGNLAGISIGWKKNNNAHHIAC 132
 DB 218 AAFMAFMHQLVFTADHAGNEITGKSEIDHVIIVIGIINPGLSLGWMKNNNAHHIAC 217
 QY 133 NSLDYDPDLOHMPVAVSSRFFNSITSHXGRKCEPDIXALFLCYQHFFVPCVAV 192
 DB 278 NHEHDPDLOHMPVAVSSRFFNSITSHXGRKCEPDIXALFLCYQHFFVPCVAV 192
 QY 193 NYLQTLILFSSKXKODRALNIMGILVFWTWFLFLA-----LTFVPI 236
 DB 338 NLRSLFALVLTCKNVRTRLVGLITFFVWGSLSLTPNTNINIAIMSYMLTFPL 397
 QY 237 QHIOFWLNLH 245
 DB 398 -HVQITLSH 405

RESULT 6
 T26280
 N/Alternate names: Deltac6 fatty acid desaturase
 C/Species: Caenorhabditis elegans
 C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 03-Jun-2002
 C/Accession: T26280, T37238
 R/Swindburne, J.; Ahnecough, R.
 submitted to the EMBL Data Library, March 1996
 A/Reference number: Z20188
 A/Accession: T26280
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-473 <WIL>
 A/Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2.4
 A/Experimental source: clone W08D2
 R/Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
 Biochem. J. 330, 611-614, 1998
 A/Title: Identification of a Caenorhabditis elegans Deltac6-fatty-acid-desaturase by heterologous complementation
 A/Reference number: Z21637; M01D:98149727; PMID:9480865
 A/Accession: T37238
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-38,69-430, 'V', 432-473 <NAP>
 A/Cross-references: EMBL:AF031477; M1D:G308519; PIDN:AAC15586.1; PID:G308520
 C/Genetics:
 A/Map position: 4
 A/Intons: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
 C/Superfamily: Caenorhabditis elegans Deltac6 fatty acid desaturase
 C/Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 17.0%; Score 224.5; DB 1; Length 473;

Best Local Similarity 26.7%; Pred. No. 9.1e-14;
 Matches 70; Conservative 36; Mismatches 115; Indels 41; Gaps 8;

QY 10 LSDHTYSAAS-----SDYKLFSDLSALNLFNRKHTTSLSLTL-----PLSVC 58
 DB 119 VSAVDYVVAQKMYESFEKLRQKHDDGLM--KANETFLPKASTLSIMPAFLQYL 176
 QY 59 GVLFSSTFVHLSAALIGFLWISQGWIGHDSGHYVNLSSRLNRAIQILSGNLAGIS 118
 DB 177 G-----WYTSACLALAMQGFGLTHFCHQOPTORPLNDTSLPFGNLFQFSR 228
 QY 119 GWMKNNNAHHIACNSLDYDPDLOHMPVAVSSRFFNSITSHXGRKCEPDIXALFLCY 178
 DB 229 DMWKDGNTHAATNVDHDDGIDLAFLAF-----IPGLCKYKAFEXALIKIVP 281
 QY 179 QHFFVPCVAVNLVLTILFSSKXKODRALNIMGILVFWTWFLFLA-----LTFVPI 229
 DB 282 QHLYFTAMLPMLRFSQVQVWFENQMEYKVVORNAFWEQATIVG--HWAVFYOL 338
 QY 230 ALLFV-PIQHIOFWLNLH 250
 DB 339 FLPTWPLRVAYFIISQMGGL 360

RESULT 7
 T43319
 Deltac5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
 C/Accession: T43319, T24875
 R/Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
 FEBS Lett. 439, 215-218, 1998
 A/Title: Functional identification of a fatty acid desaturase gene from Caenorhabditis elegans
 A/Reference number: Z22422; M01D:99059458; PMID:9845325
 A/Accession: T43319
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-447 <MIC>
 A/Cross-references: EMBL:AF078796; M1D:G4003522; PIDN:AAC95143.1; PID:G4003523
 R/Swindburne, J.
 submitted to the EMBL Data Library, October 1996
 A/Reference number: Z19947
 A/Accession: T24875
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-197, 'VSHIENN', 198-447 <WIL>
 A/Cross-references: EMBL:Z61122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
 A/Experimental source: clone T13F2
 C/Genetics:
 A/Map position: 4
 A/Intons: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
 C/Superfamily: Caenorhabditis elegans Deltac6 fatty acid desaturase
 C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 15.3%; Score 201.5; DB 1; Length 447;
 Best Local Similarity 25.1%; Pred. No. 1.4e-11;
 Matches 64; Conservative 43; Mismatches 101; Indels 47; Gaps 10;

QY 19 SSVYKLFSDLSALNLFNRKHTTSLSLTLPLPVSQVLFSDSTFVHVL----- 71
 DB 102 SAQINKSPFDLMMRRARABLMD--GSPFLYIKIETIT-----ILFAFYQHTTYLP 154
 QY 72 SAALIGFLWISQGWIGHDSGHYVNLSSRLNRAIQILSGNLAGISIGWKKNNNAHHIAC 131
 DB 155 SALMGVAMQQLGWLILHEFAHQLFKNRYNDLASVFGNPLQGFSSGGCKQOHVHNA 214
 QY 132 NSLDYDPDLOHMPVAVSSRFFNSITSHXGRKCEPDIXALFLCYQHFFVPCVAV 191
 DB 215 TTVVGRDGLDLPVPAVATVAEHLNYSQ-----DSWVTLFRWQHVHTFMLPFLR 265
 QY 192 NYLQTLILFSSKXKODRALNIMGILVFWTWFLFLA-----LTFVPI 233

Db 266 LSMLOSIFVSGMPTHYDYRNNTAIYEQ---VGLSLHMAWSLGQLYFLPDMSTRIME 321

Qy 234 VPIQHI--OPWLNHL 246

Db 322 FLVSHLVGFLSHV 336

RESULT 8

H88791

protein T13F2.1 (imported) - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C/Accession: H88791

R/Anonymous, The C. elegans Sequencing Consortium.

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_ele

A/Note: published extrata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: H88791

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-454 <STO>

A/Cross-references: GB:chr_IV; PIDN:CAB03352.1; PID:93879828; GSPDB:GNO00022; CESP:T13F2.

C/Genetics:

A/Map position: 4

C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match 14.3%; Score 188; DB 2; Length 454;

Best Local Similarity 24.4%; Pred. No. 2.8e-10;

Matches 64; Conservative 43; Mismatches 101; Indels 54; Gaps 11;

Qy 19 SSDYRKLFSDL-----SALNPNKRGHTTSLLSLTLFLPLSVCGVLPFSDTFPHVL--- 71

Db 102 SAQINNSFTDLRRKVRABGLMD--GSDPLFYRKLETFITF---ILFAFLYLYHTYLLP 154

Qy 72 SALIGFLWIGSGWIGDGHVNMVLSRLNRAIQLSGNLA-----GISGWMKMN 124

Db 155 SALMGVAMQQLGHLIEFPAHQLFKRYNDLASIVGVNFOVSHIFNNQSSGCKEQ 214

Qy 125 HNAHHTACNSLDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYHPTFY 184

Db 215 HNVHAAATNVVGRDGLDLPFVATVAEHLNNYSQ-----DSVWMTLFRQVHWMT 265

Qy 185 PWCVARVNIYLQITILL-----FSRXKQDANLIMGLVWTFPL---FL-- 228

Db 266 FMUPFLSLWLSQIFVSGMPTHYDYRNNTAIYEQ---VGLSLHMAWSLGQLYFLPD 321

Qy 229 --LALLFVPIQHI--OPWLNHL 246

Db 322 WSTRIMEFLVSHLVGFLSHV 343

RESULT 9

JG0180

Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000

C/Accession: JG0180

R/Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.

Biochem. Biophys. Res. Commun. 255, 575-579, 1999

A/Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des

A/Reference number: JG0180; MUID:99160394; PMID:10049752

A/Accession: JG0180

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-444 <AKI>

A/Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BA075496.1; PID:94514722

C/Superfamily: cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynth

F;18-94/Domain: cytochrome b5 core homology <CBS>

F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 12.9%; Score 170; DB 2; Length 444;

Best Local Similarity 24.9%; Pred. No. 1.4e-08;

Matches 64; Conservative 33; Mismatches 114; Indels 46; Gaps 8;

Qy 16 SAASDYRKLFSDLSALNPNKRGHTTSLLSLTL-----PLSVCGVLPFSDTFPHV 70

Db 107 SQITDEFRALKKTAEDMNLFTKTNHLFFPILLSHIIWESIAWFIIS----YFNGMIPTV 162

Qy 71 LSALIGFLWIGSGWIGDGHVNMVLSRLNRAIQLSGNLAISIGWKKNNHNAHI 130

Db 163 ITAFVILATSOAQAGWLQHDYGHLSVYKKSIMWNIHVKFVIGHLKGSANWNNRHFOHNA 222

Qy 131 ACSNLDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYHPTFYPMVCA 190

Db 223 KPIHFKDPIKSLHNFV-----GEMQPEYCKK---KTKLPNNHQHEVFFLGPP 273

Qy 191 RVNLYD--QTILLFSRXKVDRA-----LNIWGLVFWTFPLFLLAL 232

Db 274 LHMVYQYQIMTMRIRRDVLDLWALISYARFFTYIPFYGILGALVFLNFRFLSHW 333

Qy 233 FVPIQHIQFW---LNLHL 246

Db 334 FV-----WVTQNMHI 343

RESULT 10

T13155

linoleoyl-CoA desaturase (EC 1.14.19.3) [validated] - human

N/Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1

C/Species: Homo sapiens (man)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002

C/Accession: T13155; T08765

R/Cho, H.P.; Nakamura, M.T.; Clarke, S.D.

J. Biol. Chem. 274, 471-477, 1999

A/Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desat

A/Reference number: T13155; MUID:99085046; PMID:9867867

A/Accession: T13155

A/Status: preliminary; translated from GB/EMBL/DDJ

A/Molecule type: mRNA

A/Residues: 1-444 <CHO>

A/Cross-references: EMBL:AF126799; NID:94406527; PID:94406528; PIDN:AAD20018.1

R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, March 1999

A/Reference number: Z16471

A/Accession: T08765

A/Molecule type: mRNA

A/Residues: 'RTRG', 138-428, 'D', 430, 'W', 432-444 <WAM>

A/Cross-references: EMBL:AL050118

A/Experimental source: adult uterus; clone DKFZp586C201

C/Genetics:

A/Gene: GDB:FADS6

A/Residues: GDB:9956652

A/Cross-references: GDB:9956652

A/Note: DKFZp586C201.1

C/Superfamily: cytochrome b5 core homology

C/Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty

F;18-94/Domain: cytochrome b5 core homology <CBS>

F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match

Best Local Similarity 23.7%; Score 162; DB 2; Length 444;

Matches 60; Conservative 39; Mismatches 116; Indels 38; Gaps 8;

Qy 16 SAASDYRKLFSDLSALNPNKRGHTTSLLSLTLFLPLSVCGVLPFSDTFPHV--SAA 74

Db 107 SKITDEFRALKKTAEDMNLFTKTNHLFFPILLSHIIWESIAWFIIS----YFNGMIPTV 166

Qy 75 LIGFLWIGSGWIGDGHVNMVLSRLNRAIQLSGNLAISIGWKKNNHNAHIACS 134

Db 167 VLTATSOAQAGWLQHDYGHLSVYKKSIMWNIHVKFVIGHLKGSANWNNRHFOHNAK 226

Qy 135 LDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYHPTFYPMVCAVNL 194

Db 227 FHKDPDVNMLHVLGE--WQPI---EYGRK---KIKYLPYNHGEYFLLICEPPLIIPM 277
 QY 195 YL--QTLLLFSSRXKVDRA-----LNINGILVFWTWFLFLALLFVPI 236
 Db 278 YPQYQIIMTVIKHWDLMAVSYIRFTIYPIFGIIGALLFLNFIPLFSHWV-- 335
 QY 237 QHIOFW--LNHL 246
 Db 336 -----WYQMNHI 343

RESULT 11
 T36617
 Probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
 C/Accession: T36617
 R/Oliver, K.; Hartley, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A/Reference number: Z21610
 A/Accession: T36617
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-345 <OLI>
 A/Cross-references: EMBL:AL078610; PIDN:CA844385.1; GSPDB:GN00070; SCOEDB:SCH35.42c
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCOEDB:SCH35.42c
 C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 11.9%; Score 157; DB 2; Length 345;
 Best Local Similarity 23.7%; Pred. No. 2e-07;
 Matches 55; Conservative 47; Mismatches 104; Indels 26; Gaps 7;

QY 20 SDYRKFSDSLALNFKKHTTISLILTLFPLSVCCVLFSDTFVHLSAALIGFL 79
 Db 15 SDFARLSKRVADAGLGRPGYVTLRTAVTGLYAGMAFVLVGSMTLATAAFIAVM 74
 QY 80 WISGWIHDSGHYNWLSRLRAIQLISGNILA--GISIGMKNNHNAHHIACNSLD 136
 Db 75 YGVALVAMHARQVFRRRASE---LSGRIGASIGMSYGMWDKRRHIANPTED 130
 QY 137 YDDDL-QHMFVAVSSRFNSITSHXGRKKEFDXIXFLICYQHTFYPVMCVARNLY 195
 Db 131 LDDDIGEDILWSPDQARATGPRLLGR-----WQAFIFFLTLLEGFNLA 177
 QY 196 LQITLLLFSSRXKQDRLNIMGILVFWTWFLFLALLFV--PIQHIQFWLNH 245
 Db 178 VASGRAMANR-RUKRRALD--GALLLAHCAVYLTALFWLVPGLMAIAFLAVH 226

RESULT 12
 S35157
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synecocystis sp.
 C/Species: Synecocystis sp.
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S35157; S76243
 R/Reddy, A.S.; Nucchio, M.L.; Gross, L.M.; Thomas, T.L.
 Plant Mol. Biol. 22, 293-300, 1993
 A/Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synecocystis
 A/Reference number: S35157; MUID:93283633; PMID:8389613
 A/Accession: S35157
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <RED>
 A/Cross-references: GB:L11421; NID:g349562; PIDN:AAA27286.1; PID:g349563
 R/Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S76243

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <KAN>
 A/Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BA16502.1; PID:d101923;
 A/Experimental source: PCC 6803
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.6%; Score 114; DB 2; Length 359;
 Best Local Similarity 20.1%; Pred. No. 0.0027;
 Matches 45; Conservative 39; Mismatches 76; Indels 64; Gaps 8;

QY 37 RKCHTTSILSLITLPLSVCG-VLPSDSTF-----VHVSALIGFLMIOGIGHD 89
 Db 34 QRNPSPMYKTLITLVLMLFSAMAFVFAVIFPVRLGGCVLALAAAF-----SPNVGHD 89
 QY 90 SGHYVWLSRLRAIQLISGNILAGISIGWKKNNN-AHHIACNSLDVD----- 138
 Db 90 ANNAVSSNPHINRVGMTYD--FVGLSSFLWRKRYRHHYTHHTYTNLIGHDVEIHDGAVR 147
 QY 139 --PDQHMVFVAVSSRFNSITSHXGRKKEFDXIXFLICYQHTFYPVMCVARNLY 196
 Db 148 MSDEQEHVGIYR-----FQOFYIWGLYLFIPYWF 178
 QY 197 QTLLLFSSRXKQDRLNIMGILVFWTWFLFLALLFV--PIQHIQFWLNH 245
 Db 179 YDVIYLVNKKKXHDHKKIPFQPLELASLIGIKLWLGYYFGLPL 222

RESULT 13
 F71969
 hypothetical protein jhp0131 - Helicobacter pylori (strain J99)
 C/Species: Helicobacter pylori
 A/Variety: strain J99
 C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999
 R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Meberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A/Reference number: A71800; MUID:99120557; PMID:9923682
 A/Accession: F71969
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-482 <ARN>
 A/Cross-references: GB:AE001452; GB:AE001459; NID:g4154639; PIDN:AA05710.1; PID:g4154643
 A/Experimental source: strain J99
 C/Genetics:
 A/Gene: jhp0131
 C/Superfamily: 2-oxoglutarate/malate translocator

Query Match 8.4%; Score 110.5; DB 2; Length 482;
 Best Local Similarity 25.8%; Pred. No. 0.0081;
 Matches 67; Conservative 36; Mismatches 72; Indels 85; Gaps 15;

QY 28 DLSANLFPKRGHTTISLILTLFPLSVCCVLFSDTFVHLSAALF-----GLMWIQ 82
 Db 264 ELESWGRFSLKE---LMLSTLT--LALLGWIFFKSGLSHSAVALVIMVLMACCKV 316
 QY 83 SGWIGHDSGHYNWLSRLRAIQLISGNIL--AGI-SIGWKKNNHNAHHIACNSLDY- 137
 Db 317 S-----YEDITKKAQAFNIFLLGSLITMAGLKKVGPANFGNA---AQNLEHA 364
 QY 138 --DP--DLQHMVFVAVSSRFNSITSHXGRKKEFDXIXFLICYQHTFYPVMCVARNY 192
 Db 365 HNDPLAVLAVFIALFYLISHYFPASITAHVSA-----LPALFVIGSSH-----IOGV 410
 QY 193 NLYIQITLLLFSSRXKQDRLNIMGILV-----FWTW-----FLF 227
 Db 411 NQIQLSLFLMLDS-----LGIMGILTPYGTGSPSTIYVGSYIOSKDPKMGIFIGFLY 462
 QY 228 LVALFVPIQHIQF-----WL 243

Db 463 LIVLISVCAPWVFIAYRWL 482

RESULT 14

552650 omega-3 fatty acid desaturase (EC 1.14.99.-) - *Synechocystis* sp. (strain PCC6803)

N/Alternate names: delta 15 desaturase

C/Species: *Synechocystis* sp.

A/Variety: PCC 6803

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C/Accession: S52650; S75843

R/Sakamoto, T.; Los, D.A.; Higashi, S.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.

Plant Mol. Biol. 26, 249-263, 1994

A/Title: Cloning of omega-3 desaturase from cyanobacteria and its use in altering the de

A/Reference number: S52649; MUID:95035996; PMID:7524725

A/Accession: S52650

A/Molecule type: DNA

A/Residues: 1-359 <SAK>

A/Cross-references: GB:D13780; NID:G600596; PIDN:BA02924.1; PID:G600598

A/Note: the authors translated the initiation codon GTG for residue 1 as Val

R/Kaneho, T.; Sato, S.; Kotori, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shino, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S75843

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-359 <KAN>

A/Cross-references: EMBL:D90913; GB:AB001339; NID:G1653348; PIDN:BA18302.1; PID:G165338

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Genetics:

A/Start codon: GTG

C/Superfamily: omega-3 fatty acid desaturase

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.1%; Score 107; DB 2; Length 359;

Best Local Similarity 21.9%; Pred. No. 0.013;

Matches 51; Conservative 32; Mismatches 100; Indels 50; Gaps 9;

QY 46 LSLILTLFPLSVCGVLFSDSTFVHLSAALLIGFLWIGSNGIHDGSHYMLSRRLRAI 105
 Db 51 VGLIAGFYALAA---YLDSPFYPIFWLIGTLFWMLFVGHGDCGHSFSKSTLNWI 106
 QY 106 QILSGNIIAGISIGWKKMNNNAHIIACNSLDYDPDLQHPVAVSSRFNSITSHXGRK 165
 Db 107 GHLSTHTPIL-VPYHGMRISHRTHNANTGIDTDES-----WYPVSEOKYNQM 152
 QY 166 XEFDXIAXF---LICV-----QHFTFYPVMCVARVNLVLTILLFSRXKQDR 211
 Db 153 AWTEKLRFLPLIAPYIYFRSPNROGSHFMPGSPFPRGEKAVLSTFALAA--- 208
 QY 212 ALNIMGILVFWTW---FLFLALLFVPIQHIFW-----LNHIAENTL--YXG 253
 Db 209 ---FVGFLGFLTWQFGWLFLKRYVAAYLVFVWMLDVTFLHHTEDNIWPYRG 258

RESULT 15

T07687

omega-6 desaturase FAD2-1, microsomal - soybean

C/Species: Glycine max (soybean)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000

C/Accession: T07687

R/Hepard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.

Plant Physiol. 110, 311-319, 1996

A/Title: Developmental and growth temperature regulation of two different microsomal omeg

A/Reference number: Z16095; MUID:96151506; PMID:8587990

A/Accession: T07687

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-387 <HEP>

A/Experimental source: seed

C/Genetics:

A/Gene: FAD2-1

C/Function:

A/Description: involved in production of polyunsaturated lipids; plays a major role in c

A/Note: strongly expressed in developing seeds

C/Superfamily: omega-3 fatty acid desaturase

Query Match 7.8%; Score 103; DB 2; Length 387;

Best Local Similarity 20.1%; Pred. No. 0.034;

Matches 52; Conservative 37; Mismatches 88; Indels 82; Gaps 11;

QY 43 SLILSLTLFPLSVCGVLFSDSTFVHLSA--ALIGF--LWIOSG-----W-IGHDSG 91
 Db 53 SLTSTSYVYDLSFAFIRYIATYTHLHPQPSLAWPIYWLQGCCLLTGQVAVIAHEG 112
 QY 92 HYNVWLSRLRLRAIQILSGNIIAGISIGWKKMNNNAHIIACNSLDYDPDLQHP----- 145
 Db 113 HNAFSKYQWVDVVGTLSTLL-VPYFSWKISHRHHSNTGSLDRDEVFVPRKSKRVAM 171
 QY 146 -----VPAVSSRFNSITSHXGRKXERFDXIAFLICV 178
 Db 172 FSKYLNPLGRAVSLVLTLTGMPYLAFNVSGRPYDSFASH----- 213
 QY 179 QHFTFYPVMCV---ARVNLVLTILLFSRXKQVODRALNIMGILVFWTWFLFLALLFY 234
 Db 214 ---YHPAPYISNRRLILYSDV-ALFSVTYSLRVATIGLV--WLLCYGVPLLV 266
 QY 235 P-----IQHIFWLNH 245
 Db 267 NGFLVTITVLOHTHFALPH 285

Search completed: January 1, 2004, 06:39:41
 Job time: 10.5223 secs

Best Local Similarity 22.1%; Pred. No. 2.6e-07;
Matches 58; Conservative 42; Mismatches 118; Indels 44; Gaps 7;

QY 16 SAASDVRKLPFSDLSALNLRKQHTSILSLILTFPLSVGCVFSDSTFPAVLSAL 75
DB 107 AALVEFRALREERLEAGCEKCTOPLPFALHGHILILEALAFMMVWFYFGINTLLVAV 166
QY 76 I-GFLMIGSGMIGDGHVYVMLSRRLNRAIQILSGNLAGISIGWKMNN-AHIIACNS 134
DB 167 ILATAGSQAGMLQHDHFLSVFTKSGNNHLYHKVIGHLQAGAGMNNHHFQHHAKPNI 226
QY 135 LDVDPDLQHPVPAVSSRFNSITSHYGRKKEPFXIAXFLICYHFTFYVNCVAVNL 194
DB 227 FKQDPVNMNAFVY-----GNQPVVEYGVK---KIKHLPVNHQHKYFFIGPILLIPV 277
QY 195 YLQTLILFESRXKQVADALNIMGL-----VFPT-----WEL 226
DB 278 YFQ--FOIFNMISHGMVVLMLWCISYVRYFLCTYQFYGVAIILFNFRMESHMFV 335
QY 227 FLTALFVPI-----QHTQFMLN 244
DB 336 WVTQMSHIFMNIYERKQDMIS 357

RESULT 2

LCSD_SYNY3 STANDARD; PRT: 359 AA.

AC Q08871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE linoicoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
GN DSS6 OR SL10262.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP MEDLINE=93283633; PubMed=8389613.
RX Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RT "Isolation of a delta 6-desaturase gene from the cyanobacterium
RT Synechocystis sp. strain PCC 6803 by gain-of-function expression in
RT Arabidopsis sp. strain PCC 7120."
RL Plant Mol. Biol. 22:293-300(1993).
RN [2]
RP MEDLINE=97061201; PubMed=8905231;
RX Kaneho T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpō S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: linoicoyl-CoA + AH(2) + O(2) = gamma-
CC linoenoyl-CoA + A + 2 H(2)O.
CC -1- COFACTOR: IRON.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L11421; AAA27286.1; -
CC DR EMBL: D90914; BAA1502.1; -
CC DR InterPro: IPR005804; FA_desat_fam.
CC Pfam: PF00487; FA_desaturase_1.
CC ProDom: PD001081; FA_desat_fam; 1.

KM Oxidoreductase; Iron; Complete proteome.
SQ SEQUENCE 359 AA; 41425 MW; 33F8165AEB98C05F CRC64;

Query Match 8.6%; Score 114; DB 1; Length 359;
Best Local Similarity 20.1%; Pred. No. 0.0028;
Matches 45; Conservative 39; Mismatches 76; Indels 64; Gaps 8;

QY 37 RKCHTSSILSLILTFPLSVCG-VLPDSTF-----AHVLSAALIGFLMIGSGMIGHD 89
DB 34 QRDNPENMYLKTLLIYVLMFSANAFLVFAVIFPVRLGCGVLAIALAFL-----SFVGH 89
QY 90 SGHYVNLRLNRAIQILSGNLAGISIGWKMNN-AHIIACNSLDYD----- 138
DB 90 ANHNNAVSSNPHIRVLTGYTD--FVGLSSFLMRRYRNNLHHTYTNILGHVDEIHGDGAVR 147
QY 139 --PDLOHMPVPAVSSRFNSITSHYGRKKEPFXIAXFLICYHFTFYVNCVAVNL 196
DB 148 MSPBOEHVGIYR-----FOQFYIWLILYFIPYWFL 178
QY 197 QTLILFESRXKQVADALNIMGL-----NINGILVFWTFLPLAL 231
DB 179 YDYLVLANKYTHDKIPPEPPLSLGLIKLMIGYFGPL 222

RESULT 3

FD12_MORAP STANDARD; PRT: 400 AA.

AC Q918H5; Q96TH3; Q9UVV4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP MEDLINE=9234062; PubMed=10215899;
RX Sakurada E., Kobayashi M., Ashikari T., Shimizu S.;
RT "Identification of delta12-fatty acid desaturase from arachidonic
RT acid-producing Mortierella fungus by heterologous expression in the
RT yeast Saccharomyces cerevisiae and the fungus Aspergillus oryzae."
RL Eur. J. Biochem. 261:812-820(1999).
RN [2]
RP MEDLINE=99406036; PubMed=10478922;
RX Huang Y.-S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chan G.M., Kirchner S.J., McKelji P., Knutson D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae."
RL Lipids 34:649-659(1999).
RN [3]
RP MEDLINE=97061201; PubMed=8905231;
RX Kaneho T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpō S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: linoicoyl-CoA + AH(2) + O(2) = gamma-
CC linoenoyl-CoA + A + 2 H(2)O.
CC -1- COFACTOR: IRON.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L11421; AAA27286.1; -
CC DR EMBL: D90914; BAA1502.1; -
CC DR InterPro: IPR005804; FA_desat_fam.
CC Pfam: PF00487; FA_desaturase_1.
CC ProDom: PD001081; FA_desat_fam; 1.

CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB020033; BAB1754.1; -
 DR EMBL: AF110509; AAF08684.1; -
 DR EMBL: AF17244; AAL1300.1; -
 DR GO: GO:0016491; F:oxidoreductase; IDA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IDA.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
 FT TRANSMEM 91 111
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT DOMAIN 112 116 HISTIDINE BOX-1.
 FT DOMAIN 148 152 HISTIDINE BOX-2.
 FT DOMAIN 339 343 HISTIDINE BOX-3.
 FT CONFLICT 17 19 STS -> TTT (IN REF. 3).
 FT CONFLICT 21 23 APT -> PN (IN REF. 2).
 FT CONFLICT 95 95 A -> V (IN REF. 2).
 FT CONFLICT 107 107 I -> V (IN REF. 2).
 FT CONFLICT 179 179 N -> S (IN REF. 3).
 FT CONFLICT 180 182 AAA -> VAV (IN REF. 1).
 FT CONFLICT 261 261 A -> T (IN REF. 1).
 FT CONFLICT 280 280 V -> I (IN REF. 3).
 FT CONFLICT 358 358 Y -> I (IN REF. 1).
 FT CONFLICT 392 392 H -> Q (IN REF. 2).
 SQ SEQUENCE 400 AA; 46001 MW; 40B2PC1C1E01F93F CRC64;

Query Match 8.5%; Score 111.5; DB 1; Length 400;
 Best Local Similarity 19.5%; Pred. No. 0.0053;

Matches 58; Conservative 40; Mismatches 109; Indels 91; Gaps 13;

QY 2 PAESTSHRLSDHTVSAASDYKRLPSDSLALNLFNRKHTTSLSLTLPLPSVGV 61
 DB 27 PAFERNYQLPEFTI-----KEIRECIPIAHCFERSG-----LRGCHVAIDLTASL 73
 QY 62 FSDSTFVHLVSAALIGFL-----WIOSG-----WI-GHDSGHVYVNLRRRLNRAIQILS 109
 DB 74 FLAATQIDKEFNPRLIRYLAMPAYWIMQIVCTGIVLWLAHECHGQSFTSKTLNN----- 127
 QY 110 GNLAGISIGW-----WKNNHNAHHIACNSLDYDPLQHPVAVASRP----- 153
 DB 128 -----TVGMILHSMVLVPHYSWRISHSKHKAATGHTKD-----QVFVPKTRSGVGL 174
 QY 154 -----FNSITSHXGKKEFDXIAFLICYQHTFTFVPMCV-----ARVNL 194
 DB 175 PKENAAAANVOEDMSVHL---DEEAPITVLFPMVIOFLFGWPAYVLIIMNASGODYGRWTS 231
 QY 195 YIQTILLFSRXKVDRAINIMGI-----LVFWTWFLFLAL---LVPIQHIOFWL 243
 DB 232 HFTTSPIFEPNPFDIITISDLGVALAALGALIVASMQSLTLVTKYIIVPYLVNFWL 289

RESULT 4
 FD12 MORIS

ID FD12 MORIS STANDARD; PRT; 400 AA.

AC P59668;
 DT 15-SEP-2003 (Rel. 42, Last Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Delta-12 fatty acid desaturase (EC 1.14.99.-)
 OS Mortierella isabellina (Unbelopis isabellina).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
 OC Mucorales incertae sedis; Umbelopsis.
 NC NCBI_TaxID=91625;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=M6-22;
 RA Liu L., Li M., Xing L., Hu G.;

RT "Delta 12 fatty acid desaturase mRNA of Mortierella isabellina."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
 CC to linoleic acid (delta9, delta12-18:2) (By similarity).
 CC 1- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC 1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC 1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC -----

DR EMBL: AF17245; AAL1301.1; -
 DR GO: GO:0016491; F:oxidoreductase; IDA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IDA.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
 FT TRANSMEM 91 111
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT DOMAIN 112 116 HISTIDINE BOX-1.
 FT DOMAIN 148 152 HISTIDINE BOX-2.
 FT DOMAIN 339 343 HISTIDINE BOX-3.
 SQ SEQUENCE 400 AA; 46016 MW; F5512D3F8210BBD2 CRC64;

Query Match 8.4%; Score 110.5; DB 1; Length 400;
 Best Local Similarity 19.1%; Pred. No. 0.0066;

Matches 57; Conservative 41; Mismatches 109; Indels 91; Gaps 13;

QY 2 PAESTSHRLSDHTVSAASDYKRLPSDSLALNLFNRKHTTSLSLTLPLPSVGV 61
 DB 27 PAFERNYQLPEFTI-----KEIRECIPIAHCFERSG-----LRGCHVAIDLTASL 73
 QY 62 FSDSTFVHLVSAALIGFL-----WIOSG-----WI-GHDSGHVYVNLRRRLNRAIQILS 109
 DB 74 FLAATQIDKEFNPRLIRYLAMPAYWIMQIVCTGIVLWLAHECHGQSFTSKTLNN----- 127
 QY 110 GNLAGISIGW-----WKNNHNAHHIACNSLDYDPLQHPVAVASRP----- 153
 DB 128 -----TVGMILHSMVLVPHYSWRISHSKHKAATGHTKD-----QVFVPKTRSGVGL 174
 QY 154 -----FNSITSHXGKKEFDXIAFLICYQHTFTFVPMCV-----ARVNL 194
 DB 175 PKENAAAANVOEDMSVHL---DEEAPITVLFPMVIOFLFGWPAYVLIIMNASGODYGRWTS 231
 QY 195 YIQTILLFSRXKVDRAINIMGI-----LVFWTWFLFLAL---LVPIQHIOFWL 243
 DB 232 HFTTSPIFEPNPFDIITISDLGVALAALGALIVASMQSLTLVTKYIIVPYLVNFWL 289

RESULT 5
 FD61 SOYBN

ID FD61 SOYBN STANDARD; PRT; 387 AA.

AC P48630;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum isoform 1
 DE (EC 1.14.19.-).
 GN FAD2-1.
 OS Glycine max (Soybean).
 OC Glycine; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

Query Match	Best Local Similarity	7.8%	Score 103;	DB 1;	Length 387;
Matches	52;	Conservative 37;	Mismatches 88;	Indels 82;	Gaps 11;
43	SIILSLILTLPLSLVCGVLFSDSTFVHLSA--ALIGF--LWISGS-----W-IGHSGS	91			
53	SILTSFSYVVDLSAPFLFYATFYTHLPQFSLAMPYVWLOGCLLTGWVIAHBCG	112			
92	HYNVALSRRLNRAIQILISGNILAGISIGMWKNNNAHHIACNSLDYDPLQHP-----	145			
113	HHAFSKYQWVDVVGELTLHSTLL-VPRFSWKISHRRHNSNNGSDRDREVFAPRKSKYAM	171			
146	-----VPAVSSRFNSITSHXGKXKXEPDXIAXFLICY	178			
172	FSKYLNINPLGRAVSLVLTLLTGIGPMYLLFNVSIGREYDSFASH-----	213			
179	QHFTFYPMCV-----ARVNLVYQITLLLSRKXKQDRLNIMGILVFTWFLFLALLFV	234			
214	---VHPAPLYTSNERRLLIYSDV-ALFSVTYSLYRAVTLKGIV--WLLCVYGVPLLIIV	266			
235	P-----IQHIQFVLNH	245			
267	NGFLVITTYLQHTHALPH	285			

ID	CRTM_ALCSP	STANDARD	PRT	242 AA
AC	Q44261			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Beta-carotene ketolase (EC 1.13.1.1) (Beta-carotene oxygenase)			
OS	Alcaligenes sp.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
OC	Alcaligenaceae; Alcaligenes.			
OX	NCBI_TaxID=512;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95251715; PubMed=7733978;			
RA	Misawa N., Kajiura S., Kondo K., Yokoyama A., Satomi Y., Saito T.,			
RA	Miki W., Ohtani T.;			
RT	"Canthaxanthin biosynthesis by the conversion of methylene to keto			
RT	groups in a hydrocarbon beta-carotene by a single gene.";			
RL	Biochem. Biophys. Res. Commun. 209:867-876(1995)			
CC	FUNCTION: CONVERTS BETA-CAROTENE TO CANTHAXANTHIN VIA ECHINENONE.			
CC	-1- PATHWAY: CAROTENOID BIOSYNTHESIS. INVOLVED IN ASTHAXANTHIN			
CC	BIOSYNTHETIC PATHWAY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; D58422; BA009596.1; .			
DR	InterPro; IPR005804; FA_desat_fam.			
DR	Pfam; PF00487; FA_desaturase; 1.			
DR	ProDom; PD001081; FA_desat_fam; 1.			
KW	Carotenoid biosynthesis; Oxidoreductase.			
SQ	SEQUENCE 242 AA; 26939 MW; 077DA83FAAD1484 CRC64;			
Query Match	7.6%; Score 100.5; DB 1; Length 242;			
Best Local Similarity	28.6%; Pred. No. 0.032;			
Matches	58; Conservative 19; Mismatches 71; Indels 55; Gaps 13			
QY	39 GHTTSILIS-LITFLPLSVCGVLPSDSTFVHVLISA-ALIGFLWISGW--IGHDSGHY 93			
DB	17 GLTAAIILCMTVLAHFAITMLV-----DAAAHPLIYAVLCGLGTLWSGLFLIADDAHG 70			
QY	94 NVMLISR-RLNRAIQLISNLIAGISIGWMK--NHNNAHIAICSLDVPDQLH-MPVAV 149			
DB	71 SVVGRPRPANAIIQLALMTLYAGFS-MPKLIAMTHHRIHAGT-DNDPDGHGSPV-- 124			
QY	150 SSRFSNISTSHXGRKKEFDXIAFLICY-----QHFTFVPMCAVARNLYLQITLL 201			
DB	125 --RNYGSGVSTYFGWR-BGLLLPIYITVTTAYALLIDRMMYVYFVWPVAV----- 169			
QY	202 LFSRXKVQDRALNTMGILVFWTW 224			
DB	170 -----LASIQIFVFGTW 181			
RESULT 7				
ID	CRTM_AGRAU	STANDARD;	PRT;	242 AA.
AC	P54972;			
DT	01-OCT-1986	(Rel. 34, Created)		
DT	01-OCT-1986	(Rel. 34, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Beta-carotene ketolase (EC 1.13.1.1) (Beta-carotene oxygenase)			
GN	Agrobacterium aurantiacum.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.			
OX	NCBI_TaxID=44155;			

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96062243; PubMed=7592436;
 RA Misawa N., Satomi Y., Kondo K., Yokoyama A., Kajiwara S., Saito T.,
 RT Ohtani T., Miki W.;
 RT "Structure and functional analysis of a marine bacterial carotenoid
 biosynthesis gene cluster and astaxanthin biosynthetic pathway
 proposed at the gene level."
 RL J. Bacteriol. 177:6575-6584 (1995).
 CC -1- FUNCTION: CONVERTS BETA-CAROTENE TO CANTHAXANTHIN VIA ECHINENONE.
 CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS. INVOLVED IN ASTAXANTHIN
 CC BIOSYNTHETIC PATHWAY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D58420; BAA09591.1; -
 CC InterPro: IPR005804; FA_desat_fam.
 CC Pfam: PF00487; FA_desaturase; 1.
 CC ProDom: PD001081; FA_desat_fam; 1.
 CC Carotenoid biosynthesis; Oxidoreductase.
 KM SEQUENCE 242 AA; 27128 MW; 6AEB5BF60BE3D8 CRC64;
 SQ
 Query Match 7.5%; Score 99.5; DB 1; Length 242;
 Best Local Similarity 25.8%; Pred. No. 0.039;
 Matches 59; Conservative 30; Mismatches 77; Indels 63; Gaps 14;
 QY 27 SDLSALNLFNRKHTTSTLS--LILFLPLSCGVFSDSTFVHLSA--LGLFLMIOS 83
 DB 9 ADLTA-----TSLIVSGGIIAMALHVAHMLFDAAHPIALINPGLTSLV 58
 QY 84 GM---IGHDSGHVYMLSR--RLNRAIQLSGNLAGISIGMKV--NHNHAIACNSLDYD 138
 DB 59 GLPIAHDAHSGVPRPANAAMGQLVLMYAGFS--WRKQIVKMAHRIAGT-DDD 115
 QY 139 PDLQHPFVAVSSRFNSITSHYXGKPEDXIAXFLICYOHTFYVPMCVARVNYLQT 198
 DB 116 PFDHGGPVMYARFIST-----YFGW-----REGLLPV 145
 QY 199 LILFSSKXKQDRAINMGLVPTWTFLLALLFPVPIQIQR--WLNH 245
 DB 146 IIVTVYALI-LGDRMYV---VFWP-----LPSILASIQLFVPGTWLPH 184
 RESULT 8
 COXI_LEITA
 ID COXI_LEITA STANDARD; PRT; 549 AA.
 AC P14544;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JUN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cytochrome c oxidase polypeptide I (EC 1.9.3.1).
 GN COI.
 OS Leishmania tarentolae (Sauroleishmania tarentolae).
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85079995; PubMed=6096360;
 RA de la Cruz V.F., Neckelmann N., Simpson L.;
 RT "Sequences of six genes and several open reading frames in the
 RT kinetoplast maxicircle DNA of Leishmania tarentolae."
 RL J. Biol. Chem. 259:15136-15147 (1984).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- PATHWAY: Respiratory chain; terminal step.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR PIR; D30010; D30010.
 DR HSSP; P18401; 1FFT.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1; 1.
 DR PRINTS; PR00077; COX1; 1.
 DR PROSITE; PS00077; COX1; 1.
 KW Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
 KW Respiratory chain; Inner membrane.
 FT METAL 243 243 IRON (HEME A AXIAL LIGAND) (PROBABLE).
 FT METAL 64 64 IRON (HEME A AXIAL LIGAND) (PROBABLE).
 FT METAL 247 247 COPPER B (PROBABLE).
 FT METAL 292 292 COPPER B (PROBABLE).
 FT METAL 293 293 COPPER B (PROBABLE).
 FT METAL 378 378 IRON (HEME A3 AXIAL LIGAND) (PROBABLE).
 FT METAL 380 380 IRON (HEME A AXIAL LIGAND) (PROBABLE).
 FT CROSSLINK 243 247 1'-histidyl-3'-tyrosine (By similarity).
 SQ SEQUENCE 549 AA; 63271 MW; F6DD04815A4917C2 CRC64;
 Query Match 7.4%; Score 97; DB 1; Length 549;
 Best Local Similarity 24.1%; Pred. No. 0.16;
 Matches 64; Conservative 40; Mismatches 108; Indels 54; Gaps 14;
 QY 23 RLKPSDLALNLFNRKHTTSTLSLTLF-----PLSCGVLFSDSTFVHLSAALIGF 76
 DB 176 KRFFSFLS--WSLPIAALITALLITLTPVLAVGVTLLCDRNFTSFYDVGGDLILF 234
 QY 79 ---LWIOSGIGHDSGHVYMLSR-----RLNRAIQLSGNLAGISIGMKV 121
 DB 235 QHIFW---FPGHPE-VYIILPVGGLISTIVYVGFRCVFSTVAMITYMILLAI-LGMF 288
 QY 122 KWNHNAHIAACNSLDYDPD-----LQHPFVAVSSRFNSITSHYXGKPEDXIAX 173
 DB 289 VM---AHMFFVVGMDVDSRAVFGVSIILGLPTCV---KLPMYISFLY---TDMIT 337
 QY 174 FLICYOHTFYVPMCVARVNYLQTI---LILFSSKXKQDR--ALNMGILVPTWTF 227
 DB 338 FVYVPIVIMFIMFLGAVTGLPLSNVGIDIMLDTFVGVGHVYLSLCAVVGFTGFIH 397
 QY 228 LIALFLVPIQIQLFWMNLHAEMLYXG 253
 DB 398 FLA-KWPIELLYLFMMFYISTLFTIG 422
 RESULT 9
 DUFE_MOUSE
 ID DUFE_MOUSE STANDARD; PRT; 334 AA.
 AC Q90U16; Q35970; Q91YB6; Q920X0; Q920X1; Q920X2; Q920X3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Duffy antigen/chemokine receptor.
 GN FY OR DRY OR DAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97458170; PubMed=9314499;
 RA Luo H., Chaudhuri A., Johnson K.R., Neote K., Zbrzezna V., He Y.,
 RA Pogo A.O.;
 RT "Cloning, characterization, and mapping of a murine promiscuous
 RT chemokine receptor gene: homolog of the human Duffy gene".
 RL Genome Res. 7:932-941 (1997).

[2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Tournamille C., Colin Y.;
 RT "Murine skeletal muscle diffy antigen/receptor for chemokine
 RT glycoprotein (DARC)."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99449053; PubMed=10520743;
 RA Tang T., Owen J.D., Du Y., Walker C.L., Richmond A.;
 RT "Molecular cloning and characterization of a mouse gene with homology
 RT to the Duffy antigen receptor for chemokines."
 RL DNA Seq. 9:129-143(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BLG2/Msf, BFW/2msf, C57BL/10SnJ, CAST/Ei, HMI/Msf, MSM/Msf,
 RA Liu Y., Kitano T., Koide T., Shiotaishi T., Moriaki K., Saitou N.;
 RT "Conspicuous differences among gene genealogies of 21 nuclear genes of
 RT five Mus musculus subspecies."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleno M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Canninci P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Blatterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Non-specific receptor for many chemokines (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in liver and brain.
 CC -1- SIMILARITY: BELONGS TO FAMILY DUPLY OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: AF016697; AAC53360.1; -
 DR EMBL: AF016584; AAC53354.1; -
 DR EMBL: AF109159; AAF14225.1; -
 DR EMBL: U88431; AAF08328.1; -
 DR EMBL: AB039074; BAB68598.1; -
 DR EMBL: AB039075; BAB68599.1; -
 DR EMBL: AB039076; BAB68600.1; -
 DR EMBL: AB039077; BAB68601.1; -
 DR EMBL: AB039078; BAB68602.1; -
 DR EMBL: AB039080; BAB68604.1; -
 DR EMBL: AB039081; BAB68605.1; -
 DR EMBL: AB039082; BAB68606.1; -

DR EMBL: BC005583; AAH05583.1; -
 DR MGD: MGI:1097689; DfY.
 DR GO: GO:0006954; P:Inflammatory response; IMP.
 DR InterPro: IPR005384; DuffAntigen.
 DR PRINTS: PR01559; DUFFYANTIGEN.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 DR EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 61
 FT TRANSMEM 62 82
 FT DOMAIN 83 93
 FT TRANSMEM 94 114
 FT DOMAIN 115 124
 FT TRANSMEM 125 145
 FT DOMAIN 146 164
 FT TRANSMEM 165 185
 FT DOMAIN 186 205
 FT TRANSMEM 206 226
 FT DOMAIN 227 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 285
 FT TRANSMEM 286 306
 FT DOMAIN 307 334
 FT CARBOHYD 16 16
 FT CARBOHYD 26 26
 FT CARBOHYD 32 32
 FT CARBOHYD 285 285
 FT VARIANT 10 10
 FT VARIANT 56 56
 FT VARIANT 61 61
 FT VARIANT 76 76
 FT VARIANT 178 178
 FT VARIANT 188 188
 FT VARIANT 194 194
 FT VARIANT 207 207
 FT VARIANT 221 221
 FT VARIANT 256 256
 FT VARIANT 268 268
 SQ SEQUENCE 334 AA; 36693 MW; 21AC4B6147D840C8 CRC64;
 Query Match 7.2%; Score 94.5; DB 1; Length 334;
 Best Local Similarity 21.7%; Pred. No. 0.16; 86; Indels 77; Gaps 12;
 Matches 55; Conservative 35; Mismatches 86; Indels 77; Gaps 12;
 QY 11 SDHTVNASSDYKRLFSDLSALNLFNRKG-----HTTSLILSLTLFPLSV-----58
 DB 39 SDVSLTPAACVSCNLDRLSLEFPLVTSVGLMAGSILFALRPFHHQICPSPIIA 98
 QY 59 -----GVLFSDSTFV-----HVLSAALIGFLWITQSGWIGHSGHYNM-----LS 98
 DB 99 ELAVGSLFIAVPIIAPILAPGLSHASTALCNIGY-----WWTYSAFAQALLIGCYACLN 152
 QY 99 RLRLRAIQLISGNTLAGISIGMKKNNHNAHICNSLSDPDLDQHMPVPAVSSRFRNSIT 158
 DB 153 PRLN--IGQIRGFTL-GLSVGLMG-----AAALSGPLV-ALADVDVNGFC 193
 QY 159 SHXVGRKXEPDXIAXFLICVQHTFPYVPMCVARVNIYLQITILLFRXKXQDAPALNMG- 217
 DB 194 TPSSRDMEALKTHYALCTITFTVPLTILAAKGLKI-----ALS-KGP 237
 QY 218 ---ILVFWTWLFL 227
 DB 238 GPMVSVLMWIF 250

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RESULT 10
UNC7 CAEBL
ID UNC7 CAEBL STANDARD; PRT; 522 AA.
AC 003412;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inexin unc-7.
GN UNC-7 OR R07D5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN 11
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93202469; PubMed=7681023;
RA Starich T.A., Herman R.K., Shaw J.E.;
RT "Molecular and genetic analysis of unc-7, a Caenorhabditis elegans
RT gene required for coordinated locomotion.";
RL Genetics 133:527-541(1993).
RN 12
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smay R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: STRUCTURAL COMPONENTS OF THE GAP JUNCTIONS. REQUIRED FOR
CC COORDINATED LOCOMOTION.
CC -1- SUBUNIT: HETEROOLIGOMER OF UNC-7 AND UNC-9 (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DEVELOPMENTAL STAGE: PRESENT IN ALL DEVELOPMENTAL STAGES BUT MOST
CC ABUNDANT IN L1-L3 LARVAE.
CC -1- SIMILARITY: Belongs to the innoxin family.
CC
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CC -----
CC EMBL: Z19122; CAA79529.1; -
CC EMBL: Z70685; CAA94607.1; -
CC F.R.; T24027; T24027.
CC WormPep; R07D5.1; CE06279.
CC InterPro; IPR000990; Innoxin.
CC Pfam; PF00876; Innoxin.1.
CC PRINTS; PR01262; INNOXIN.
CC Gap junction; Transmembrane.
CC DOMAIN 20 25
CC FT TRANSMEM 151 171 POTENTIAL.
CC FT TRANSMEM 221 241 POTENTIAL.
CC FT TRANSMEM 320 340 POTENTIAL.
CC FT TRANSMEM 405 425 POTENTIAL.
CC SQ SEQUENCE 522 AA; 950DTAFBA961120 CRC64;
Query Match 7.1%; Score 94; DB 1; Length 522;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 66; Conservative 52; Mismatches 117; Indels 140; Gaps 17;
QY 1 LPAFST-----SH-RLSDHTVSA-----SSDYRKLFSDL 29
DB 78 LPSYQAKLDGSHQIDSHHVGSAHGAGGCHGKHKEGPAMIIYLLASAFRALYPRLL 137
QY 30 -----SALNLFNKRKHTSILSLILTL-----PLSYCGVLFSTSTVHLSAALIG 77
DB 138 DDDFVFKLNTY-----YTTTLLASFALLVSAKQYVGFIQ-CWV---PATTDAMEQYTEN 189
QY 78 FLWIQSG-WIGHDSGHYNWLSRLRN-----AIQLISGNIAGISIGWKKWN 124

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Db 190 YCWQNTYVWPMQEDIPREIYSRR-NRQIGYQWVPFLIALEALFYVPCILRGSLYWH 248
QY 125 HNAH-----HIACNSLDYDPDLOHMPFAVSSKFFNSISHXGRKE-----FDXIAXFL 175
DB 249 SGINLQGLVQMACDALMDSIEIKRTVTYTMARRMODEVOLTNIDRGHSRSCFSNLQGA 308
QY 176 ICYOHFTFPYVWCVARV-----NLVLTILL----- 201
DB 309 NCRHRCGCYVMTLYIGIKVLVSANVLLQFFLNHLGSDLVAGFSLDLMAHIMEQT 368
QY 202 -LFSRKKVODRALINWG-----ILVFTWPL-----FLI 229
DB 369 GMEPRVTLCDPEVRVYGNHRTVQCVMINMENEXIFLFWMFYTCGIVTCNTMYM 428
QY 230 ALLFVPIQHIOFWLNL 246
DB 429 LWFIPSGMSFVRKYL 445
RESULT 11
D12 CREAL
ID D12 CREAL STANDARD; PRT; 375 AA.
AC 081931;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta(12) fatty acid dehydrogenase (EC 1.14.99.33) (Crepennate
DE synthase) (Delta-12 fatty acid acetylase).
OS Crepis alpina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichoriaceae; Crepis.
OX NCBI_TaxId=72610;
RN 11
RC SEQUENCE FROM N.A.
RX MEDLINE=98239771; PubMed=9572738;
RA Lee M., Lemman M., Banas A., Bafor M., Singh S., Schweizer M.,
RA Nilsson R., Liljeborg C., Dahlqvist A., Gunneron P.O., Sjoedahl S.,
RA Green A., Stymne S.;
RT "Identification of non-heme diron proteins that catalyze triple bond
RT and epoxy group formation.";
RL Science 280:915-918(1998).
CC -1- FUNCTION: CHANGES THE DELTA-12 DOUBLE BOND OF LINOLEIC ACID INTO A
CC TRIPLE BOND IN THE BIOSYNTHESIS OF CREPENYNIC ACID.
CC -1- CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepenynate + A +
CC H(2)O.
CC -1- COFACTOR: Iron.
CC -1- PATHWAY: polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- TISSUE SPECIFICITY: Seed.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/
CC OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC -----
CC EMBL: Y16285; CAA76158.2; -
CC InterPro; IPR005804; FA desat fam.
CC Pfam; PF00487; FA desaturase.1.
CC ProDom; PD001081; FA desat fam. 2.
CC Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Iron.
CC FT TRANSMEM 54 74 POTENTIAL.
CC FT TRANSMEM 77 97 POTENTIAL.
CC FT TRANSMEM 110 130 POTENTIAL.
CC FT TRANSMEM 172 192 POTENTIAL.
CC FT TRANSMEM 218 238 POTENTIAL.

```

FT TRANSNM 242 262 POTENTIAL.
 FT DOMAIN 98 102 HISTIDINE BOX-1.
 FT DOMAIN 134 138 HISTIDINE BOX-2.
 FT DOMAIN 308 312 HISTIDINE BOX-3.
 SQ SEQUENCE 375 AA; 43382 MW; B31F5A64DDC2926 CRC64;
 Query Match 6.8%; Score 89.5; DB 1; Length 375;
 Best Local Similarity 25.2%; Pred. No. 0.53;
 Matches 32; Conservative 21; Mismatches 49; Indels 25; Gaps 6;

QY 73 AALIGFLWISGMIQHSCHYVWMLSRRLNRAIOLISGNILAGISGMKNNNAHIAC 132
 DB ASITGLTMV-----IGHGCHGHAIFSDYQWVDYTGFIHSPIMTPYFS-WKXSHRNHANT 141
 QY 133 NSLDYDLDLOHMPVFAVSSRFNSITSHXGRKKEPFIAXFLCYQHFE-YPMCVAR 191
 DB 142 NSLNDL--VYIFSKAKVALYKVLNHPER-----LLMFTFTLIGFP----- 184

QY 192 VNLVLOT 198
 DB 185 --LVLT 169

RESULT 12
 PD6C SOYBN STANDARD; PRT; 424 AA.
 AC P48628;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 OS Glycine max (soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 NC NCB1_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=94345008; PubMed=8066133;
 RA Hiltz W.D., Carlson T.J., Booth J.R. Jr., Kinney A.J., Stecca K.L.,
 RA Yadao N.S.;
 RT "Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
 and its expression in a cyanobacterium.";
 RL Plant Physiol. 105:635-641(1994).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL, L29215; AA050158.1; -;
 DR PIR, T07742; T07742.
 DR InterPro, IPR005804; FA_desat_fam.
 DR Pfam, PF00487; FA_desaturase_1.
 DR ProDom, PD001061; FA_desat_fam; 2.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Translet peptide.
 FT TRANSIT 1 63 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 64 424 OMEGA-6 FATTY ACID DESATURASE.

FT DOMAIN 165 169 HISTIDINE BOX-1.
 FT DOMAIN 201 205 HISTIDINE BOX-2.
 FT DOMAIN 361 365 HISTIDINE BOX-3.
 SQ SEQUENCE 424 AA; 49641 MW; 4F3D52D4B1A2009 CRC64;
 Query Match 6.8%; Score 87; DB 1; Length 424;
 Best Local Similarity 21.7%; Pred. No. 1;
 Matches 58; Conservative 42; Mismatches 97; Indels 70; Gaps 15;

QY 19 SSDYRK-LFSDLSALNLFNRKHTTS--ILSLILFLPLSYC-----GYLPSDST 66
 DB 75 SAERYQLADYD-----FRQVGEPLSDDYTLKQVINPLPKVEVEIDDVAKMSVLSTVS 130
 QY 67 F---VHVLAA---LLGLFLWISGM-----IGHGCHYVWMLSRRLNRAIOLISGNIL 113
 DB 131 YALGLFMISKAPRYLPLAWWTGTATITGFPVGHGCAH---RSTSSKLVEDIYGT-L 185
 QY 114 AGISGM---WKNNNAHHIACNSLDYDLDLOHMPVFA--VSSRFNSITSHXGRKX 166
 DB 186 AFMPLIYYPVPRFKDHRHAKTNML--REDTAMHVPWVWDEPSTPLRKALITYGQPR 243
 QY 167 EPDXIAXFLICYQHFFPYPMCVARNVLIQTI-----LLLSRKXVDRLAINIG 217
 DB 244 CWMISAHMLMMHDLKKFRPSEVPRVKISLACVFARIGWPLIYK-----TGIMG 295

QY 218 ILVFWTWFLPLALLFPVPIQHIFWLN 244
 DB 296 WKFW-----LMPWLGYHFWMS 312

RESULT 13
 PD6C ARATH STANDARD; PRT; 448 AA.
 AC P46312; G9M094;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxID=3702;
 RN [1]
 RP SEQUENCE OF 1-418 FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95148736; PubMed=7846158;
 RA Falcone D.L., Gibson S., Lemieux B., Somerville C.R.;
 RT "Identification of a gene that complements an Arabidopsis mutant
 deficient in chloroplast omega 6 desaturase activity.";
 RL Plant Physiol. 106:1453-1459(1994).
 CC [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Meyer K.F.X., Schneller C., Mandut R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansoorge W., Brandt P., Griwall L., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
 RA Kreis M., Dalseny M., Puigdomenech P., Watson M., Schmidthein T.,
 RA Reichert B., Portelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohiseil J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bitham L., Robben J.,
 RA Van der Schuren J., Grymoprez B., Chuang Y.-J., Vandenbusche F.,
 RA Braeken M., Weltjens I., Voet M., Baetiaens I., Aert R., Defoor E.,
 RA Weitenegger T., Bothé G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke P.,
 RA Woolfman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Bernier S., Hempel S., Feldpausch N., Lambert S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,

RA Petzelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharte M., Grimm M., Loehner T.H.,
 RA Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argirou A., Vitale D., Liguori K., Piravandi E.,
 RA Messeret O., Quigley F., Clabaud G., Mwendileh A., Felber R.,
 RA Schindl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chefred F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Glibons T., Weber N., Vandendol M., Bargeue M., Terol J., Torres A.,
 RA Perez-Perez A., Punnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bieleke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Seshon K., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spiehl J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Cotton M., Joseph C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Grant S., Shohdy N., Hasegawa A., Hameed A., Lochi M., Johnson A.,
 RA Chen E., Marra M., Mathiesen R., McCombie W.R.,
 RT "sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana,"
 RL Nature 402:769-777(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGECC)."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).
 CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: U09503; AAA92800.1; -;
 DR EMBL: AL022198; CA18198.1; -;
 DR EMBL: AL161578; CAB79813.1; -;
 DR EMBL: AY045621; AAK73979.1; -;
 DR EMBL: AY058078; AAL24186.1; -;
 DR EMBL: AY058852; AAL24240.1; -;
 DR PIR: D83562; D83562.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desat_fam; 1.
 DR ProDom: PD001081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KM Transist peptide.
 FT TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 70 448 OMEGA-6 FATTY ACID DESATURASE.
 FT DOMAIN 171 175 HISTIDINE BOX-1.
 FT DOMAIN 207 211 HISTIDINE BOX-2.
 FT DOMAIN 367 371 HISTIDINE BOX-3.

SQ SEQUENCE 448 AA; 51225 MW; C3AC72FB28FBF287 CRC64;
 Query Match 6.6%; Score 87; DB 1; Length 448;
 Best Local Similarity 20.3%; Pred. No. 1.1; Indels 74; Gaps 11;
 Matches 55; Conservative 39; Mismatches 103;
 QY 12 DHTVSAASDPRKLFSDLSANLNFNRKHTTSLLSLITLPLPLSGVLFSD-----ST 66
 DB 84 DRQGLAESYGFRIIGDL-----PENVTLNDIMDTLPKEVFEI--DDKLKLSV 130
 QY 67 FVHVLAAALIGFLWISGW-----IGHDSGHVNMLSRLNRAIQI 107
 DB 131 LLSVTSYTLGLFPIAKSPWLLPLAWMTGTAITGPFVIGHDCAH-----KSFKNKLVED 186
 QY 108 LSGNIIAGISIGW-----WKNNHNAHIIACNSLDYDDLDQMPVFAV--SSRFFRSISHX 162
 DB 187 IVGT-LAFPLVPLVPEPWRKCDHRNKAKTMTLVDHAWQVPEPEPSSVPMKAIIFG 245
 QY 163 GRKCEPDIXAFPLICQHFPEYPMCVARVNLVQTI-----LLFSRXKVDRAI 213
 DB 246 GFRFPLSLAHVNMWFMFLKFRPASEVNRVKISLACVFAFMVGVPLIYK-----V 297
 QY 214 NINGILVFWTWFLFLLALLFVPIQHIQFWLN 244
 DB 298 GLIGWVKFW-----LMPWLGTHFWMS 318
 RESULT 14
 ID UHPB_ECOLI STANDARD; PRT; 500 AA.
 AC P09835; P76729;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sensor protein uhpB (EC 2.7.3.-).
 GN UHPB OR B3668.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87279903; PubMed=3301805;
 RA Friedrich M.J., Kadner R.J.,
 RT "Nucleotide sequence of the uhp region of Escherichia coli,"
 RL J. Bacteriol. 169:3556-3563(1987).
 RN [2]
 RP REVISIONS.
 RA Kadner R.J.,
 RT Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92234930; PubMed=1569007;
 RA Ireland M.D., Wei B.-Y., Kadner R.J.,
 RT "Structure and function of the uhp genes for the sugar phosphate
 RT transport system in Escherichia coli and Salmonella typhimurium,"
 RL J. Bacteriol. 174:2754-2762(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=93315143; PubMed=7686887;
 RA Birtand V.D., Plunkett G., III, Daniels D.L., Blattner F.R.,
 RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
 RT genome: organizational symmetry around the origin of replication,"
 RL Genome 16:551-561(1993).
 CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM UHPB/UHPA
 CC INVOLVED IN THE REGULATION OF THE UPTAKE OF HEXOSE PHOSPHATES.
 CC UHPB FUNCTIONS AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT
 CC PHOSPHORYLATES UHPA IN RESPONSE TO ENVIRONMENTAL SIGNALS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: Contains 1 histidine kinase domain.
 CC -----
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 DR EMBL: M17102; AAA24721.1; ALT_SEQ.
 DR EMBL: M94478; AAA24725.1; ALT_INIT.
 DR EMBL: L10328; AAA62020.1; ALT_INIT.
 DR EMBL: AE000444; AAC76691.1; ALT_INIT.
 DR PIR: E65168; RGCUB.
 DR EcoGene; EG11052; unpb.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR005467; His_kinase.
 DR Pfam; PF02518; HATPase_c1.
 DR SMART; SM00387; HATPase_c1.
 DR PROSITE; PS50109; HIS_KIN_1.
 KM Sensory transduction; Transferrase; Kinase; Phosphorylation;
 KM Transmembrane; Inner membrane; Sugar transport; Complete proteome.

FT TRANSMEM 8 28 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT TRANSMEM 112 132 POTENTIAL.
 FT TRANSMEM 140 160 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT DOMAIN 311 499 HISTIDINE KINASE.
 FT MOD RES 313 313 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 500 AA; 56305 MW; A7353FC1FD53152 CRC64;

Query Match 6.5%; Score 86; DB 1; Length 500;
 Best Local Similarity 23.3%; Pred. No. 1.5; Indels 62; Gaps 11;
 Matches 51; Conservative 33; Mismatches 73;

40 HTTSILSLITLTFPLSCVCLFSDSTFVH-----VLSALIGFLMIQS-GWIGHDS 90
 82 HFLPLMIGSLTLTLPLVALI-----SNRYRQRMRTLLGALTAALQSLPWLHCK 135

QY 91 GHYNNMISRLNRAIQILSGNIIAGISIGWKNNNNAHIAACS-LDYDPDLOHMPVFAV 149
 DB 136 ESNNAAL-----LTLTGTLTAPICLVFW-----HYLANNTWPLGSPSLVSQPT--- 179

QY 150 SSRFFNSITSHXGKKEPFIXXFLCYQHFFTFYPCVAVNLVYQITLL-LFSKXV 208
 DB 180 -----NMGR-----HLVWYLLFV--ISLWQLQGLPELSKFTP 212

QY 209 QDBALNMGILVFTWFLFLALFLVPIQH--QFWLNH 245
 DB 213 FCLALPIALAMHYGQAGALITLMAIALIASQTWADH 251

RESULT 15
 FD3E TOBAC STANDARD; PRT; 379 AA.
 AC P48626;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).
 GN PAD3.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxId=4097;
 RN [1]
 RC SEQUENCE FROM N. A.
 RC STRAIN=cv. SRI, TISSUE=leaf;
 RX MEDLINE=95011632; PubMed=7926817;
 RA Hamada T., Kodama H., Nishimura M., Iba K.;
 RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase";
 RL Gene 147:293-294(1994).

CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEDOWN IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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 DR EMBL: D26509; BA05515.1; -.
 DR PIR: JC2555; JC2555.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase_1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KM Transmembrane.

FT TRANSMEM 52 72 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX-1.
 FT DOMAIN 133 137 HISTIDINE BOX-2.
 FT DOMAIN 300 304 HISTIDINE BOX-3.
 SQ SEQUENCE 379 AA; 44149 MW; 87221A21AB02E1B2 CRC64;

Query Match 6.5%; Score 85.5; DB 1; Length 379;
 Best Local Similarity 22.2%; Pred. No. 1.2;
 Matches 47; Conservative 29; Mismatches 89; Indels 47; Gaps 9;

QY 52 LPLFLSCGV-LPSDSTFVNVLSALIGFLMIQSGWGHYNNMISRLNRAI-QILS 109
 DB 60 IFVATLIGIALIHDSWLFPLVWALQGTWFMALFVIGHDCGHSFSDQLNNVGHILH 119

QY 110 GNILAGISIGWKNNNNAHIAACS-LDYDPDLOHMPVFAVSSRFNSITSHXGKXEPD 169
 DB 120 SAIL--VPTNGMRISHTKHQNHGNETDESNVMP-----EKLYKV--GYSTKFLAY 169

QY 170 XIAXFLICY-----QHFTFY-----PVMC---VARVNLVLOTT 199
 DB 170 KIPFPLALPYMLMKRSPKSGSHFNPYSDLPQPHRKVVVSTLCWVMAALLVYLCTA 229

QY 200 LLLFSRXKQDRAALNMGILVFTWFLFLAL 231
 DB 230 FGSLSQMFKIYGA-----YLIFVMWLDFTVYL 256

Search completed: January 1, 2004, 06:30:56
 Job time : 7.56688 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 22.707 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-6
Perfect score: 1318
Sequence: 1 LPAGSTSHRLSDHTVSAASS.....VPIOHIOFWINHLAENLYXG 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteria: *
17: sp_archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	822	62.4	446	10	Q92TY9
2	780.5	59.2	449	10	Q81B96
3	780.5	59.2	449	10	Q81B96
4	778.5	59.1	449	10	Q81B96
5	768.5	58.3	446	10	Q81B96
6	765.5	58.1	446	10	Q81B96
7	747.5	56.7	458	10	Q81B96
8	740.5	56.2	448	10	Q81B96
9	735.5	55.8	448	10	Q81B96
10	730.5	55.4	448	10	Q81B96
11	729.5	55.3	448	10	Q81B96
12	686.5	52.1	469	10	Q81B96
13	678.5	51.5	448	10	Q81B96
14	377.5	28.6	523	3	Q9H8G8
15	342.5	26.0	573	3	Q8NKG8
16	317	24.1	568	3	Q8NKG9

17	263	20.0	467	3	Q96VC3	Q96VC3 mucor circi
18	251.5	19.1	457	3	Q9HEV4	Q9HEV4 mortierella
19	249.5	18.9	457	3	Q8X173	Q8X173 mortierella
20	247.5	18.8	457	3	Q9UVY3	Q9UVY3 mortierella
21	247.5	18.8	457	3	Q9UVY3	Q9UVY3 mortierella
22	244.5	18.6	483	10	Q9LENO	Q9LENO ceratodon p
23	244	18.5	477	10	Q8RXB0	Q8RXB0 phaeodactyl
24	234.5	17.8	357	3	Q9HDP4	Q9HDP4 mortierella
25	234.5	17.8	457	3	Q9HEV1	Q9HEV1 mortierella
26	234.5	17.8	457	3	Q8X174	Q8X174 mortierella
27	232	17.6	419	10	Q9SKO9	Q9SKO9 euglena gra
28	227	17.2	459	10	Q944W4	Q944W4 pythium lit
29	224.5	17.0	443	5	Q61388	Q61388 caenorhabdi
30	224.5	17.0	443	5	Q23221	Q23221 caenorhabdi
31	212.5	16.1	520	10	Q9LEW9	Q9LEW9 ceratodon p
32	204	15.5	525	10	Q9ZNM2	Q9ZNM2 physcomittr
33	201.5	15.3	447	5	Q9XTB7	Q9XTB7 caenorhabdi
34	197	14.9	350	16	Q9F2M3	Q9F2M3 streptomyce
35	172	13.1	444	11	Q920R9	Q920R9 mus musculu
36	170	12.9	444	11	Q92122	Q92122 rattus norv
37	164	12.4	347	16	Q9FC35	Q9FC35 streptomyce
38	162	12.3	386	4	Q9EH07	Q9EH07 homo sapien
39	162	12.3	422	4	Q9H3G3	Q9H3G3 homo sapien
40	162	12.3	444	4	Q95864	Q95864 homo sapien
41	160.5	12.2	444	4	Q96139	Q96139 homo sapien
42	160.5	12.2	444	4	Q9VYX1	Q9VYX1 homo sapien
43	160.5	12.2	444	4	Q96T10	Q96T10 homo sapien
44	160.5	12.2	444	4	Q60427	Q60427 homo sapien
45	160.5	12.2	501	4	Q8NCC7	Q8NCC7 homo sapien

ALIGNMENTS

RESULT 1
Q92TY9 PRELIMINARY; PRT; 446 AA.
ID Q92TY9
AC Q92TY9;
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Desaturase/cytochrome b5 protein.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotyledons; Malvales; Euphorbiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3968;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed endosperm;
RX MEDLINE=97268723; PubMed=910811;
RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
RL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC EMBL; AF005096; AAD01240.1; -.
DR HSSP; P00171; IISU.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Heme
SQ SEQUENCE 446 AA; 51418 MW; A1954FDB2DB600F CRC64;
Query Match 62.4%; Score 822; DB 10; Length 446;
Best Local Similarity 57.5%; Pred. No. 5.6e-70;
Matches 154; Conservative 38; Mismatches 60; Indels 16; Gaps 3;


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QY 1 LPAFSTSHRLSDHTVGAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPFLVSGV 60
DB 71 LDFEFGYHMLKXSVSETSDYRLVAEFKLG-FEKGHIAITLVSWMMLALSTYGV 129
QY 61 LPSDSTFVHVALIGFLMTIGSGWIGHDSGHYVNLSSRLNRAIQLISGNIAGISIGW 120
DB 130 LGSNSTWVHLISGGLGFMWIGWIGHDSGHYVNMSSRFRNLQAQLISGNCIAGISIAW 189
QY 121 WKNNHNAHIAACNSLDVDPDQHMPPFAVSSRFNSITSHYGRKKEFDXIAEFLICYH 180
DB 190 WKNNHNAHIAACNSLDVDPDQHMPPFAVSSRFNSITSHYGRKKEFDXIAEFLICYH 249
QY 181 FFYPMCVARVNLVYQITLLLFSSKXKVDRAINIGILVFTWFLFLA-----LL 232
DB 250 LTFYPMCAKRIULFPOSISLISKRVANRGOEILGVLVFWLWYPLVSLCENMGERRV 309
QY 233 FVP-----IOHIOFWNLHLENLYXG 253
DB 310 FVAASPSVTRIOHVQFCNLHNFSSSVYLG 337

RESULT 2
Q8LB96 PRELIMINARY; PRT; 449 AA.
AC Q8LB96;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 23, Last sequence update)
DE Delta-8 sphingolipid desaturase.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.,
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RT Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.,
RT "Full-length cDNA from Arabidopsis thaliana."
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AY087345; AAM64895.1; -.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 449 AA; 51744 MW; A1EB557B8CE03E18 CRC64;

Query Match 59.2%; Score 780.5; DB 10; Length 449;
Best Local Similarity 54.8%; Pred. No. 5e-66;
Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;
QY 6 TSHRLSDHTVGAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPFLVSGVLFSDS 65
DB 78 TGYHNDPQVSEVSRDYRMAAEFKLGFEKNGHVTLTATFAVAMPFLRVLGVLACS 137
QY 66 TTVHVALSALLIGFLMTIGSGWIGHDSGHYVNLSSRLNRAIQLISGNIAGISIGW 125
DB 138 VFAHQIAAALLGLMTIGSAYIGHSYVIMSNKSNRFAQLISGNCITGISIAWKKTH 197
QY 126 NAHHLACNSLDVDPDQHMPPFAVSSRFNSITSHYGRKKEFDXIAEFLICYHFTFP 185

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DB 198 NAHHLACNSLDVDPDQHMPPFAVSSRFNSITSHYGRKKEFDXIAEFLICYHFTFP 257
QY 186 WCVARVNLVYQITLLLFSSKXKVDRAINIGILVFTWFLFLA-----LV--- 234
DB 258 WVCGRINLFIQITLLLFSSKREVPDRALNPAFLVFTWFLVSLPNNPERRFFVFTG 317
QY 235 ---PIOHIOFWNLHLENLYXG 253
DB 318 FVYTAHQIQTILNHPADVYTG 340

RESULT 3
Q9ZRP8 PRELIMINARY; PRT; 449 AA.
AC Q9ZRP8;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DE Delta-8 sphingolipid desaturase.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxId=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Drakkar; TISSUE=ripening embryos;
RC MEDLINE=99003197; PubMed=976850;
RA Sperling P., Zaehlinger U., Heinz E.,
RT "A sphingolipid desaturase from Higher Plants Identification of a New
RT Cytochrome b5 Fusion Protein."
RT J. Biol. Chem. 273:28590-28596(1998).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AJ224160; CA11857.1; -.
DR HSSP: P82291; ICXY.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 449 AA; 51490 MW; FEEB37AF9D390C1 CRC64;

Query Match 59.2%; Score 780.5; DB 10; Length 449;
Best Local Similarity 54.0%; Pred. No. 5e-66;
Matches 141; Conservative 44; Mismatches 61; Indels 15; Gaps 2;
QY 8 HRLSDHTVGAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPFLVSGVLFSDSTF 67
DB 80 YVKKDHVSDVRDYRRLAERFKGLFPKKGHVLTLYTLCVAAAMLAAYVYGVACTSIW 139
QY 68 VVHVALSALLIGFLMTIGSGWIGHDSGHYVNLSSRLNRAIQLISGNIAGISIGWKKNNHA 127
DB 140 AHLISAVLGLMTIGSAYVGHDSGHYVNLSTPCNKLVOGLSGNCTGISIAWKKTHNA 199
QY 128 HHIAACNSLDVDPDQHMPPFAVSSRFNSITSHYGRKKEFDXIAEFLICYHFTFPYV 187
DB 200 HHISGNSLDHDDDLGHIIPVLAVSNKFKMTSRFGRKLTFFPLARFLISYQHWSTFPM 259
QY 188 CVARVNLVYQITLLLFSSKXKVDRAINIGILVFTWFLFLA-----LVFV----- 234
DB 260 CVGRINLFIQITLLLFSSRYVDPDRALNIGILVFTWFLVSLPNNQERITFVFLSMA 319
QY 235 ---PIOHIOFWNLHLENLYXG 253
DB 320 VTAHQIQTILNHPADVYTG 340

RESULT 4

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Q9ZRP7 PRELIMINARY; PRT; 449 AA.

AC Q9ZRP7;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE Delta-8 sphingolipid desaturase (AT3G61580/P2A19_180).

GN SLD1 OR F2A19.180 OR AT3G61580.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsids.

OC NCBI_TaxID=3702;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia; TISSUE=flower; MAINLY GREEN PARTS, and Root;

RX MEDLINE=99003197; PubMed=9786850;

RT Sperlberg P., Zaehring U., Heinz E.;

RT "A sphingolipid desaturase from higher plants. Identification of a new cytochrome b5 fusion protein."

RT J. Biol. Chem. 273:28590-28596(1998).

RL [2]

RP SEQUENCE FROM N.A.

RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RL [3]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Ban J., Bower L., Carrini P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neuman G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natsuka M., Nguyen M., Onda C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;

RA "Arabidopsis cDNA clones";

RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RL [5]

RP SEQUENCE FROM N.A.

RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T., Carrini P., Chen H., Cheuk R., Chan M.C., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A., Kawai J., Kim C.J., Natsuka M., Quach H.L., Sakurai T., Satou M., Seki M., Shin P., Tang C.C., Toriumi M., Wallender B.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Ecker J., Theologis A., Davis R.W.;

RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

DR EMBL: AL132962; CAB71088.1; -

DR EMBL: AF428420; AAL16189.1; -

DR EMBL: BF000442; AAN17419.1; -

DR HSP: P00171.1; I15U.

DR InterPro: IPR001199; Cyt B5.

DR InterPro: IPR005804; FA_decat_fam.

DR Pfam: PF00487; FA_decatase; 1.

DR Pfam: PF00173; heme_1; 1.

DR ProDom: PD000612; Cyt B5; 1.

DR ProDom: PD001081; FA_decat_fam; 1.

DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.

DR Heme.

SC SEQUENCE 449 AA; 51675 MW; 145048F9FD35964 CRC64;

Query Match 59.1%; Score 778.5; DB 10; Length 449;

Best Local Similarity 54.8%; Pred. No. 7.7e-66;

Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVASAASDYRLTFLSALNLFNRKHTTSLILTLPLPLSCVGLFSDS 65

DB 78 TGYHIRDQVSEVSDYRRMAEFRLGLFENKGVHTVLTFLAFVAMFGLVGYVLACTS 137

QY 66 TTVHVLTAALIGFLWIGSGHDSGHVNMVLSRLNRAIQLSGNIIAGISIGWKKMH 125

DB 138 VFAHDIQAALIGLWIGVYGHDSGHVNMVLSRLNRAIQLSGNIIAGISIGWKKMH 197

QY 126 NAHHLACSLDVPDPLQHPVAVSSRFENSTSHXGKXEDXIAFLICYOHTFPYP 185

DB 198 NAHHLACSLDVPDPLQHPVAVSSRFENSTSHXGKXEDXIAFLICYOHTFPYP 257

QY 198 NAHHLACSLDVPDPLQHPVAVSSRFENSTSHXGKXEDXIAFLICYOHTFPYP 257

DB 198 NAHHLACSLDVPDPLQHPVAVSSRFENSTSHXGKXEDXIAFLICYOHTFPYP 257

QY 198 NAHHLACSLDVPDPLQHPVAVSSRFENSTSHXGKXEDXIAFLICYOHTFPYP 257

DB 198 NAHHLACSLDVPDPLQHPVAVSSRFENSTSHXGKXEDXIAFLICYOHTFPYP 257

QY 235 ----FIOHGFNLNLAENLYXG 253

DB 318 FTVTALQHIQFTLNHPADVVG 340

RESULT 5

Q9FR82 PRELIMINARY; PRT; 446 AA.

AC Q9FR82;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE Delta-8-sphingolipid desaturase.

GN SLD1.

OS Borago officinalis (Boraginaceae) (Borage).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Lamiales; Boraginaceae; Borago.

OX NCBI_TaxID=13363;

RL [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=21092516; PubMed=11162428;

RA Libisch B., Michelson L.V., Lewis M.J., Shewry P.R., Napier J.A.;

RT "Chimeras of Delta6-fatty acid and Delta8-sphingolipid desaturases."

RT Biochem. Biophys. Res. Commun. 279:779-785(2000).

RL [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=2160464; PubMed=11368168;

RA Sperlberg P., Libisch B., Zaehring U., Napier J.A., Heinz E.;

RT "Functional identification of a delta 8-sphingolipid desaturase from Borago officinalis."

RT Arch. Biochem. Biophys. 388:293-298(2001).

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

DR EMBL: AF133728; AAG43277.1; -

DR HSP: P00171.1; I15U.

DR InterPro: IPR001199; Cyt B5.

DR InterPro: IPR005804; FA_decat_fam.

DR Pfam: PF00487; FA_decatase; 1.

DR Pfam: PF00173; heme_1; 1.

DR ProDom: PD000612; Cyt B5; 1.

DR ProDom: PD001081; FA_decat_fam; 1.

DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.

DR Heme.

SC SEQUENCE 446 AA; 50926 MW; EBD579F035A3AFOC CRC64;

Query Match 58.3%; Score 768.5; DB 10; Length 446;

Best Local Similarity 55.9%; Pred. No. 6.9e-65;

Matches 147; Conservative 35; Mismatches 66; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVASAASDYRLTFLSALNLFNRKHTTSLILTLPLPLSCVGLFSDS 65

DB 76 TGYHLEDVLSISIDYRKRLASEFSEKAGLFEKKGHTVTCISFILLGCGVYGLCSNS 135

QY 66 TTVHVLTAALIGFLWIGSGHDSGHVNMVLSRLNRAIQLSGNIIAGISIGWKKMH 125

DB 136 LNVHMLSGMLGMCPTIOAYLGHDSGHVNMVLSRLNRAIQLSGNIIAGISIGWKKMH 195

QY 126 NAHHLACSLDVPDPLQHPVAVSSRFENSTSHXGKXEDXIAFLICYOHTFPYP 185

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Db 196 NAHIIICNSLDYDPDLOHLPFAVPSSFFKSLSRFGRLTDTGSLRFLVSQHTTIV 255
Qy 186 VMCVAVNVLQTLTLLFSRXKQODRALNMGILVFTWFLFLA-----LTV--- 234
Db 256 VMFGINLVYQFELLFSTRKVPDRALNIGILVYTWTPYVLSCLPNMNERVLEVLNC 315
Qy 235 ----PIOHIOFWNLHLENLYXG 253
Db 316 FSVTALOHIOFTLNHFAADYVVG 338

RESULT 6
Q8LUD7 PRELIMINARY; PRT; 446 AA.
AC Q8LUD7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Sphingolipid long chain base delta 8 desaturase.
OS Aquilegia vulgaris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Ranunculaceae; Aquilegia.
OC NCBI_TaxID=3451;
RN [1]
RP SEQUENCE FROM N.A.
RA Longman A.V., Michaelson L.V., Napier J.A.;
RT "Isolation and characterization of a cDNA encoding a delta 8
sphingolipid desaturase from Aquilegia vulgaris.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF406816; AAN03619.1; -.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;

Query Match 58.1%; Score 765.5; DB 10; Length 446;
Best Local Similarity 54.1%; Pred. No. 1.3e-64;
Matches 140; Conservative 43; Mismatches 61; Indels 15; Gaps 2;

Qy 10 LSDHTVAASSDYRKLFSDSLALNLFNRKGTTSILSLITLFPPLSVCGVLFSDSFTVH 69
Db 79 LKDYTSEVSKDYRKLVAFESKAGLYDKGHHLLFSFTTILMAISVMGVLCSDKTMAH 138
Qy 70 VLSAALIGFLWISGMIHGDSGHYNNVLSRLNRAIQILSGNTLAGISIGMKWNNAH 129
Db 139 LSAVAALVGLIMWIGFVGHDSGHYNNVLTPLKLNRFMQIFGNCITGISIGMKWNNAH 198
Qy 130 IACNSLDYDPDLOHMPVFAVSSRFPNSITSHXGRKKEPFXIXFLICYGHFFPYMCV 189
Db 199 IAVNSLDYDPDLOHIFPLAVSSDIFFSLTSKFGKKTTPDIRFLISFOHMTFFYPMAI 258
Qy 190 ARVNLVQLTLLFSRXKQODRALNMGILVFTWFLFLALL-----FVPI----- 236
Db 259 ARINLPAQSTFILLSKRPVTDRLBELGLNFMCMVSLIACLPNMGERRAMTVAMSFVNS 318
Qy 237 --OHIOFWNLHLENLYXG 253
Db 319 GYQHIOFCLNHFSAHTYVG 337

RESULT 7
Q43469 PRELIMINARY; PRT; 458 AA.
AC Q43469;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE Delta-8 sphingolipid desaturase.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteroceae; Asteroideae;
OC Heliantheae; Helianthus.
OC NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Indred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=96028121; PubMed=7588718;
RA Sperling P., Schmidt H., Heinz E.;
RT "A cytochrome b5-containing fusion protein similar to plant acyl lipid
desaturases.";
RL Eur. J. Biochem. 232:798-805 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Indred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=21116801; PubMed=1171153;
RA Sperling P., Blume A., Zaehring U., Heinz E.;
RT "Further characterization of delta 8-sphingolipid desaturases from
higher plants.";
RL Biochem. Soc. Trans. 28:638-641 (2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: X87143; CA60621.1; -.
DR HSSP: P00171; 1F03.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 458 AA; 52231 MW; D182287AB0E99245 CRC64;

Query Match 56.7%; Score 747.5; DB 10; Length 458;
Best Local Similarity 52.8%; Pred. No. 7e-63;
Matches 140; Conservative 40; Mismatches 66; Indels 19; Gaps 4;

Qy 6 TSHRLSDHTVAASSDYRKLFSDSLALNLFNRKGTTSILSLITLFPPLSVCGVLFS 63
Db 87 TGYHLKDYOVSDISRDKLASBFAKAGFEKKGH--GVYSLCFVSLLSACVGVLS 144
Qy 64 DSTFVAVLSAALIGFLWISGMIHGDSGHYNNVLSRLNRAIQILSGNTLAGISIGMKW 123
Db 145 GSFVHMLSGALIGLAWMOIAYLGHDAGHYQWATRGMKKFGIFGNCITGISIAMWKM 204
Qy 124 NNAHHIACNSLDYDPDLOHMPVFAVSSRFPNSITSHXGRKKEPFXIXFLICYGHFF 183
Db 205 TNAHHIACNSLDYDPDLOHMPVFAVSSRFPNSITSHXGRKKEPFXIXFLICYGHFF 264
Qy 184 YPMVCVAVNVLQTLTLLFSRXKQODRALNMGILVFTWFLFLALL-----FV- 234
Db 265 YPMVCVAVNVLQTLTLLFSRXKQODRALNMGILVFTWFLFLAVSRPNMNERVLEVLNC 315
Qy 235 ----PIOHIOFWNLHLENLYXG 253
Db 325 VSECVTGIHIOFTLNHFAADYVVG 337

RESULT 8
Q8VZ22 PRELIMINARY; PRT; 448 AA.
AC Q8VZ22;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)

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DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
 DE Delta-6-desaturase.
 GN D6DS.
 OS Echium gentianoides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Echium.
 NCBI_TaxID=173991;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 RT Echium: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055117; AL23580.1; --
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW SEQUENCE 448 AA; 51428 MW; C2A937951B87C183 CRC64;
 SQ
 Query Match 56.2%; Score 740.5; DB 10; Length 448;
 Best Local Similarity 48.5%; Pred. No. 3,2e-62;
 Matches 130; Conservative 59; Mismatches 64; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILTLTLPPLSVCGV 60
 DB 72 LDFPFTGYLLKDYSSVEVSKDRLKVFERNKRGLEPKGHYLVTVFPLAMMFAMSVYGV 131
 QY 61 LFSDFVAVLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIQILSGNLAGISGM 120
 DB 132 LFCEGVVHLLAGLGMFWIOWGIGHAGHYIVPNPRLNLMGIVASNCISGISGM 191
 QY 121 WKNNNAHHIACNSLDYDPDLQHPFVAVSSRFNSITSHXGKKEPDXIAXFLICYOH 180
 DB 192 WKNNNAHHIACNSLDYDPDLQIPLVYSSKLFSSLTSHPEKKTLPDLSRFVSHOH 251
 QY 181 FFYPMVCARVNLVQTLILFSSRXKQDRALNIGLIVPTWF-----L 226
 DB 252 WFFYPMVCARVNLVQTLILFSSRXKQDRALNIGLIVPTWF-----L 226
 QY 227 FLALLFVP-IOHIOFWNLHLENLYXG 253
 DB 312 FVVASLSTVGTGQVQPSLNHFPASVYVG 339
 RESULT 9
 Q8VZ21 PRELIMINARY; PRT; 448 AA.
 AC Q8VZ21;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 GN D6DS.
 OS Echium pitardii var. pitardii.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Echium.
 NCBI_TaxID=174255;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 RT Echium: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055116; AL23581.1; --

DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW SEQUENCE 448 AA; 51394 MW; 4B6D6EA4905DE263 CRC64;
 SQ
 Query Match 55.8%; Score 735.5; DB 10; Length 448;
 Best Local Similarity 48.1%; Pred. No. 9,5e-62;
 Matches 129; Conservative 59; Mismatches 65; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILTLTLPPLSVCGV 60
 DB 72 LDFPFTGYLLKDYSSVEVSKDRLKVFERNKRGLEPKGHYLVTVFPLAMMFAMSVYGV 131
 QY 61 LFSDFVAVLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIQILSGNLAGISGM 120
 DB 132 LFCEGVVHLLAGLGMFWIOWGIGHAGHYIVPNPRLNLMGIVASNCISGISGM 191
 QY 121 WKNNNAHHIACNSLDYDPDLQHPFVAVSSRFNSITSHXGKKEPDXIAXFLICYOH 180
 DB 192 WKNNNAHHIACNSLDYDPDLQIPLVYSSKLFSSLTSHPEKKTLPDLSRFVSHOH 251
 QY 181 FFYPMVCARVNLVQTLILFSSRXKQDRALNIGLIVPTWF-----L 226
 DB 252 WFFYPMVCARVNLVQTLILFSSRXKQDRALNIGLIVPTWF-----L 226
 QY 227 FLALLFVP-IOHIOFWNLHLENLYXG 253
 DB 312 FVVASLSTVGTGQVQPSLNHFPASVYVG 339
 RESULT 10
 Q9SAU5 PRELIMINARY; PRT; 448 AA.
 AC Q9SAU5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Borago.
 NCBI_TaxID=13363;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA TISSUE=Seed;
 RA Numborg A.N., Beremand P.D., Thomas T.L.;
 RT "Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
 RT (GLA)."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF007561; AAD01410.1; --
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW SEQUENCE 448 AA; 51626 MW; EAC3F0BF22E0DE00 CRC64;
 SQ
 Query Match 55.4%; Score 730.5; DB 10; Length 448;
 Best Local Similarity 48.9%; Pred. No. 2,9e-61;
 Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILTLTLPPLSVCGV 60
 DB 72 LDFPFTGYLLKDYSSVEVSKDRLKVFERNKRGLEPKGHYLVTVFPLAMMFAMSVYGV 131

Db 72 LDKFTGYLKDYSVEVSQDYRKLYVEFSKMGJYDKKGMIFATLFCIFAMLPAMSVYGV 131
 QY 61 LFDSDTFVHYLSAALIGFLWIOSGMIGHDSGHYVMSRLNRAIOILSGNIIAGISIGM 120
 Db 132 LFCGCVLHFLFSCGLMGFLWIOSGMIGHDSGHYVMSRLNRAIOILSGNIIAGISIGM 191
 QY 121 WKNHNNAHIIACNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFXDIAAXFLICYQH 180
 Db 192 WKNHNNAHIIACNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFXDIAAXFLICYQH 251
 QY 181 FTFFYPVACVAVNLYIQTILLFSSRKXKVDORALNIMGILVFWTF-----L 226
 Db 252 WFFYPIIMCARLNMVYQSLIMLTKRNVSYRAQELLGLVFSIWIYPLVSCLPNMGIRIM 311
 QY 227 FLTALLFVP-IOHIOFNLHLENIYXG 253
 Db 312 FVIALSLVTGMQOVQFSLNHFSSSVYGV 339

RESULT 11

004353 PRELIMINARY; PRT; 448 AA.
 AC 004353;
 DT 01-JUL-1997 (TEMBLrel. 04, Created)
 DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Delta 6 desaturase.
 OS Borago officinalis (Borragace) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Borago.
 NC NCB1_TaxID=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268723; PubMed=9108131;
 RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 RT cytochrome b5 domain results in the accumulation of high levels of
 RT delta6-desaturated fatty acids in transgenic tobacco."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; U79010; AAC49700.1; -.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00467; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51635 MW; B62BEE701680909F CRC64;

Query Match 55.3%; Score 729.5; DB 10; Length 448;
 Best Local Similarity 48.9%; Pred. No. 3.5e-61;
 Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;

QY 1 LPAFSTSHRLSDTVAASDYRKLFSDSLALNLFNRKHTTSLILTLPLSYGV 60
 Db 72 LDFEFGYLYKDVSEVSQDYRKLYVEFSKMGJYDKKGMIFATLFCIFAMLPAMSVYGV 131
 QY 61 LFDSDTFVHYLSAALIGFLWIOSGMIGHDSGHYVMSRLNRAIOILSGNIIAGISIGM 120
 Db 132 LFCGCVLHFLFSCGLMGFLWIOSGMIGHDSGHYVMSRLNRAIOILSGNIIAGISIGM 191
 QY 121 WKNHNNAHIIACNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFXDIAAXFLICYQH 180
 Db 192 WKNHNNAHIIACNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFXDIAAXFLICYQH 251
 QY 181 FTFFYPVACVAVNLYIQTILLFSSRKXKVDORALNIMGILVFWTF-----L 226
 Db 252 WFFYPIIMCARLNMVYQSLIMLTKRNVSYRAQELLGLVFSIWIYPLVSCLPNMGIRIM 311

QY 227 FLTALLFVP-IOHIOFNLHLENIYXG 253
 Db 312 FVIALSLVTGMQOVQFSLNHFSSSVYGV 339

RESULT 12

092UT8 PRELIMINARY; PRT; 469 AA.
 AC 092UT8;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE S276.
 GN S276.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 NC NCB1_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ET3;
 RA Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;
 RT "Aluminum tolerance in yeast conferred by over-expression of wheat
 RT gene.";
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF031194; AAD10250.1; -.
 DR HSP; P00171; 1150.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR InterPro; IPR001092; HhH_baslc.
 DR Pfam; PF00467; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 469 AA; 52617 MW; 16F223C1F79740D CRC64;

Query Match 52.1%; Score 686.5; DB 10; Length 469;
 Best Local Similarity 48.1%; Pred. No. 4.6e-57;
 Matches 125; Conservative 46; Mismatches 74; Indels 15; Gaps 1;

QY 9 RLSDDHTVAASDYRKLFSDSLALNLFNRKHTTSLILTLPLSYGVLFSDSTFV 68
 Db 100 RLTDYVPPASADFRRLAOLSSAGLFERYGHTPKFLVAMSVLFCIALYCVLACSTGA 159
 QY 69 HVLSAALIGFLWIOSGMIGHDSGHYVMSRLNRAIOILSGNIIAGISIGMKNHNAH 128
 Db 160 HMFAGLIGFLWIOSGMIGHDSGHYVMSRLNRAIOILSGNIIAGISIGMKNHNAH 219
 QY 129 HIACNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFXDIAAXFLICYQHFTFVAVC 188
 Db 220 HISCNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFXDIAAXFLICYQHFTFVAVC 279
 QY 189 VARVNLVYIQTILLFSSRKXKVDORALNIMGILVFWTFELTALL-----F 233
 Db 280 FARINLVQSIYFLITQKKRORWLEIAGVAFVWVYPLVSCLPNMGIRVAFVLSFVY 339
 QY 234 VPIQHIQFNLHLENIYXG 253
 Db 340 TGIQHVQFCLNHFSSSVYGV 359
 RESULT 13
 08L717 PRELIMINARY; PRT; 448 AA.
 AC 08L717;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, last annotation update)
 DE Delta-6-desaturase.
 OS Argania spinosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Sapotaceae; Argania.
 NCBI_TaxID=85884;
 RN
 RP SEQUENCE FROM N.A.
 RA El Filali A., Anderson M., Abbas K.;
 RT "Characterization and cloning of delta-6-desaturase in Argania spinosa
 fruit.";
 RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY131238; AAM94345.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;
 Query Match 51.5%; Score 678.5; DB 10; Length 448;
 Best Local Similarity 46.6%; Pred. No. 2.5e-56;
 Matches 125; Conservative 49; Mismatches 79; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDYKRLPSDLALNLFNRKGGTSLILSLTLPLSLVCGV 60
 DB 72 LDFEFTGYLYKDYVSBSVDYKLVPEFSKMGLYDKAGHIMPATLCFIMLFAMSYGV 111
 QY 61 LPSDSTFVYVLSAALIGFLMIGSGHGHGHNWLSRLNALIQLSGNIAGISIGV 120
 DB 132 LRCEGVVHLFSGCLMGFLMIGSGHGHGHNWLSRLNALIQLSGNISIGV 191
 QY 121 WKNHNAHHIACSLDYPDLOHMPVAFVSSRFNSTSHXGRKXEPDXIAFLCYOH 180
 DB 192 SKNNHNAHHIACSLDYPDLOHMPVAFVSSRFNSTSHXGRKXEPDXIAFLCYOH 251
 QY 181 FTFYVWCARVNLVLTILLFSSRXKVDRAINIMGILVFWTF-----L 226
 DB 252 WTFYTIMCARLMMYQSLIMLTGRNVSYRAHEILGCLVFSIMPLVSLPNNGERIM 311
 QY 227 FLIALLFVP-IGHIQEWLHLENLIXG 253
 DB 312 FVIASLSVTGMQOVFSINHFSSSVYVG 339
 RESULT 14
 Q9HDG8 PRELIMINARY; PRT; 523 AA.
 AC Q9HDG8;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, last annotation update)
 DE Delta-6 desaturase.
 OS Mucor rouxii.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 NCBI_TaxID=29923;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 24905;
 RX MEDLINE=20563795; PubMed=11112411;
 RA Laoteng K., Mannontarat R., Tanticharoen M., Cheevadhanarak S.;
 RT "Delta(6)-desaturase of Mucor rouxii with high similarity to plant
 delta(6)-desaturase and its heterologous expression in Saccharomyces
 cerevisiae.";
 RT Biochem. Biophys. Res. Commun. 279:17-22(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF296076; AAG36960.1; -

DR EMBL: AF296083; AAG36959.1; -
 DR HSP: P00173; 1EX.
 DR InterPro: IPR001525; C5_DNA_mech.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS00095; C5_MTASE_2; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 523 AA; 60622 MW; A03727AF39EB7857 CRC64;
 Query Match 28.6%; Score 377.5; DB 3; Length 523;
 Best Local Similarity 32.5%; Pred. No. 1.3e-27;
 Matches 81; Conservative 46; Mismatches 87; Indels 35; Gaps 5;
 QY 22 YRLLFSDLSALNLFN-----RKG--HTTSLILSLTLPLSLVCGVLSFSDTFVYVLS 72
 DB 167 YRLLFSDLSALNLFN-----RKG--HTTSLILSLTLPLSLVCGVLSFSDTFVYVLS 217
 QY 73 AALIGFLMIGSGHGHGHNWLSRLNALIQLSGNIAGISIGWKMNNHNAHHIAC 132
 DB 218 AAFMAFMHQLVFTADAGHNETGKSEIDHVGIVIANPISGLSGWKMNNHNAHHIAC 277
 QY 133 NSLDYDPLQHPVAFVSSRFNSTSHXGRKXEPDXIAFLCYOHFTFYVWCARV 192
 DB 278 NHEHDPDIOHVPFMAITTKFPNNISTYVYKRLPFDASRFVRQHLYLYLISFGRF 337
 QY 193 NYLQTLILFSGXKQDQALNIMGLVFWTFWFLPLA-----LLEVP 236
 DB 338 NHRISFAYLLTCNVRTLELVGITFPFVWGSLSTLPTNIRIAYIMSYMLTFPL 397
 QY 237 OHIQEWLH 245
 DB 398 -HVQITLSH 405
 RESULT 15
 Q9NKG8 PRELIMINARY; PRT; 573 AA.
 AC Q9NKG8;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, last annotation update)
 DE Putative delta 8-sphingolipid desaturase.
 OS Kluyveromyces fragilis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_TaxID=28985;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=IFO 1090;
 RA Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
 RT "Isolation and characterization of the genes encoding delta 8-
 sphingolipid desaturase from Saccharomyces kluyveri and Kluyveromyces
 fragilis.";
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AB085690; BAB93118.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 573 AA; 67065 MW; 9383EBA4323F1A57 CRC64;
 Query Match 26.0%; Score 342.5; DB 3; Length 573;
 Best Local Similarity 29.2%; Pred. No. 3.1e-24;

	Matches	75;	Conservative	53;	Mismatches	92;	Indels	37;	Gaps	5;
Qy	19	SSDYRKLFDLSALNENRKGHTTSLILTLFPLSVGVLPSDSTFY----	HVLSA	73						
Db	195	ASEYRKLHGRTAAGLYQ-----	CNYRYLREFLRIGTLFGISFYLLSLKWPALSA	245						
Qy	74	ALIGFLMISGWIIGHDSGHYNVMSRLNRAIOILSGNLAGISIGWKNHNAHIACN	133							
Db	246	ICIGFAMQQLVFIADHAGHISITHNYQVDNIGMTVASWIGSLGWMKRNHDVHHLVTN	305							
Qy	134	SLDYDPDLQMPVPAVSSRFNSITSHXGKXKXEDXIAFLICYOHFTFYPMCVARVN	193							
Db	306	DPVHDDPIDHTLPEFAVSTRLFHNVTSTYDPLFLFDKFAQKVVPIDHLYYPILCFGRFN	365							
Qy	194	LY-LQTIILLFSRXKVQDRA-----	ININGILVFWTWFLFLALLFVP-----	235						
Db	366	LYRLSMWHVLLGGQPRGRKAMFRYYELAEISFPNYWFFYLITYKKOMPTNAERPKYVMIS	425							
Qy	236	-----IQHIQFWLNHLA	247							
Db	426	HIATMTVHVQITLSHFA	442							

Search completed: January 1, 2004, 06:33:55
 Job time : 23.907 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 : Search time 8.78981 Seconds
(without alignments)
1217.848 Million cell updates/sec

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Perfect score: 1318
Sequence: 1 LPASTSHRLSDHTVSAASS.....VPIQHIFWNLHLENLYXG 253

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/6CTOS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753.5	57.2	452	4	US-08-934-254-27 Sequence 27, Appl
2	730.5	55.4	448	1	US-08-366-779-5 Sequence 5, Appl
3	730.5	55.4	448	1	US-08-789-936-5 Sequence 5, Appl
4	730.5	55.4	448	2	US-08-934-254-5 Sequence 5, Appl
5	721.5	54.7	446	2	US-08-833-610-5 Sequence 5, Appl
6	721.5	54.7	446	3	US-08-834-033A-15 Sequence 15, Appl
7	682.5	51.8	252	2	US-08-834-655-7 Sequence 7, Appl
8	682.5	51.8	252	2	US-08-834-033A-8 Sequence 8, Appl
9	682.5	51.8	252	4	US-09-363-574-7 Sequence 7, Appl
10	682.5	51.8	252	4	US-09-363-526-7 Sequence 7, Appl
11	291	22.1	104	2	US-08-834-655-6 Sequence 6, Appl
12	291	22.1	104	3	US-08-834-033A-7 Sequence 7, Appl
13	291	22.1	104	3	US-09-363-574-6 Sequence 6, Appl
14	291	22.1	104	4	US-09-363-526-6 Sequence 6, Appl
15	247.5	18.8	457	2	US-08-834-655-2 Sequence 2, Appl
16	247.5	18.8	457	3	US-08-834-033A-2 Sequence 2, Appl
17	247.5	18.8	457	4	US-09-363-574-2 Sequence 2, Appl
18	247.5	18.8	457	4	US-09-363-526-2 Sequence 2, Appl
19	247.5	18.8	457	4	US-09-330-235-18 Sequence 18, Appl
20	247.5	18.8	458	4	US-09-439-261-10 Sequence 10, Appl
21	247.5	18.8	458	4	US-09-439-261-44 Sequence 44, Appl
22	247.5	18.8	458	4	US-09-227-613-11 Sequence 11, Appl
23	247.5	18.8	458	4	US-09-227-613-41 Sequence 41, Appl
24	245.5	18.6	355	2	US-08-834-655-5 Sequence 5, Appl
25	245.5	18.6	355	3	US-08-834-033A-6 Sequence 6, Appl
26	245.5	18.6	355	3	US-09-363-574-5 Sequence 5, Appl
27	245.5	18.6	355	4	US-09-363-526-5 Sequence 5, Appl

28	245.5	18.6	457	2	US-08-833-610-4 Sequence 4, Appl
29	245.5	18.6	457	3	US-08-834-033A-14 Sequence 14, Appl
30	241.5	18.3	323	4	US-09-439-261-17 Sequence 17, Appl
31	241.5	18.3	323	4	US-09-227-613-17 Sequence 17, Appl
32	160.5	12.2	360	4	US-09-439-261-41 Sequence 41, Appl
33	160.5	12.2	360	4	US-09-227-613-39 Sequence 39, Appl
34	160.5	12.2	444	4	US-09-439-261-11 Sequence 11, Appl
35	160.5	12.2	444	4	US-09-227-613-12 Sequence 12, Appl
36	160.5	12.2	445	4	US-09-439-261-39 Sequence 39, Appl
37	160.5	12.2	445	4	US-09-439-261-45 Sequence 45, Appl
38	158	12.0	432	4	US-09-439-261-9 Sequence 9, Appl
39	158	12.0	432	4	US-09-227-613-9 Sequence 9, Appl
40	158	12.0	465	4	US-09-439-261-40 Sequence 40, Appl
41	158	12.0	465	4	US-09-227-613-38 Sequence 38, Appl
42	156.5	11.9	444	4	US-09-048-888-3 Sequence 3, Appl
43	153.5	11.6	444	4	US-09-439-261-43 Sequence 43, Appl
44	153.5	11.6	444	4	US-09-227-613-42 Sequence 42, Appl
45	150.5	11.4	445	4	US-09-048-888-1 Sequence 1, Appl

ALIGNMENTS

```

RESULT 1
US-08-934-254-27
; Sequence 27, Application US/08934254
; Patent No. 6355861
;
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF INVENTIONS: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832XXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-934-254-27
;
; Query Match 57.2%, Score 753.5, DB 4, Length 452;
; Best Local Similarity 53.2%, Pred. No. 1e-76;
; Matches 142, Conservative 37, Mismatches 73, Indels 15, Gaps 2;
;
; QY 2 PAFSTSHRLSDHTVSAASSDYRKLPDSIALNLNFKGHTTSLSLTLTPPLSVCCVL 61
; DB 74 PLFGCYVYVLAALIGFLMIQSGWIGHDSGHYNNWLSRLRATQILSGNLIAGISIGMW 121
; QY 62 FSDSTFVYVLAALIGFLMIQSGWIGHDSGHYNNWLSRLRATQILSGNLIAGISIGMW 121

```


Db 134 ASBVSCHMLGCLLGLWLTQAAVYGHDSGHYQVMPFRGNRTQTLIAGNLTGISIAWM 193
Qy 122 KNNHNAHHIACNSLDYDPLQHMFPVAVSRFRNSITSHXGKKEFDXIAFLICYOH 181
Db 194 KNNHNAHHIACNSLDYDPLQHMFPVAVSRFRNSITSHXGKKEFDXIAFLICYOH 253
Qy 182 TFPVAVCARVNLVYQTLILLFSRXKQVDRALNMGILVFWTWL-F- 227
Db 254 TFPVAVCARVNLVYQTLILLFSRXKQVDRALNMGILVFWTWL-F- 313
Qy 228 -LALLFVPIQHIQFWLNLAEMLYXG 253
Db 314 VLISPAVTAIQHVQFTLNHFSGDTYVG 340

RESULT 2
US-08-366-779-5
Sequence 5, Application US/08366779
Patent No. 5614393
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-366-779-5

Query Match 55.4%; Score 730.5; DB 1; Length 448;
Best Local Similarity 48.9%; Pred. No. 4e-74;
Matches 11; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
Qy 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKCHTTSILSLITLTPPLSVCGV 60
Db 72 LKFFFGYLLKXSVSEVSKDVRKLVFERSKMGLYKKGHIMFATLCFIAMLPAMSVYGV 131
Qy 61 LPSDSTFVHVALSALIGFLMIQSGWIGHDSGHYVNLMSRLNRAIQLISGNILAGISIGW 120
Db 132 LFCBGLVHLFSGCLMGFLMIQSGWIGHDSGHYVNLMSRLNRAIQLISGNILAGISIGW 191

Qy 121 KNNHNAHHIACNSLDYDPLQHMFPVAVSRFRNSITSHXGKKEFDXIAFLICYOH 180
Db 192 KNNHNAHHIACNSLDYDPLQHMFPVAVSRFRNSITSHXGKKEFDXIAFLICYOH 251
Qy 181 TFPVAVCARVNLVYQTLILLFSRXKQVDRALNMGILVFWTWL-F- 226
Db 252 TFPVAVCARVNLVYQTLILLFSRXKQVDRALNMGILVFWTWL-F- 311
Qy 227 FLALLFVPIQHIQFWLNLAEMLYXG 253
Db 312 VLISPAVTAIQHVQFTLNHFSGDTYVG 339

RESULT 3
US-08-789-936-5
Sequence 5, Application US/08789936
Patent No. 5789220
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,936
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
US-08-789-936-5

Query Match 55.4%; Score 730.5; DB 1; Length 448;
Best Local Similarity 48.9%; Pred. No. 4e-74;
Matches 11; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
Qy 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKCHTTSILSLITLTPPLSVCGV 60
Db 72 LKFFFGYLLKXSVSEVSKDVRKLVFERSKMGLYKKGHIMFATLCFIAMLPAMSVYGV 131
Qy 61 LPSDSTFVHVALSALIGFLMIQSGWIGHDSGHYVNLMSRLNRAIQLISGNILAGISIGW 120
Db 132 LFCBGLVHLFSGCLMGFLMIQSGWIGHDSGHYVNLMSRLNRAIQLISGNILAGISIGW 191

Db 312 FVIALSLVTGMOQVQFSLNHFSSSVYVG 339

RESULT 6

US-08-834-033A-15
; Sequence 15, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KUNITZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300, USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-033A-15

Query Match 54.7%; Score 721.5; DB 3; Length 446;
Best Local Similarity 48.5%; Pred. No. 4.1e-73;
Matches 130; Conservative 50; Mismatches 73; Indels 15; Gaps 2;

QY 1 LPAFSTSHRLSDTVAASADYRKLFSDSLNLFNKRGHTSILSLITLPLSLVCGV 60
Db 72 LDFEFGYVIXKDVSVBVSQVYRKLVEFESKMGIDKKGIMFATLCFIMLTFAMSVYGV 131
QY 61 LPSDSTFVHVALIGFLWIGSGWIGHDSGHYVNMLSRLNRAIQILSGNLAGISIGW 120
Db 132 LFCEGVLVHFLSGCLMGFLWIGSGWIGHDSGHYVNMVSDSLNFKFMGIFANCLSGISIGW 191
QY 121 WKNNHNAHNLACNSLDYDPPDLOHMPVAVSSRFNSITSHXGKKEFDXIAFLICYQH 180
Db 192 WKNNHNAHNLACNSLDYDPPDLOHMPVAVSSRFNSITSHXGKKEFDXIAFLICYQH 251
QY 181 FTFYPMCAVARNLVYQITILLFSRKKVODRALNIMGILVFWTWF-----L 226
Db 252 WFTYPMCAVARNLVYQITILLFSRKKVODRALNIMGILVFWTWF-----L 226
QY 227 FLIALFLVP-IGHIQFWLNLAEVLXXG 253
Db 312 FVIALSLVTGMOQVQFSLNHFSSSVYVG 339

RESULT 7

US-08-834-655-7
; Sequence 7, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KUNITZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-655-7

Query Match 51.8%; Score 682.5; DB 2; Length 252;
Best Local Similarity 59.5%; Pred. No. 4.7e-69;
Matches 125; Conservative 27; Mismatches 43; Indels 15; Gaps 2;

QY 59 GVLPSDSTFVHVALIGFLWIGSGWIGHDSGHYVNMLSRLNRAIQILSGNLAGISIGW 118
Db 5 GVLACTSVPAHQIAAALLGLWIGSAYIGHDSGHYVIMENKSYNRPAAQLSGNCLTGISIGW 64
QY 119 GAKKNNHNAHNLACNSLDYDPPDLOHMPVAVSSRFNSITSHXGKKEFDXIAFLICY 178
Db 65 AAKKNNHNAHNLACNSLDYDPPDLOHMPVAVSSRFNSITSHXGKKEFDXIAFLICY 124
QY 179 QHFTFYPMCAVARNLVYQITILLFSRKKVODRALNIMGILVFWTWF-----L 232
Db 125 QHFTFYPMCAVARNLVYQITILLFSRKKVODRALNIMGILVFWTWF-----L 232
QY 233 --FV-----PIQHIQFWLNLAEVLXXG 253
Db 185 FFEVFTSFTVYALQHIQFLLNHFADVVYVG 214

RESULT 8
US-08-834-033A-8
; Sequence 8, Application US/08834033A
; Patent No. 6075183

CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-7

Query Match 51.8%; Score 682.5; DB 4; Length 252;
Best Local Similarity 59.5%; Pred. No. 4,7e-69;
Matches 125; Conservative 2; Mismatches 43; Indels 15; Gaps 2;

QY 59 GVLPSTFVHVLSAALIGFLMTQSGMIGDSGHYNVMSRLNRAIQIISGNIAGISL 118
DB 5 GVLACTSVFPAHQIAALIGLMTQSAVIGHDSGHVYMSKNRYRFAQLISGNCILGISL 64

QY 119 GWMKMNHNHHICNSLDYDPDLOHMPVFAVSSRFPSISHXYYGRXEPDIXAFICV 178
DB 65 AMKMKTHNHHILCNSLDYDPDLOHLPFPAVSTKFSLSRYDRKLTGPARPLVSY 124

QY 179 OHFTFVPMCVARVNLVLTLLFSRXKVQDRALNIMGILVFWTFLPLALL----- 232
DB 125 QHFTFVPMCVGFINLFIQTFLLFSRXKVQDRALNIMGILVFWTFLPLALL----- 184

QY 233 --FV-----PIQIQTQFWNLHAEINLYXG 253
DB 185 FFEVFTSFVTALQIQTQFWNLHAEINLYXG 214

RESULT 11
US-08-834-655-6
Sequence 6, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KUNTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-6

Query Match 22.1%; Score 291; DB 2; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLFPLS-----VCCVLPSTFVHVLSAALIGFLMTQSGMIGDSGHYNVMSRLNRAIQIISGNIAGISL 100
DB 1 VTLVTLFPAVANSIGLVGLVACPSVPHQIAAGLGLMTQSAVIGHDSGHVYMSKNRYRFAQLISGNCILGISL 104

QY 101 LNRALQILSGNLAGISIGMWMKMNHNHHIACNSLDYDPDLOHMP 145
DB 61 NNAFQLISGNCILGISIGMWMKMNHNHHIACNSLDYDPDLOHMP 104

RESULT 12
US-08-834-033A-7
Sequence 7, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUNTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716

TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-7

Query Match 22.1%; Score 291; DB 3; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLFPLS-----VCGVLFSDSTFVHLSAALIGFLMIQSGWIGHDSGHYNWLSRR 100
DB 1 VTLVTLAFPAANSLSGLVGLVACPSVXPHQIAAGLGLMIQSAVIGXDSGHYVMSNKS 60
QY 101 LNRATQILSGNLAGISIGWKKNNNAHHIACNSLDYDPDLQHP 145
DB 61 NNXPQQLLSGNCLTGI-IAMWKTHNAHHLACNSLDYGNLQHIP 104

RESULT 13
US-09-363-574-6
Sequence 6, Application US/09363574
Patent No. 6136574

GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-6

Query Match 22.1%; Score 291; DB 3; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLFPLS-----VCGVLFSDSTFVHLSAALIGFLMIQSGWIGHDSGHYNWLSRR 100
DB 1 VTLVTLAFPAANSLSGLVGLVACPSVXPHQIAAGLGLMIQSAVIGXDSGHYVMSNKS 60
QY 101 LNRATQILSGNLAGISIGWKKNNNAHHIACNSLDYDPDLQHP 145
DB 61 NNXPQQLLSGNCLTGI-IAMWKTHNAHHLACNSLDYGNLQHIP 104

RESULT 14
US-09-363-526-6
Sequence 6, Application US/09363526
Patent No. 6410288

GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-6

Query Match 22.1%; Score 291; DB 4; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLFPLS-----VCGVLFSDSTFVHLSAALIGFLMIQSGWIGHDSGHYNWLSRR 100
DB 1 VTLVTLAFPAANSLSGLVGLVACPSVXPHQIAAGLGLMIQSAVIGXDSGHYVMSNKS 60
QY 101 LNRATQILSGNLAGISIGWKKNNNAHHIACNSLDYDPDLQHP 145
DB 61 NNXPQQLLSGNCLTGI-IAMWKTHNAHHLACNSLDYGNLQHIP 104

RESULT 15
US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:

APPLICANT: KUTITZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A.
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 18.8%; Score 247.5; DB 2; Length 457;
Best Local Similarity 26.7%; Pred. No. 1.5e-19;
Matches 64; Conservative 45; Mismatches 110; Indels 21; Gaps 6;
QY 19 SSDYRKLFSLSALNLFNRKHTTSLILTLFPLS--VCGVLESDSTFVVLSPALL 76
Db 101 AAEVRKRLTFLFOSLIGYDSSKAYAFVSPNLCTWGLSTVIYAKWGOTSTLANVLSALL 160
QY 77 GFLMISGWIHDSGHYVWLSRLNRAIQILSGNLAGISIGWKKNNHNAHHIACNSLD 136
Db 161 GLFWQCGWLAHPLHGHVQDFRFGDLFGAFLGVCQCGSSSWKDKKNTHTHAAPVHG 220
QY 137 YDPLQHPVFAVSS--REFNSTSHXYGRKKEFDXIAFLICYHFTFYVWCVARVN 193
Db 221 EDDPIDTHPLTWSEHALFEMFSDVPDEBLTRMW----SRFVNLQTWFFYFPLISFARLS 275
QY 194 LVIQTILLF-----SRXKVQDRALNTMGILVFTWTFLLALLFV--PIQHIOFWL 243
Db 276 WCLQSILFLVLPNGOAHKPSGARVPISLVEQLSLAMHTWYLATM-FLFKDPVNMVLYFL 334

Search completed: January 1, 2004, 06:38:14
Job time: 9.98981 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:37:05 ; Search time 48.1975 Seconds
(without alignments)
1053.214 Million cell updates/sec

Title: US-09-857-524B-6
Perfect score: 1338
Sequence: 1 IFAFSTSHRLSDHTVSAASS.....VPIQHIFWNLHAEVLYXG 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues
Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753.5	57.2	452	US-10-029-756-27	Sequence 27, Appl
2	747.5	56.7	458	US-10-340-779A-11	Sequence 11, Appl
3	730.5	55.4	448	US-10-029-756-5	Sequence 5, Appl
4	729.5	55.3	448	US-10-340-779A-13	Sequence 13, Appl
5	352.5	26.7	366	US-10-369-493-4137	Sequence 4137, Ap
6	258.5	19.6	453	US-09-769-863-14	Sequence 14, Appl
7	258.5	19.6	453	US-10-054-534B-14	Sequence 14, Appl
8	258.5	19.6	453	US-10-431-952-14	Sequence 14, Appl
9	247.5	18.8	457	US-10-278-391-4	Sequence 4, Appl
10	247.5	18.8	457	US-10-191-513A-11	Sequence 11, Appl
11	247.5	18.8	458	US-10-191-513A-41	Sequence 41, Appl
12	241.5	18.3	323	US-10-191-513A-17	Sequence 17, Appl
13	227	17.2	459	US-09-967-477B-8	Sequence 8, Appl
14	225.5	17.1	443	US-10-340-779A-20	Sequence 20, Appl
15	224.5	17.0	473	US-10-369-493-6108	Sequence 6108, Ap

16	198.5	15.1	448	US-10-340-779A-4	Sequence 4, Appl
17	189	14.3	454	US-10-369-493-6107	Sequence 6107, Ap
18	176	13.4	365	US-10-156-761-9835	Sequence 9835, Ap
19	175	13.3	353	US-10-156-761-9130	Sequence 9130, Ap
20	160.5	12.2	360	US-10-191-513A-39	Sequence 39, Appl
21	160.5	12.2	444	US-10-191-513A-12	Sequence 12, Appl
22	158	12.0	432	US-10-191-513A-9	Sequence 9, Appl
23	158	12.0	465	US-10-191-513A-38	Sequence 38, Appl
24	157	11.9	439	US-09-769-863-29	Sequence 29, Appl
25	157	11.9	439	US-10-054-534B-29	Sequence 29, Appl
26	157	11.9	439	US-10-431-952-29	Sequence 29, Appl
27	156.5	11.9	444	US-10-262-617-3	Sequence 3, Appl
28	154	11.7	439	US-10-054-534B-31	Sequence 31, Appl
29	153.5	11.6	444	US-10-191-513A-42	Sequence 42, Appl
30	150.5	11.4	445	US-10-262-617-1	Sequence 1, Appl
31	147	11.2	430	US-10-120-637A-69	Sequence 69, Appl
32	147	11.2	433	US-10-120-637A-55	Sequence 55, Appl
33	144	10.9	442	US-10-054-534B-35	Sequence 35, Appl
34	143	10.8	456	US-10-054-534B-33	Sequence 33, Appl
35	141.5	10.7	182	US-10-191-513A-20	Sequence 20, Appl
36	141	10.7	356	US-10-191-513A-18	Sequence 18, Appl
37	140	10.6	347	US-10-191-513A-40	Sequence 40, Appl
38	139.5	10.6	439	US-09-967-477B-4	Sequence 4, Appl
39	138	10.5	219	US-10-191-513A-19	Sequence 19, Appl
40	138	10.5	287	US-10-191-513A-14	Sequence 14, Appl
41	138	10.5	288	US-10-191-513A-15	Sequence 15, Appl
42	137.5	10.4	266	US-10-102-806-650	Sequence 650, App
43	136	10.3	261	US-10-104-047-2586	Sequence 2586, Ap
44	114	8.6	359	US-10-340-779A-12	Sequence 12, Appl
45	114	8.6	359	US-10-369-493-2766	Sequence 2766, Ap

ALIGNMENTS

RESULT 1
US-10-029-756-27
Sequence 27, Application US/10029756
Publication No. US20020108147A1
GENERAL INFORMATION:
Applicant: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029, 756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934, 254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19, 827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-10-029-756-27

Query Match 57.2%; Score 753.5; DB 14; Length 452;
 Best Local Similarity 53.2%; Pred. No. 2.8e-70;
 Matches 142; Conservative 37; Mismatches 73; Indels 15; Gaps 2;

QY 2 PAFSTSHRLSDHTVSAASDYRKLFSDSLALNLFNRKHTTSLILSLTLFPLSVCL 61
 DB 74 PLFTGYLLKDFEYSEISKYRRLNEMSRSGIFEEKGHIMTFVGVAVMAIYGV 133
 QY 62 FDSSTFVHLSALIGLWIOSGMIGDSGHYVNLRLNRAIQILSGNIIAGISIGW 121
 DB 134 ASSEVGHMLCGALLGLMIAVYVGHDSGHYVMPTRGYNRTQLIAGNIIAGISIAW 193
 QY 122 KMNHNAAHIIACNSLDYDPLQHMVPFAVSSRPFNSITSHXGRKXEPDIXAFIQCQHF 181
 DB 194 KTHNAAHIIACNSLDYDPLQHIFPVAVSTRLNSTSVYGYLKFDEVARFLVSYQHW 253
 QY 182 TFPVNCVARNLYQTILLFSRKKVQDRALNIMGLVFWTF-LF----- 227
 DB 254 TYPVNI FGRVNLFIQTFLLLTRRDVDRALMLGIAVFWTFPLFVSCLPNMPERFGF 313
 QY 228 -LLALLFVPIQHIOFWNLNLAENLYXG 253
 DB 314 VLISFAVTALQHVQFTLNHPSGDTYVG 340

RESULT 2

US-10-340-779a-11
 ; Sequence 11, Application US/10340779A
 ; Publication No.: US20030152983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Napier, Johnathan A.
 ; APPLICANT: Michaelson, Louise
 ; APPLICANT: Stobart, Keith
 ; TITLE OF INVENTION: Desaturase
 ; FILE REFERENCE: 005407.00004
 ; CURRENT APPLICATION NUMBER: US/10/340, 779A
 ; PRIOR FILING DATE: 2003-03-24
 ; PRIOR APPLICATION NUMBER: US 09/582, 034
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: PCT/GB98/03895
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: UK 9814034.6
 ; PRIOR FILING DATE: 1998-06-29
 ; PRIOR APPLICATION NUMBER: UK 9727256.1
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 458
 ; TYPE: PRT
 ; ORGANISM: Helianthus annuus
 ; US-10-340-779a-11

Query Match 56.7%; Score 747.5; DB 12; Length 458;
 Best Local Similarity 52.8%; Pred. No. 1.2e-69;
 Matches 140; Conservative 40; Mismatches 66; Indels 19; Gaps 4;

QY 6 TSHRLSDHTVSAASDYRKLFSDSLALNLFNRKHTTSLILSLTLFPLSVCL 63
 DB 87 TGYHLNDYQSDISRDYRKLASEPAKGFEEKGH--GVYSLCFVSLISACVGYLV 144
 QY 64 DSFFVHLSALIGLWIOSGMIGDSGHYVNLRLNRAIQILSGNIIAGISIGW 123
 DB 145 GSFVHMLSGAILGLMIAVYVGHDSGHYVMPTRGYNRTQLIAGNIIAGISIAW 204
 QY 124 KMNHNAAHIIACNSLDYDPLQHMVPFAVSSRPFNSITSHXGRKXEPDIXAFIQCQHF 183

DB 205 THNAAHIIACNSLDYDPLQHIFPMLAVSSKLFNSITSVFGRQLTFPDLARFVSQHYLY 264
 QY 184 YPNCVARNLYQTILLFSRKKVQDRALNIMGLVFWTFPLFALLL-----FV- 234
 DB 265 YPIMCVARNLYQTILLISKRKIPDRGLNITGLIFWTFPLVSRLENMPERVAFL 324
 QY 235 -----PIQHIOFWNLNLAENLYXG 253
 DB 325 VSFCTVGIQHIOFTLNHPSGDTYVG 349

RESULT 3

US-10-029-756-5
 ; Sequence 5, Application US/10029756
 ; Publication No.: US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/10/029, 756
 ; APPLICATION NUMBER: US/10/029, 756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-10-029-756-5

Query Match 55.4%; Score 730.5; DB 14; Length 448;
 Best Local Similarity 48.9%; Pred. No. 6.9e-68;
 Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;

QY 1 LPASTSHRLSDHTVSAASDYRKLFSDSLALNLFNRKHTTSLILSLTLFPLSVCL 60
 DB 72 LDKFTGYLLKDFEYSEISKYRRLNEMSRSGIFEEKGHIMTFVGVAVMAIYGV 131
 QY 61 LFSSTFVHLSALIGLWIOSGMIGDSGHYVNLRLNRAIQILSGNIIAGISIGW 120
 DB 132 LFCEGVVHLSALIGLWIOSGMIGDSGHYVNLRLNRAIQILSGNIIAGISIGW 191
 QY 121 KMNHNAAHIIACNSLDYDPLQHMVPFAVSSRPFNSITSHXGRKXEPDIXAFIQCQHF 180
 DB 192 KMNHNAAHIIACNSLDYDPLQYIPFLVSSKFGSLTSHFEKRLTFPDLISRFVSYQH 251

Qy 118 IGMWKNHNAHIAAC-----SLDDPDLOHMPFAVSSRFFNSITSHYGRKKKEFX 170
 Db 201 VQWKKKNTHTAIPLHATPEIAFHGDDPDIDIMPLASLK-----MAGHAVD-----SP 251
 Qy 171 IAXFLICYOHFFPYPMCAVNVLYQITILLF-----SRKKVODRALINIGILVFWT 223
 Db 252 VGLFFMRQAYLYPFLILFARISWVIOQAMAFYVNGPGCTDVKQYPLLEBRAGLLIYVG 311
 Qy 224 WFLFL-----ALLFV 234
 Db 312 WNLGLVYAAANMSLQAAAFLEFV 333

RESULT 7

US-10-054-534B-14
 ; Sequence 14, Application US/10054534B
 ; Publication No. US20030167525A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer M.
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763 US, P1
 ; CURRENT APPLICATION NUMBER: US/10/054,534B
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: US 09/769,863
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolegnia diclina
 ; US-10-054-534B-14

Query Match 19.6%; Score 258.5; DB 12; Length 453;
 Best Local Similarity 26.3%; Pred. No. 1.5e-18;
 Matches 69; Conservative 52; Mismatches 98; Indels 43; Gaps 9;

Qy 3 AFSTSHRLSDHTVSAAS---SDYRKLFSDLSALNLF--NRKGHTTSILSLITLFPPLSV 57
 Db 85 AVDTG--ISDEVKKSQSDPIASRYKRLVKKLGYDSKLYLYKCASTLSIALVSAAI 142
 Qy 58 CGVLFSDDSTFVHLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIOILSGNIIAGIS 117
 Db 143 C--LHFDSTAMTMVAAILGLFYQCGWLAHDFLHHQVEFNHLFGDLVGVMTGNLMQGPS 200
 Qy 118 IGMWKNHNAHIAAC-----SLDDPDLOHMPFAVSSRFFNSITSHYGRKKKEFX 170
 Db 201 VQWKKKNTHTAIPLHATPEIAFHGDDPDIDIMPLASLK-----MAGHAVD-----SP 251
 Qy 171 IAXFLICYOHFFPYPMCAVNVLYQITILLF-----SRKKVODRALINIGILVFWT 223
 Db 252 VGLFFMRQAYLYPFLILFARISWVIOQAMAFYVNGPGCTDVKQYPLLEBRAGLLIYVG 311
 Qy 224 WFLFL-----ALLFV 234
 Db 312 WNLGLVYAAANMSLQAAAFLEFV 333

RESULT 8

US-10-431-952-14
 ; Sequence 14, Application US/10431952
 ; Publication No. US20030190733A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer

; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763 US, O1
 ; CURRENT APPLICATION NUMBER: US/10/431,952
 ; CURRENT FILING DATE: 2003-05-08
 ; PRIOR APPLICATION NUMBER: US/09/769,863
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolegnia diclina
 ; US-10-431-952-14

Query Match 19.6%; Score 258.5; DB 12; Length 453;
 Best Local Similarity 26.3%; Pred. No. 1.5e-18;
 Matches 69; Conservative 52; Mismatches 98; Indels 43; Gaps 9;

Qy 3 AFSTSHRLSDHTVSAAS---SDYRKLFSDLSALNLF--NRKGHTTSILSLITLFPPLSV 57
 Db 85 AVDTG--ISDEVKKSQSDPIASRYKRLVKKLGYDSKLYLYKCASTLSIALVSAAI 142
 Qy 58 CGVLFSDDSTFVHLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIOILSGNIIAGIS 117
 Db 143 C--LHFDSTAMTMVAAILGLFYQCGWLAHDFLHHQVEFNHLFGDLVGVMTGNLMQGPS 200
 Qy 118 IGMWKNHNAHIAAC-----SLDDPDLOHMPFAVSSRFFNSITSHYGRKKKEFX 170
 Db 201 VQWKKKNTHTAIPLHATPEIAFHGDDPDIDIMPLASLK-----MAGHAVD-----SP 251
 Qy 171 IAXFLICYOHFFPYPMCAVNVLYQITILLF-----SRKKVODRALINIGILVFWT 223
 Db 252 VGLFFMRQAYLYPFLILFARISWVIOQAMAFYVNGPGCTDVKQYPLLEBRAGLLIYVG 311
 Qy 224 WFLFL-----ALLFV 234
 Db 312 WNLGLVYAAANMSLQAAAFLEFV 333

RESULT 9

US-10-278-391-4
 ; Sequence 4, Application US/10278391
 ; Publication No. US20030159164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOPCHIK, JOHN J.
 ; APPLICANT: KELLER, BRUCE
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: KIRCHNER, STEPHEN J.
 ; APPLICANT: MUKERJI, PRADIP
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
 ; PRODUCTS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MEDLEN & CARROLL, LLP
 ; STREET: 220 MONTGOMERY STREET, SUITE 2200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/278,391
 ; FILING DATE: 23-Oct-2002
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/087,578
 ; FILING DATE: 29-MAY-1998

ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-03348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
SPRANDEDNESS: NO. US20030159164A1 Relevant
TOPOLOGY: NO. US20030159164A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-278-391-4

SEQUENCE DESCRIPTION:	SEQ ID NO: 4:
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Query Match	18.8%	Score 247.5;	DB 12;	Length 457;
Best Local Similarity	26.7%	Pred. No. 2.1e-17;		
Matches 64;	Conservative 45;	Mismatches 110;	Indels 21;	Gaps 6

QY 1 SSSRYLTFDLSALNLFNNKHTTSLILSLITLTPPLS -VCGVLPDSPTFVHTLSALI 76
Db 101 AAETVKRLTFLFOSLGYYDSKAYVAFKSFNNCTIGLSTVIVAKGQSTSLANLSTALL 160
QY 77 GFLMTQSGVIGHDSGHYVNLRSRLNRAIQLISGNIILGISIGVMKNHNAHIACSLD 136
Db 161 GLFMQCGGLAHDFLHHQVFDPRFMGDLFGALFSGVCCGFSSSMKKCKAHTNHAAAPVHG 220
QY 137 YPBDLOHMFVFAVS--RFNFSITSHXGGRKCEFDXIAKFLICYQHETFYVPMCVARN 193
Db 221 EDPDIDITHFLITWSEHALEMFSADVDEBELTRKM-----SRMVLNQTFEYFPIILSFARLS 275
QY 194 LVYQTLILF-----SRKKVDORALNMGILVFMTPLEPLALLFV--PIQHIOFWL 243
Db 276 WCLOSILFLFVNGQAHKPSGARVPSLVEQSLAHNMHWIYATL-FLFIKDPVNMVLYFL 334

RESULT 10
US-10-191

;; Sequence 11, Application US/10191513A
; Publication No. US20030104596A1
: GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pardeep
 APPLICANT: Leonard, Amanda E.
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Tapaa, Das
 TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/191,513A

; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613

PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US98/07422

PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: USC 08/0932 610

PRIOR FILING DATE: 1997-04-11

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; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4
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; SEQ ID NO 11
; LENGTH: 458

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TYPE: PRT
ORGANISM: Homo sapiens

CONSTRUCTION: MONO BAYLENS
FEATURE:
WAVE/KRY WATERWAY

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; NAME/KEY: VARIANT
; LOCATION: (458) ... (458)

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OTHER INFORMATION: Xaa = Unknown or other amino acid
US-10-191-513A-11

Query Match	18.8%	Score 247.5;	DB 15;	Length 458;
Best Local Similarity	26.7%	Pred. NO. 2.1e-17;		
Matches 64;	Conservative 45;	Mismatches 110;	Indels 21;	Gaps 6

[illegible][illegible]

RESULT 11
US-10-191-513A-41

Publication No. US20030104596A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Paridip
 APPLICANT: Leonard, Amanda E.
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Tapas, Das
 TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 FILE REFERENCE: 6295.US.D3
 CURRENT APPLICATION NUMBER: US/10/191,513A
 CURRENT FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: US 09/227,613
 PRIOR FILING DATE: 1999-01-08
 PRIOR APPLICATION NUMBER: PCT/US98/07422
 PRIOR FILING DATE: 1998-04-10

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; NUMBER OF SEQ ID NOS: 54
;
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 41
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; LENGTH: 458
; TVPR: DPT
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; ORGANISM: Homo sapiens
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; FEATURE:
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; NAME/KEY: VARIANT
; LOCATION: (458) .. (458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
;
; OS=10-191-513A-41

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Query Match 18.8%; Score 247.5; DB 15; Length 458;

Best Local Similarity 26.7%; Pred. No. 2,1e-17;
Matches 64; Conservative 45; Mismatches 110; Indels 21; Gaps 6

19 SSDYRKLFSDISALNLENRKGHMTTSLTTLPLIS--VCGYLFSDSTEVHVSALIT 76

101 ::||| : :| :||| : || :|||:

DD 101 AAEVKRKLIFVUSDOIUSSKATIAFNVSFNLCIMGSIIVIVANMGZISIDWVNSPNUU 100

77 GFLWQSGWIGHDSGHYNVWMLSRRLNRAIQILSGNLAGISIGWKKMNNHAHLIACNSLD 136

Db 161 GTFWQCGSLANDFLHHQVFQDRPWGDLFGAFLGGVCQGFSSSWKKDKNTTHAAPNVHG 220

QY 137 YDPLQIMPVFAVSS---RPFNSITSHXGKKEFDXIAFLICYQHFTFYPMCVARVN 1933

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db      221 EDPDIDTHPLLTWSEHALEMFSDVDEELTRMM-----SRFMVLNQITWFYFPILSPARLS 275
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194 LYLOIILFF-----SRXKQDRALNIMGILVFPTWPELILALLFV--PIQHIOFWL 243

276 WCLOSILFVLPNGOAHKPSGARVYISLVEOLSLMEHWYIATM-FLFTKDPVNMILVYEL 334

RESULT 12
US-10-191-513A-17

Db 252 QHLYFTAMLPMLRFSWTGSGVQWFKENQNEYKYQNNAFWEQATIVG---HWAWVFYQL 308
QY 230 ALFLV-PIQHIOFWLNHLAENL 250
Db 309 FLPLPTWPLRVAVYFIISQMGGL 330

RESULT 15

US-10-369-493-6108
; Sequence 6108, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6108
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6108

Query Match 17.0%; Score 224.5; DB 12; Length 473;

Best local Similarity 26.7%; Pred. No. 5.5e-15;
Matches 70; Conservative 36; Mismatches 115; Indels 41; Gaps 8;

QY 10 LSDHTVSAAS-----SDYRKLFSDSLALNLFNRKHTTSLLSLILTL-----PPLSYC 58
Db 119 VSAVDVSAQEKWVESFEKLRLQKLDHDDLM--KANETVFLPKAISTLSIMAFAYLQYL 176
QY 59 GVLFSDSTFVHVLSALLIGFLMIQSGWIGHSCHYVNLRSRLNRAIQILSGNLAGIST 118
Db 177 G-----WYITSACLALAMQOFGWLTPECHQOPTKNRPLNDTISLFFGNFLOGFSR 228
QY 119 GWWKKNHNAHHCNSLDYDPLQHMVPFAVSSRFNSITSHXGGRKXEFDXIAXFLICY 178
Db 229 DMWKDGNHTTHAATNVIHDGDIIDLAFLFAF-----IPGDLCKTKASFKAILKIVPY 281
QY 179 QHFTFYVAVCVARVNLVLTITLLFSRXKVQDRA-----LNIINGILVFWTWFLFL 229
Db 282 QHLYFTAMLPMLRFSWTGSGVQWFKENQNEYKYQNNAFWEQATIVG---HWAWVFYQL 338
QY 230 ALFLV-PIQHIOFWLNHLAENL 250
Db 339 FLPLPTWPLRVAVYFIISQMGGL 360

Search completed: January 1, 2004, 06:58:36
Job time : 49.1975 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:39:42 ; Search time 4853.01 Seconds
(without alignments)
16303.117 Million cell updates/sec

Title: US-09-857-524B-7

Perfect score: 1934

Sequence: 1 gcacgcacacacacagtaaaaa.....aaaaaaaaaaaaaaaaaaaaa 1934

Scoring table: IDENTITY NUC

Gapop 10.0, Gapept 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBankl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sbs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sbs:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pin:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_hgo_hum:*

40: em_hgo_mus:*

41: em_hgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	35.7	1594	6 AX007239	AX007239 Sequence
2	690	35.7	1610	8 BNAJ4160	AX224160 Brassica
3	677.2	35.0	1869	8 AF133728	AF133728 Borago of
4	672.8	34.8	110149	8 AC005397	AC005397 Arabidops
5	643.4	33.3	1856	8 AF005096	AF005096 Ricinus c
6	642.8	33.2	1591	8 HACTB5RN	X87143 Helianthus
7	642.8	33.2	1606	6 AX007273	AX007273 Sequence
8	642.6	33.2	1491	8 BT003379	BT003379 Arabidops
9	642.6	33.2	1652	8 AY087345	AY087345 Arabidops
10	642.6	33.2	1678	6 AX007241	AX007241 Sequence
11	642.6	33.2	1704	8 AF428420	AF428420 Arabidops
12	642.6	33.2	1705	8 ATAJ4161	AJ224161 Arabidops
13	642.6	33.2	1743	8 BT000442	BT000442 Arabidops
14	642.6	33.2	95993	8 AT2A19	AL122962 Arabidops
15	639.2	33.1	1350	6 AX505863	AX505863 Sequence
16	622.6	32.2	1478	8 AY055117	AY055117 Echium ge
17	618.4	32.0	1684	6 AR076814	AR076814 Sequence
18	618.4	32.0	1684	6 AR084177	AR084177 Sequence
19	618.4	32.0	1684	6 BD062571	BD062571 A sunflow
20	618.4	32.0	1684	6 BD070919	BD070919 An oleosl
21	618.4	32.0	1685	6 AR020904	AR020904 Sequence
22	618.4	32.0	1685	6 AR200408	AR200408 Sequence
23	618.4	32.0	1685	6 I38430	I38430 Sequence 4
24	618.4	32.0	1685	6 AF007561	AF007561 Borago of
25	616.8	31.9	1687	8 BOUT9010	U79010 Borago offi
26	616.2	31.9	1450	8 AY055118	AY055118 Echium pl
27	604.4	31.3	1341	8 AF406816	AF406816 Aquilegia
28	603.6	31.2	1633	8 AF001394	AF001394 Arabidops
29	600.8	31.1	1347	8 AY131238	AY131238 Argania b
30	567.6	29.3	1385	8 AY234126	AY234126 Primula v
31	559	28.9	1681	8 AY234124	AY234124 Primula f
32	555	28.7	1702	6 AR200409	AR200409 Sequence
33	524.4	27.1	1410	8 AY234125	AY234125 Primula f
34	502	26.0	1788	8 AF031194	AF031194 Trilium
35	487.6	25.2	96312	2 AP005554	AP005554 Oryza sat
36	399.4	20.7	1618	8 AY234127	AY234127 Primula v
37	191	9.9	535	6 AX058838	AX058838 Sequence
38	153	7.9	291	6 AR246607	AR246607 Sequence
39	138.8	7.2	1572	8 AB090360	AB090360 Mucor cfr
40	138.8	7.2	1572	8 AF290983	AF290983 Mucor rou
41	138.8	7.2	1572	8 AF296076	AF296076 Mucor rou
42	121.4	6.3	322194	8 CNG09845	EX088700 DNA cent
43	112	5.8	266	6 AR247897	AR247897 Sequence
44	77.4	4.0	1467	6 AX058832	AX058832 Sequence
45	77.4	4.0	2040	6 AX058830	AX058830 Sequence

ALIGNMENTS

RESULT 1

AX007239 1594 bp DNA 1linear PAT 06-SRP-2000

LOCUS AX007239

DEFINITION Sequence 1 from Patent WO0000593.

ACCESSION AX007239

VERSION AX007239.1 GI:9995105

KEYWORDS

SOURCE

ORGANISM

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS 1

TITLE Zaehringer,U., Heinz,B., Schmidt,H. and Sperling,P.

Sphingolipid-desaturase

Pred. No. is the number of results predicted by chance to have a

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 /mol_type="mRNA"
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 /issue_type="ripening embryos"
 /dev_stage="18 to 35 DAF"
 gene 1..1610
 /gene="sld1"
 5' UTR 1..50
 /gene="sld1"
 CDS 51..1400
 /gene="sld1"
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 /evidence=experimental
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 DSGHNVSTKPCNKLVLGNCIGISIAWMKTHNHHISCNLDHDPLOHPIV
 LVSNEFESKTSRPFYGRKLTDPRLARPLISYOHMFYPMCVGRINLFIOTLLIFS
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 3' UTR
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 ORIGIN

Query Match 35.7%; Score 690; DB 8; Length 1610;
 Best Local Similarity 69.7%; Pred. No. 1,5e-140;
 Matches 933; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

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 61 AGCAAGAAGAGATTCAATTAACAGGATGATCTGAAAAACACAAACCGGAGATT 120
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 378 TATGATCTCAATTCAAGTAAGTGTATCAATCTCAATTGGGTCAAGAGACACCTG 437
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 121 TATGATCTCAATCAAGGAAAGTCTACGACGTCTCCACTGGGTCAATCCCATCCG 180
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 438 GTGATGATGTTCCAACTCTCAAACTTGCTGAGCCAGAGATGCACTGATGATCATAGCAT 497
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 181 GAGCGAAGACAGGATCTTAACCTCGCGCGTCAAAACGTCACCGCGCTTATCGCTT 240
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 498 ACCATCTGGACAGCATGCTCACACCTTGAAAAATTTCTTCACTGCTACACCATCAGTG 557
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 558 ACTTCAAGTCTCTGAGTGTCCAAAGACTTACGAAAGCTGTGATCTGATTTCTCAAAAT 617
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 301 ACCACCAAGTCTCGACGTGTCCGTCGACCTACCGTGTAAAGCGGAGATTTTCCAAAC 360
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 618 TGGGCTTTTTCACAAAGGAGCATGCTCACTTCATGACCCCTGATCTGTGCTGTTA 677
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 361 GCGGACTCTTCATAAAAAAGTCACTGACTCTTTTACAGCTCAAGTGTGCTGCTGCA 420
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 678 TGTTCCTCATTTGACTCTATGTTGTTCTGAGTGCACTAGTGTGAGGCTCATTTGGGTT 737
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 738 CAGGATGCTCTTGAAGGTTGCTTGTGATGTAAGTGTCTATGTGGCCATGATTTGCGCC 797
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 481 CCGCCCTCTTGGCGCTTCTCTGATATACAGCCCTTACGAGGACATGACTCTGCTG 540
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 798 ACTATGTGTTATGACAAACCATGATGTTTCAACAAGGTGACAGATCTCTCTGGGAAC 857
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 Qy 1218 TGCCTAATTTGGCTGAGAGAGTTATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1277
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 Qy 1578 CTGCTGCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1637
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 Db 1321 AAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
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 Qy 1638 CTGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1697
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 Db 1381 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1398
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RESULT 3
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 LOCUS AF133728
 DEFINITION Borage officinalis delta 8-sphingolipid desaturase (sld1) mRNA,
 complete cds.
 ACCESSION AF133728
 VERSION AF133728.1 GI:12002281
 KEYWORDS
 SOURCE Borage officinalis
 ORGANISM Borage officinalis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamids; Boraginaceae; Borage.
 REFERENCE 1 (bases 1 to 1869)

AUTHORS Libisch, B., Michaelson, L. V., Lewis, M. J., Shewry, P. R. and Napier, J. A.
 TITLE Chimeras of Delta6-fatty acid and Delta8-sphingolipid desaturases
 JOURNAL Biochem. Biophys. Res. Commun. 279 (3), 779-785 (2000)
 MEDLINE 21092516
 PUBMED 11162428
 2 (bases 1 to 1869)
 Sperleng, P., Libisch, B., Zahringer, U., Napier, J. A. and Heinz, E.
 TITLE Functional identification of a delta8-sphingolipid desaturase from Borago officinalis
 JOURNAL Arch. Biochem. Biophys. 388 (2), 293-298 (2001)
 MEDLINE 21260464
 PUBMED 11368168
 3 (bases 1 to 1869)
 Libisch, B., Sperleng, P., Heinz, E., Sayanova, O. and Napier, J. A.
 TITLE Direct Submission
 SUBMITTED (08-MAR-1999) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK
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[illegible]

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DEFINITION AF005096
ACCESSION AF005096
VERSION AF005096.1 GI:4101625
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SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
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1 (bases 1 to 1856)
Sayanova, O., Smith, M.A., Lapinskas, P., Stebarta, A.K., Dobson, G., Christie, W.W., Shewry, P.R. and Napier, J.A.
Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco
Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
97268723
9108131
2 (bases 1 to 1856)
Napier, J.A. and Shewry, P.R.
Direct Submission
Submitted (22-MAY-1997) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK
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BASE COUNT 493 a 326 c 388 g 648 t 1 others

ORIGIN

Query Match 33.3%; Score 643.4; DB 8; Length 1856;
Best Local Similarity 68.2%; Pred. No. 2,4e-130;
Matches 909; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

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 Asteridae; campanulide; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.

REFERENCE
 1 Zaehring, U., Heinz, E., Schmidt, H. and Sperling, P.
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 Patent: WO 0000593-A 35 06-JAN-2000;
 ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);
 SPERLING PETRA (DE); GVS GES FUER ERWERB UND VERMER (DE)
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TITLE Full-length messenger RNA sequences greatly improve genome annotation
 JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)
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 TITLE Full-length cDNA from Arabidopsis thaliana
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1652)
 AUTHORS Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R. and Feldmann K.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the w or lwer ecototypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genes carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

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Best Local Similarity 66.0%; Pred. No. 3.6e-130;
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 1 (bases 1 to 1704)
 REFERENCE
 AUTHORS
 Cheuk, R., Chen, H., Kim, C.-J., Koesema, E., Meyers, M.C., Banh, J.,
 Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
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 Davis, R.W., Theologis, A. and Ecker, J.R.
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 Unpublished
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 Cheuk, R., Chen, H., Kim, C.-J., Koesema, E., Meyers, M.C., Banh, J.,
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 Unpublished
 2 (bases 1 to 1704)
 TITLE
 JOURNAL
 Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory
 (SIGAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 COMMENT
 The Salk, Stanford, PGEC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H.,
 Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J., Bowser, L.,
 Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G.,
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 Davis, R.W., Theologis, A., and Ecker, J.R.
 Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
 this work. Shinnozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
 contributed equally to this work as PIs.
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VERSION
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ORGANISM Arabidopsis thaliana.
REFERENCE 1
AUTHORS De Haan, M., Maarse, A.C., Grievell, L.A., Mewes, H.W., Lemcke, K.,
Mayer, K.F.X., Quetier, F. and Salanoubat, M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 95993)
AUTHORS EU Arabidopsis sequencing project.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
Coordinator: Marcel Salanoubat and Francis Quetier, Groupe
d'Interet Public, Centre National de Sequencage - GENOSCOPE, 2 rue
Gaston Cremieux, BP191, 91006 Evry Cedex, France;
http://www.genoscope.cns.fr
COMMENT Information on performance of analysis and a more detailed
information of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.

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VERSION	AX505863.1	GI:23387100	

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<i>Arabidopsis thaliana</i>	
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; <i>Arabidopsis</i> .	

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Harper, J. P., Kreps, J., Wang X. and Zhu, T.	Stress-regulated genes of plants, transgenic plants containing same, and methods of use	Patent: WO 021655-A 558 28-FEB-2002; The Scripps Research Institute (US) ; Syngenta Participations AG (CH)

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Db	963	GGCCCTTCAACACACTTCAATTCACGCTTAA CAAATTCGCTGTATGTCTACGTTGCTTC	1022
OY	1330	ACCGAGTGGGAATACGTGTTTGAAGACAGACAAGTGTATCATTTGATATCTCTGTGTC	1388
Db	1023	ACCCACCGGTATGCACTGTGTTCGAAAGCAAGCGCGGGAACATTCATCTCTTGTAG	1082
OY	1390	CTCTTCATGATTTGTTTTTTCGCTGTGCTGCAATTTTCAGCTTTAGCATATTTGTTTTC	1448
Db	1083	ATCATATACATGATTTGTGTTCTTTGGTGTATTAACAATTTTCAGCTTTAGCATCATTTGTTCC	1142
OY	1450	AAGGCTACCTGAGTCCAAATTGAGAAAGATTTGCGCTTGTGTAGTACCTTTTGCAGAA	1509
Db	1143	TCGCTTACCTTCGTGTGCATCTCCGGAAAGTTTCTCCGGTGGTTCAAGAGCTTTTCCAGAA	1202
OY	1510	GCATTAATTTGCTTATAGAGCTTGTCAATTTTGGGAAGCCAAATCAGTGTGACAAATTAAGAC	1565
Db	1203	GCATTAATCTTCGTATAGAGATATGTGTGTTTGAAGCAAAATGTGTGACATTAACAC	1262
OY	1570	CCTCAGAGCTGTCCCTTCAAGCTGATAGGAACTTAA CAAACCTTCCCTCTAAGATTTGTT	1629
Db	1263	TTTGAATACAGACGCTTATCAAGCTTAAGACGTGTGCTATATCCGTTGTTAAGAACTTGT	1322
OY	1630	GTGGGAAGCTGTATATACCATGGCTGA	1657

Fri Jan 2 09:49:10 2004

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Page 20

Db 1323 TTGGGAGCTTTGAATACTCATGGCTAA 1350

Search completed: December 31, 2003, 21:04:31
Job time : 4857.01 secs

XX WPI: 2000-412336/35.
 DR P-PSDB: AAY71554.
 XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 46; 57pp; English.
 XX The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone se1.PK0017.D4:fls isolated from soybean seedling cDNA
 CC library, se1. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SO Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;
 Query Match 100.0%; Score 1934; DB 21; Length 1934;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1934; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 GTGGCTCATTTGGGTTCAAGCATGCTTAGGGTCTTGTGATGCAAGTCTTATGT 780
 Db 721 GTGGCTCATTTGGGTTCAAGCATGCTTAGGGTCTTGTGATGCAAGTCTTATGT 780
 QY 781 GGGCCATGATTTGGCCACTATGTGTTATGACCAACATGTTTCAACAGTTTGACA 840
 Db 781 GGGCCATGATTTGGCCACTATGTGTTATGACCAACATGTTTCAACAGTTTGACA 840
 QY 841 GATCTCTGTTGGGAACGCTTGAACGGGATPAAGATTTGTTGGGAAGTACTCAAA 900
 Db 841 GATCTCTGTTGGGAACGCTTGAACGGGATPAAGATTTGTTGGGAAGTACTCAAA 900
 QY 901 TGCTACCACTTGCCTGCAACAGCTTGAACCATAGACCTGATGCAAGCATCCGGT 960
 Db 901 TGCTACCACTTGCCTGCAACAGCTTGAACCATAGACCTGATGCAAGCATCCGGT 960
 QY 961 CTTTGACGTTTCTGCGGGTCTTCAATTCATACCTCTCATTTCTATGGGAGAAATT 1020
 Db 961 CTTTGACGTTTCTGCGGGTCTTCAATTCATACCTCTCATTTCTATGGGAGAAATT 1020
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 Db 1021 GGAGTTTGAATTCATGCTAGTGGTCTTGATCTGCTACAGACCTTACTTTTACC 1080
 QY 1081 AATGTGTGTCAGAGGTCAACTGTATCTGACACAATTCGCTATGTTTTCGAGCG 1140
 Db 1081 AATGTGTGTCAGAGGTCAACTGTATCTGACACAATTCGCTATGTTTTCGAGCG 1140
 QY 1141 AAAAGTGAGATAGAGCTTGAACATPAATGGGATCTTGTGTTTGAAGTTGCC 1200
 Db 1141 AAAAGTGAGATAGAGCTTGAACATPAATGGGATCTTGTGTTTGAAGTTGCC 1200
 QY 1201 TCTTTTGTGCTGCTGCTGCAATTTGGCCGAGAGGTTATGTTGCTTGTGAGCTT 1260
 Db 1201 TCTTTTGTGCTGCTGCTGCAATTTGGCCGAGAGGTTATGTTGCTTGTGAGCTT 1260
 QY 1261 TGCTGTGTGTCATCCAGACATTCAGTTCTGTTGAATCATTGCTGCAAAATGATA 1320
 Db 1261 TGCTGTGTGTCATCCAGACATTCAGTTCTGTTGAATCATTGCTGCAAAATGATA 1320
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 Db 1321 TGTGGGCGACGAGTGGAAATGACTGGTTTGAAGACAGACAGATGTGATATAT 1380
 QY 1381 CTCTTGCCCTTCGATGATGATGTTTTCGGGCTGAGTTTCAAGCTTGAGCATCA 1440
 Db 1381 CTCTTGCCCTTCGATGATGATGTTTTCGGGCTGAGTTTCAAGCTTGAGCATCA 1440
 QY 1441 TTTGTTTCAAGGCTACCTCGGTGCCAATTGAGGAATTTGCGCTTGTAGTGAACCT 1500
 Db 1441 TTTGTTTCAAGGCTACCTCGGTGCCAATTGAGGAATTTGCGCTTGTAGTGAACCT 1500
 QY 1501 TTGCAAGAGATPAATTTGCTTATPAGAGCTTGTCAATTTGGAGGCAATCAGTGAC 1560
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 Db 1561 AATTAGACCTCTCAGACTGTGCTGCTTCAAGCTTAAAGGACTTAACAAACCTGCCCC 1620
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 Db 1621 GAATTTGTGTTGGGAAGCTGTTAATACCATGCTGAGGCAATTTGAGAGTTT 1680
 QY 1681 AGAATTTGTCAAGGCTTTTGTGTTTCTTTTAAAGAAAAAATTTCTCA 1740
 Db 1681 AGAATTTGTCAAGGCTTTTGTGTTTCTTTTAAAGAAAAAATTTCTCA 1740
 QY 1741 TTTGATTTTGTAGCCCTTTCAGATTTGGGCTTGAATTTAATCTTTTGTGAG 1800
 Db 1741 TTTGATTTTGTAGCCCTTTCAGATTTGGGCTTGAATTTAATCTTTTGTGAG 1800
 QY 1801 TGTGTGTACAAATGAGATGTATCCAGATGTCTAGTCAATGCTTGTGATCAAT 1860

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Db      1801 TGTGTGTACAAAGATGATGATCCAGATGTTACTGAGTTCATGCTTGCATCAAT 1860
Qy      1861 ACAATTCATATCATATGATGCAAAAAAAGATGATGATGATGATGATGATGATGAT 1920
Db      1861 ACAATTCATATCATATGATGCAAAAAAAGATGATGATGATGATGATGATGATGAT 1920
Qy      1921 AAAAAAAAAAAAAA 1934
Db      1921 AAAAAAAAAAAAAA 1934

RESULT 2
AAZ44832 standard; DNA; 1594 BP.
XX
AC      AAZ44832;
XX
XX      27-APR-2000 (first entry)
XX
DE      B. napus sld1 DNA.
XX
XX      Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
XX      transgenic plant; crop plant; delta-8-unsaturated long-chain base;
XX      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
XX      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
XX      pharmaceutical; food; chemical raw material; ds.
XX
OS      Brassica napus.
XX
FH      Key Location/Qualifiers
FT      CDS 51..1400
FT      /*tag= a
FT      /product= "sld1"
XX
XX      DE19828850-A1.
XX
XX      30-DEC-1999.
XX
XX      27-JUN-1998; 98DE-1028850.
XX
XX      27-JUN-1998; 98DE-1028850.
XX
XX      (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
XX      Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
XX      WPI; 2000-127549/12.
XX      P-PSDB; AAY51333.
XX
XX      New sphingolipid desaturase that selectively introduces double bond
XX      into sphingolipids and capnoids -
XX
XX      Claim 11; Fig 1; 62pp; German.
XX
XX      This invention describes a novel sphingolipid desaturase that selectively
XX      introduces a double bond into the sphingobase of the ceramide residue of
XX      sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
XX      desaturase, or a vector containing the DNA sequence, can be used to
XX      produce transgenic plants, especially crop plants, with an increased or
XX      decreased delta-8-unsaturated long-chain base content or an altered
XX      delta-8-unsaturated long-chain base cis/trans ratio, especially to
XX      compensate for a delta-8-unsaturated long-chain base deficiency, to
XX      exclude production of delta-8-unsaturated bases, to increase tolerance
XX      or resistance to soil salinity, ion stress or toxicity, drought, wet
XX      conditions, cold or frost and/or phytopathogenic microorganisms, or to
XX      alter size growth and flowering time. Cells, transgenic organisms or
XX      plants containing the DNA sequence can be used to produce sphingolipids
XX      and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
XX      can be used in cosmetics, pharmaceuticals and foods and as chemical raw
XX      materials. This sequence encodes the Brassica napus sphingolipid
XX      desaturase sld1 protein described in the method of the invention.

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SQ      Sequence 1594 BP; 382 A; 369 C; 375 G; 468 T; 0 other;
Query Match 35.7%; Score 690; DB 21; Length 1594;
Best Local Similarity 69.7%; Pred. No. 1,1e-125;
Matches 933; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

Qy      318 AGAAGAGAAAGAGATCATTAACCTCAGAGAGAGCTGAAGGGTCAACAAAGAGAGAGATT 377
Db      61 AGACAAAGAGAGAGATCATTAACAGCATGATGTAAGAAAAACAAACAAACCCGAGATT 120
Qy      378 TATGATCTCAATTCAGAGTAAAGTGTACATGCTCAGATTGGGTCAAGAGACCTTG 437
Db      121 TATGATCTCAATTCAGAGTAAAGTGTACATGCTCAGATTGGGTCAAGAGACCTTG 180
Qy      438 GTGGTGAATGTTCAATCTCAACCTTGCTGGCCAGATGTCACATGATGATTCATAGAT 497
Db      181 GAGGCGAAGACGATCTTAACCTCGCCGCTCAAGAGTCACGAGCGGTTCAATCGCTT 240
Qy      498 ACCATCTGACACAGCATGATGTCACACCTTGAAAAATCTTCACTGAGTACCACTCAGTG 557
Db      241 ACCATCTGACACAGCATGATGTCACACCTTGAAAAATCTTCACTGAGTACCACTCAGTG 300
Qy      558 ACTTCAAGTCTCTGAGGTGTCAGAAAGCTACAGAAAGCTTGATCTGATGTTCAAAAT 617
Db      301 ACCACACAGTGTCCGAGTGTCCGAGTACACGTCGTTAGCCGAGATTTCAAAC 360
Qy      618 TGGGTCTTTTGACACCAAGGGGATGTCATTGATGACCCCTTGATCTGTGCTGTA 677
Db      361 GCGGACTCTTCGATTAAGAAAAAGTACAGTCTTTACAGCTCAGCTGCGTCCGCA 420
Qy      678 TGTTCCTATGTAATCTATGATGTTCTGAGAGTCACTAGTGTGAGGCTCATTTGGGT 737
Db      421 TGCTCGGGGGGCTTGTATGAGTGTGTTGTGATGACAGAGATATGGGCCCATTAATAT 480
Qy      738 CAGGATGCTCTTAAGGGTCTTTGAGTGAAGTCTTAATGAGGCTGATGATTTGCGC 797
Db      481 CCGCGCTTGTGAGGCTTCTGATGATGAGAGCGCTTACGTGAGACATGATCTGGTC 540
Qy      798 ACTATGCTTATGACAAACCAATGTTTCAACAAAGTTGACAGATCTCTCTGGAACT 857
Db      541 ATTACAAAGTACGTCACAAAGCCGTTAATAACTGTCACACTTCTGCTGTAAT 600
Qy      858 GCTTGAACGGGATTAAGATGCTTGTGGAAGTGAATCAATGATCAACCAATGCGT 917
Db      601 GCATCACCGGATATGATCGCGTGTGGAATGACGATACGCTACCATATCTCTT 660
Qy      918 GCAACAGCTTGAACATGACCTGATCTGACAGACATGCGGCTTTGCAAGTTTCTGCGC 977
Db      661 GTATATGCTTGAACAGATCTGATCTCAGACATCCCTGTCTTAGCGGTCTCAACA 720
Qy      978 GGTTCCTCAATTCATACCTCTCATTTCTATGAGGAGAAAGTTGAGATTTCATTG 1037
Db      721 AGTTCCTTAAGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy      1038 CTAGGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1097
Db      781 CTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy      1098 TCAACTGTATCTGACAGCAATCTGCTATGTTTGGAGCGCAAAAGTCAGAGATAGAG 1157
Db      841 TCAATCTTATTCACAAAGCTTACTTTTGTGATTTGCAAGAGTATGTTCTGATGAG 900
Qy      1158 CTTGAACATTAATGAGGATCTGTTGTTTGGAGTGTGCTTCTTTTATGTTGCTTGGC 1217
Db      901 CTTGAACATTAATGAGGATCTGTTTCTGAGAGTGTGCTTCTTTTATGTTATCTTCC 960
Qy      1218 TGGCAATTTGGCGAGAGGATATGTTGTTGCTGATGTTGCTGTTGTTGCTGATTC 1277
Db      961 TACCAACTGCAAGAGAGATATCTTCTTCTTTTAAAGATGCGGTACGCGCATTC 1020
Qy      1278 AGCAGATTCAGTTCTGTTTGAATCACTTGTCTGCAATGTATATGTCGCGCACCGATG 1337
Db      1021 AGCAGTTAGTTCTGTTTAAACATTTTGGGAGATGTTTACACGCGTCCGCTATG 1080

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QY 1338 GGAATGACTGGTTGGAGAGACAAGTGGTACATTGGATATCTTGGCTCTTTCGA 1397
DB 1081 GGAACGATTTGGTTTGGAGAGACAACGCTGGTACGCTTGAATATCTGTAGTGTATATA 1140
QY 1398 TGAATGGTTTTCGTTGGCTTGGAGTTTGCAGTTTGCAGTTCATCTTGTTCAGAGCTAC 1457
DB 1141 TGAATGGTTTTCGTTGGCTTGGAGTTTGCAGTTTGCAGTTCATCTTGTTCAGAGCTAC 1200
QY 1458 CTGGTGGCAATTGAGAGAGATTTCGCTTTGGTTAGTACCTTTGCAAGAGCATATAT 1517
DB 1201 CGCCTTGCATCTGAGAGAGATTTCGCTTGGTTAGTACCTTTGTAAGAGCATATATC 1260
QY 1518 TGCCTTATGAGAGCTTGTCTATTTTGGAGAGCAATCAGTACATTAGACCTTCAGGA 1577
DB 1261 TACCGTATGAGAGCTTGTCTATTTTGGAGAGCAATCAGTACCTTCAGAGCTTCAGGA 1320
QY 1578 CTGGTGGCTTACAGCTTACAGCTTACCAACCTTGCCTTACAGATTTGTGTGGAGAG 1637
DB 1321 AAGCGGCGGTTCAAGCTTACAGTACATGACTAATCTGTGTGAGAGATTTGCTATGGAGAG 1380
QY 1638 CTGTTAATACCATGCT 1655
DB 1381 CTCTGAATACTCATGCT 1398

RESULT 3
AAC42244
ID AAC42244 standard; DNA; 1465 BP.
AC AAC42244;
XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
DE Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS Epi033405-A2.
PN 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
PF 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 29-OCT-1999; 99US-0162142.

Query Match 34.8%; Score 672.8; DB 21; Length 1465;
Best Local Similarity 68.7%; Pred. No. 2,46-122;
Matches 926; Conservative 0; Mismatches 422; Indels 0; Gaps 0;

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DB 118 GCGGATCAACGAGAGAGATTCGTTACAGGAGATTTGAAAAACCAACCAACC 177
QY 370 GGGAGATTATGATCTCAATTCAAGGTAAAGGTAAATGTCAGATTGGTCAAGGA 429
DB 178 TGGAGATTATGATTTGATTCAGATTCAAGTTAAAGTTAGACGTTCCGATTGGTTAATC 237
QY 430 GCACCTGTGTGTGATGATTCATCAAACTTGTGCGCAGATGTCAGTATGCAAT 489
DB 238 TCATCCCGAGGCGAGACAGGATTCATCTGCGGCGCAGACGTCACCGACGCTT 297
QY 490 CATGACATACCATCTGCGACAGATGTCACACCTTGAAAAATTTCTACTGGCTACCA 549
DB 298 CATGCTTACCTCCGAAACCGATGCGACACCTTGAAAAAGTTTCAATGCTACCA 357
QY 550 CCTCAGTACTTCAAGGCTCTGAGGTGTCCAAAGACTACAGAAAGCTTGATCGAGTT 609
DB 358 GGTAGAGACCAACGATGTCAGAGTCTACAGTACCTGCTTTAGCCGCGAGTT 417
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QY 670 TGCTGTATGTTCTCATTTGATCTATGAGTTCTGAGTGCATGCTGTGTGGCTCA 729
DB 478 CGGGGTATGCTCCGCGGCTTCTTACGGGCTTGTGCGGTGACGACATCTGGCTCA 537
QY 730 TTGCGTTCAAGCATGCTTTAGGCTTGTGATGAAAGTCTATGCGGCATGA 789
DB 538 CTTATCTCCGCTTTTACTCGTCTCTGATCCAAAGCCTTACGTCGCGACGA 597
QY 790 TTCTGCGCACTATGTTATGACAAACAAATGTTTCAACAGGTCACAGATCTCTC 849
DB 598 TTCCGTCACACGAGTGAAGTCAACAAACGTTAAACAACTTATCCAGCTTCTC 657
QY 850 TGGGAATGCTTGAACGGGATATGACATGCTGTTGAGAGTGAAGTCAAAATGCTACCA 909
DB 658 CGGTATGCTCTACCGGACATCTCAATGCGGTGTGAAATGACGACAAACGCTCA 717
QY 910 CATGCGTGAACAGCCTTGACATGACCGGATCTGACAGACATGCGGCTTGAAGT 969
DB 718 CATGCTTGAACGCTTGAACGATCCGAGTCTCAACAACTCCGATCTTCCGCT 777
QY 970 TTCTGCGGCTTCTCAATTCATCACTCTCAATTTCTATGAGAGAGTTGAGATTGA 1029
DB 778 CTTTACAAAATTTCTCAATTCATGATGATGATGATGATGATGATGATGATGATGAT 837
QY 1030 TTTCATTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1089
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DB 898 CGAAGATCAACCTCTTCAATTCATCAACATCTTATCTATTTCTGAAAGCCGCTCC 957
QY 1150 GGAATAGACCTTGAACATTAATGAGGATCTTGTGTTTGAAGTTGCTCTCTTAAAT 1209
DB 958 AGATCGGCTTGAACATTCGCGGAATTTAGTTTCTGACATGATTCCTCTCTTAAAT 1017


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Qy      1016  AGTTGGATTGATTTATGTTAGTCTTGATCTGCTACCGAGCACTTACTTTTAC 1075
Db      823  CAGTTGACCTTTGACCCGTTAGCCCGTTCTTCTGAGCTACCGACTTATTAATTTAC 882
Qy      1076  CCGGTAATGTTGTTGGCAGGAGTCACTTGATCTGAGCAATTCGCTATGTTTTCG 1135
Db      883  CCGATCATGTTGTGTGGCCCGGCTCACTTATTTACAAACATCTGTTGCTATTTCA 942
Qy      1136  AGCGGAAAAGTGACGAGATAGAGCTTGAAACATTAATGGGATCTGTGTTTGGACTTG 1195
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Qy      1256  AGCTTTCCTGTTTGTTCATCCAGACATTCAGTTCTGTTGAATCACTTGTGCAAT 1315
Db      1063  AGCTTCTGTGTAAAGGATTAACAATTTCAATTTACACTGAAACATTTTCTGGGAT 1122
Qy      1316  GTATATGTCGGGCCACGAGTGGGAATGACTGTTTGGAGACAGACAGATGTACATTG 1375
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Qy      1376  GATATCTCTGTGTGCTCTTGCATGATGATGTTTGGTTCGCTGCTGCACTTACCTGAG 1435
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Qy      1556  TGGACATTTAGACACCTTCAGACGCTGCTCCCTTAACAGCTTACGAGGCTTACCAATCC 1615
Db      1363  ACGACCTTGAAGACGCTTAGACACGCGCTCTACAGCAGCTTACGAAACCCGCC 1422
Qy      1616  CCTAAGATTTGTTGGGAGAGCTGTTAATACCATGCTGAGGCACTTGGAGTTTATG 1675
Db      1423  CCACAGATTTAGCTTGGGAAAGCTTTCACACCCCATGATGAGCTTATCATCTATGT 1482
Qy      1676  AGTTAGATTTTGTCAAGGCTTTT 1701
Db      1483  TGGTACTCATCTCGGCTACTTTGTGT 1508

RESULT 5
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ID      AAC3846 standard; DNA, 1650 BP.
XX
AC      AAC3846;
XX
DT      17-OCT-2000 (first entry)
DE
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XX      Arabidopsis thaliana DNA fragment SEQ ID NO: 4526.
XX
XX      Hybridisation assay; genetic mapping; gene expression control;
XX      protein identification; signal transduction pathway;
XX      metabolic pathway; promoter; termination sequence; ss.
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XX
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XX
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XX
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XX
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 QY 370 GCGAGATTATGATCTCAATTCAGTAAGTGTACAAAGTCTCAGATTGGGTCAAGA 429
 DB 269 TGGAGATCTATGATCCGATTCAGGCAAGTCTACACGCTCCAGATTGGATTAAAC 328
 QY 430 GCACCTGTGTGATGATCTCAATCTCAACCTTGTGCGCAGGATGTCACTGATGACTT 489
 DB 329 TCATCTCCGAGGCGACACGAGTTCATCTCTGTGGTCAACGTCACCGATGCTTT 388
 QY 490 CATAGCATACCATCTCGGACACAGCATGGTACACACTTGAAATTTCTTACTGCGCTACCA 549
 DB 389 CATGCAATTCATCCCGAACCCTGCGACCATCTGACCATCTTCAACCGGTACCA 448
 QY 550 CCTAGTACTTCAAGTCTCTGAGTGTCCAAAGACATACGAAAGCTGTGATGACTT 609
 DB 449 CATCAGAGATTCCAAAGTCTCGAAGTCTCAAGGATTAACGTTAGTGTGCGCAATT 508
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Db      509 TCGTAACTCGTCTCTCGAAAACAAAGTCACTACTCTACACTAGCTTCGT
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Db      569 CGCCGCAATGTTCTCGAGTCTCTACGAGTCTTGGCTTGAACCTCCGCTTCGCTCA
Qy      730 TTGGGTTACGAGCATGCTTAGAGTCTTGGATCAAGTCTTATGAGCCATGA
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Qy      790 TTCTGCGCACTATGTTGTTATGACCAACCAATGTTTCAAGGTTGACAGATCTCTC
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Qy      850 TGGGAATGCTTGAACCGGAGTAAACATTTCTGTTGAGAGTCAACATGCTCAACA
Db      749 CGGTAACTGCTCCCGAATCTCAATCGCTGGTGAATGAGACTCAATGCTCATCA
Qy      910 CATTCGTCGACACAGCTTGACATGACCTGATCTGAGACATGCGGCTTTGAGT
Db      809 TCTAGCTTGAACAGCTTCATTCGATCCAGATCTACACACATCCCTGCTTCGCTC
Qy      970 TTGCTGCGGCTTCTCAATTCATACCTCTCATTTATGAGAGAAATGAGTTTGA
Db      869 CTCACCAAAATCTTCTCTCATTCATGACCTGAGATTCGAGAACTCACTTTGA
Qy      1030 TTTCATGCTAGTCTTGAATCTGCTACAGACTTTACTTTTACCCTGATGCTGT
Db      929 TCCAGTCGAGATCTTGAACACTTCAACACTTATATATCATGATATGCTCTT
Qy      1090 TGCAGGTCACACTTATCTGACACAACTCTGCTATGTTTTCGAGGGAAGTCA
Db      989 TGGAGATCAATCTTCTCATTCAAAGCTTCTCTGCTCTTCTCAAAAGTGAATCC
Qy      1150 GATAGAGCTTGAACATTAAGGGAATCTTGTGTTTGAACCTTGTCTCTTTTGT
Db      1049 AGATCGTCTTAACTTCGCGGAACTTAGTCTTGGACTTGTCCACTCTTAACT
Qy      1210 GTCTGCTGCAATGCTGCTGAGAGGTTATGTTGCTGCTGCTGCTGCTGCTT
Db      1109 CTATGCTTACCAAACTGCTGAGATTTCTCTGCTTCAAGCTTCAACCTGTC
Qy      1270 TTCATCTGAGACATTCAGTCTGTTGAACTTCTGCTGCAATGCTATAGCGGGC
Db      1169 GCGCTTCAACACTTAACTTACGCTTACACTTCTGCTGATGCTTACGTTGCTC
Qy      1330 ACCGAGTGGAGATGCTGTTTGAAGACAGACAAAGTATCATTTGATATCTTGTGC
Db      1229 ACCCAGCGTACGACTGTTTGAAGAGCAAGCGCGGAAACATCATCTCTTGTAG
Qy      1390 CTCTGATGATGTTGTTTGGTGGCTTGCAGTTTCACTGAGCATATTTGTTCC
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Qy      1450 AAGGCTACCTCGGTCGAATTTGAGAGATTTGCTTGTGTTAGTATCTTGTCAAG
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Db      1589 TTGGTTAAATTGATGCTGTTTAT 1617
RESULT 7
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DT      27-APR-2000 (first entry)
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XX
KW      Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KW      transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW      pharmaceutical; food; chemical raw material; ds.
XX
OS      Arabidopsis thaliana.
XX
FH      Key
CDS      Location/Qualifiers
FT      172..1521
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FT      /product= "sphingolipid desaturase"
XX
DE19828850-A1.
XX
PD      30-DEC-1999.
XX
PF      27-JUN-1998; 98DE-1028850.
XX
PR      27-JUN-1998; 98DE-1028850.
XX
PA      (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
PI      Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
DR      WPI; 2000-127549/12.
XX
PT      P-PSDB; AAY51334.
XX
PS      New sphingolipid desaturase that selectively introduces double bond
PS      into sphingolipids and capnoids -
XX
PS      Claim 11; Fig 3; 62pp; German.
XX
CC      This invention describes a novel sphingolipid desaturase that selectively
CC      introduces a double bond into the sphingobase of the ceramide residue of
CC      sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC      desaturase, or a vector containing the DNA sequence, can be used to
CC      produce transgenic plants, especially crop plants, with an increased or
CC      decreased delta-8-unsaturated long-chain base content or an altered
CC      delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC      compensate for a delta-8-unsaturated long-chain base deficiency, to
CC      exclude production of delta-8-unsaturated bases, to increase tolerance
CC      or resistance to soil salinity, ion stress or toxicity, drought, wet
CC      conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC      alter size growth and flowering time. Cells, transgenic organisms or
CC      plants containing the DNA sequence can be used to produce sphingolipids
CC      and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC      can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC      materials. This sequence encodes the Arabidopsis thaliana sphingolipid
CC      desaturase sld1 protein described in the method of the invention.
XX
SQ      Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 other;
Query Match 33.2%; Score 642.6; DB 21; Length 1678;
Best Local Similarity 66.0%; Pred. No. 2e-116;
Matches 930; Conservative 0; Mismatches 479; Indels 0; Gaps 0;
Qy      310 GGTGTTGAGAGAGAGAGATCACTTACCTGAGAGAGCTGAGGCTCAACAAGGA 369
Db      174 GCGGAGAGAGAGAGAGAGATCACTTACCTGAGAGAGAGATCTTAAACAAACAAATC 233

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QY 370 GGGAGATTATGATTCATTCATTCAGGTAAGGTGTAACAATGCTCAGATTGGGTCAAGGA 429
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 QY 430 GCACCTGTGTGATGATTCATTCATTCAGGTAAGGTGTAACAATGCTCAGATTGGGTCAAGGA 489
 DB 294 TCATCCGGAGGCGACAGGATTCATTCAGGTAAGGTGTAACAATGCTCAGATTGGGTCAAGGA 353
 QY 490 CATGATCATCATCTGCGACAGCATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 549
 DB 354 CATGATCATCATCTGCGACAGCATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 413
 QY 550 CCTGATGATTCAGGTAAGGTGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 609
 DB 414 CATGATGATTCAGGTAAGGTGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 473
 QY 610 CTCAAAATTTGGGTCTTTTGAACCAAGGAGGATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 669
 DB 474 TCGTAATCTGGGTCTTTGAAACCAAGGAGGATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 533
 QY 670 TGCTGATGATTCAGGTAAGGTGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 729
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 DB 774 TCTGATGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 833
 QY 970 TTCTGCGCACTATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1029
 DB 834 CTCGACCAATTTCTTCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 893
 QY 1030 TTTCAATGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1089
 DB 894 TCAAGTCCGAGATTCATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 953
 QY 1090 TGGCAGGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1149
 DB 954 TGGAGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1013
 QY 1150 GGATGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1209
 DB 1014 AGATGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1073
 QY 1210 GTCTGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1269
 DB 1074 CTCATGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1133
 QY 1270 TTCTGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1329
 DB 1134 GCGGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1193
 QY 1330 ACCGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1389
 DB 1134 ACCGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1253
 QY 1390 CTCTGATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1449
 DB 1254 ATCATATGATGATGATGTAACAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGAATGCTCAGATTGGGTCAAGGA 1313

QY 1450 AAGGCTACCTGCGGCCAATGGAAGATTCGCTTTGGTATGATGACCTTTGCAAGGA 1509
 DB 1314 TCGCTTACCTGCTTGGCATCTCGGAAAGTTCTCCGCTGTTCAAGGCTTTGCAAGGA 1373
 QY 1510 GCATATTTGCTTATGAGAGCTTGTATTTGGGAGCCCAATGATGACATTTAGGAC 1569
 DB 1374 GCATATTTGCTTATGAGAGCTTGTATTTGGGAGCCCAATGATGACATTTAGGAC 1433
 QY 1570 CCTGAGAGCTGCGCCCTACAGGAGGATTAACAACCCCTGCTTAAAGATTTGT 1629
 DB 1434 TTTGAGAGGAGGATTAACAACCCCTGCTTAAAGATTTGT 1493
 QY 1630 GTGGAAGCTGTTATATCCATGAGGATTTGAGATTTTGAAGATTTTGT 1669
 DB 1494 TTGGAAGCTTGAATCTATGCTTAAATGATTTTATCAAAACAAATATGCTTTGT 1553
 QY 1690 TCAAGTCTTTTCTTTTCTTTCT 1718
 DB 1554 TTGGAATTTGATGATGATTTTAT 1582

RESULT 8

AB212753
 ID AB212753 standard; DNA; 1350 BP.

AC AB212753;

DT 21-JAN-2003 (first entry)

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

OS Arabidopsis thaliana.

PN WO200216655-A2.

XX 28-FEB-2002.

PF 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

PR 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Harper JF, Kreps J, Wang X, Zhu T;

DR WPI, 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed

PT and producing plants with increased tolerance to these abiotic stresses

PT -

PS Claim 6; SEQ ID NO 558; 577bp + Sequence listing; English.

XX The invention relates to identifying a stress condition to which a plant

CC cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides

CC in the plant cell with an array or probes representative of the plant

CC cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used

CC in methods of the invention.

CC Note: The sequence data for this patent is not represented in the printed

CC specification but is based on sequence information supplied to Derwent by

CC the European Patent Office.

CC

Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 other;

Query Match 33.1%; Score 639.2; DB 24; Length 1350;
 Best Local Similarity 67.1%; Pred. No. 9e-116;
 Matches 905; Conservative 0; Mismatches 443; Indels 0; Gaps 0;

QY 310 GGTGTGAGAGAGAGAGAGATACATACCTCAGAGAGCTGAAGGCTCAACAAGGA 369
 DB 3 GCGGAGAGAGAGAGAGAGAGATACATACCAAGAGAGATCTTAAAAACACAAATC 62
 QY 370 GGGAGATTTAGATCTCAATTCAGAGTAAAGTGTACAAATCTCAGATGGGTCAAGGA 429
 DB 63 TGGAGATCTATGATCGGATTCAGAGCAAGGTCTACAAAGCTCTCCGATTTGAATAAC 122
 QY 430 GCACCTGGTGGTGTGATTCATCTCAACCTTGGTGGCAGAGATGTCATGATTCAT 489
 DB 123 TCATCCGAGAGGACACGAGATTCATCTCGTGGTGAAGACGTCACGATGCTTT 182
 QY 490 CATAGCATACCATCTGGCAGACAGATGTCACACCTTGAATAATCTTCACTGCTACCA 549
 DB 183 CATGCAATTCATCCCGAAGCGCTTGGCAGCATCTGACCATCTTTCACCGGTTACCA 242
 QY 550 CCTGATGATCTCAAGTCTCTGAGGTCCAAAGACTACAGAAAGCTTGCATCTGAGTT 609
 DB 243 CATCAGAGATTCAGAGTCTCCGAAGTCTCAGCGGATTCAGGATTCGCTCCGAGTT 302
 QY 610 CTCAAAATGGGCTTTTGAACCAAGGAGATGTCATTCATGCAACCTTGCATCTGT 669
 DB 303 TCGTAATCTCGGCTCTTGAAGAAAGAGTACGTTACTCTTACATCTAGAGCTTCTGT 362
 QY 670 TGTGTTATGTTCTCATTTGATCTATGTTGTTCTGAGTGTGCACTAGTGTGGGCTCA 729
 DB 363 GCGGCAATGTTCTCGAGTCTCTAGGTTTGGCTTGTACCTCCGCTTCGCTCA 422
 QY 730 TTTGGGTTCAAGCATGCTCTTAGGTTGCTTGTGATGCAAGAGTCTTATGAGCCATGA 789
 DB 423 CCAATGCGCCGCGCTTCTCGGTTCTCTGATTCAGAGCGCTTACATAGGTACAGA 482
 QY 790 TTTGGGCACTATGTTGTTATGACAAACATGTTTCAACAAGTTGACAGATCTCTC 849
 DB 483 TTTGGTATATGATTCATCATGTCGAAACAAATCTTATAAGATTCGTCGCTCTCTC 542
 QY 850 TGGGAATGCTTGAACCGGATTAAGCATGCTTGGTGAAGTGAAGTCAATGCTACCA 909
 DB 543 CGGTAATCTGTCAACCGGATTCATGATGCTGTGGAAGTGAAGTCAATGCTACCA 602
 QY 910 CATTCGTCGAACAGCTTGAACATGACCTGATCTGAGGACATGCGGCTCTTGGCAGT 969
 DB 603 TCTAGCTTGTAAAGCTCGATTAAGATTCAGATCTTACACATCCCTGTCTTGGCGT 662
 QY 970 TTTGCTGGGCTTTCATTCATTAACCTCTCATTTCTATGGAAGAAATTGAGTTGA 1029
 DB 663 CTCACCAAAATCTTCTCTCATTTGACCTCGAGATTCACATGCGAAATCACGTTTGA 722
 QY 1030 TTTGATGCTAGGTTTCTGATCTGTACACAGCATTTTATCCCGGTAATGTGCT 1089
 DB 723 TCCAGTGGCGAGATTTCTTAGTCAAGTATCAACATTAATTAATCAAGTATGCTT 782
 QY 1090 TGGCAGGCTCAACTGTATCTGACAGCAATTCGTATGTTTTCAGAGCGAAAGTGA 1149
 DB 783 TGAAGATCAATCTCTTCAATCAAGTTCTGTGCTCTTCCAAAGCTGAAGTACC 842
 QY 1150 GGATAGAGCTTGAACATATAGGGATCTTGTGTTTGAAGTGTGCTCTTTTAACT 1209
 DB 843 AGATCGGCTTAAACCTCGCGGAAATCTTGTGCTTCTGAGCTTGGTCCACCTTAAGT 902
 QY 1210 GTCTTGCTGCGCAATGCTGAGAGAGGATATGTTGCTGCTAGCTTGTGCTTTG 1269
 DB 903 CTCATGTTACCAACTGCGCTGAGAGATCTTCTTCTGCTTCAACAGCTTACCGTAC 962
 QY 1270 TTTGATCCAGACATTCAGTTCTGTTGATCACTTGTGCTCAATGATATGTCGAGCC 1329
 DB 963 GGGCTTCAACACATTCATTCAGGCTTAACCATTTGCTGTATGTCTAGTTGGTCC 1022

QY 1330 ACCGAGTGGGAATGATGTTTGGAGACAGACAAGTGTATGATGATATCTTGTGC 1389
 DB 1023 ACCGACGGTATGACATGCTTTCAGAGAGACAGCGCGGAAACATCATATCTTTGAG 1082
 QY 1390 CTCTTCATGATGATGTTTTCGTTGCTTGCAGTTTCAGCTTGAAGATCAATTTGTTCC 1449
 DB 1083 ATCATATCATGATGATGTTTCTTGTGATTAACATTTCACTTGAAGATCATTTGTTCCC 1142
 QY 1450 AAGCTACCTCGGTGCCAATTTAGAGAAAGATTTGCCCTTTGTTAGTACCTTTCAGAA 1509
 DB 1143 TCGCTTACCTCGGTGCCATCTCCGAAAGTTCCTCCGTTGTCMAAGCTTTCAGAA 1202
 QY 1510 GCATATTTGCTTATGAGAGCTTGTCAATTTGGGAGGCGCAATGAGCAATTTAGAC 1569
 DB 1203 GCATATCTTCCGTAAGAGATATGCTGTTGTAAGCAATGTTGACATTTACAC 1262
 QY 1570 CCTCAGGACTGCTGCCCTTACAGCTAGAGACTTAACAACCTTCCCTTAAGATTTGTT 1629
 DB 1263 TTTGAAGACAGACCTTATCAGCTAGAGAGCTGCTATTCGCTGTTAAGAACTTGT 1322
 QY 1630 GTGGAAAGCTGTTAATACCATGCTGA 1657
 DB 1323 TTGGGAAGCTTGTGAATCTCATGCTTAA 1350

RESULT 9
 AAV34398
 ID AAV34398 standard; DNA, 1684 BP.
 XX AAV34398;
 AC AAV34398;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Borage delta-6 desaturase gene.
 XX
 KW Upstream region; regulatory region; sunflower; albumin; seed; expression;
 KW lipid metabolism; delta-6 desaturase; transgenic plant; ds.
 XX
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..1389
 FT primer_bind /tag= a
 FT primer_bind /product= "delta-6 desaturase"
 FT primer_bind complement (616..632)
 FT primer_bind /tag= b
 FT primer_bind 1165..1181
 FT primer_bind /tag= c
 XX
 FN W09845460-A1.
 XX
 PD 15-OCT-1998.
 XX
 PE 09-APR-1998; 98MO-US07178.
 XX
 PR 09-APR-1997; 97US-0831570.
 XX
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 XX
 PI Beremand PD, Nunberg AN, Thomas TL,
 XX
 DR WPI: 1998-583201/49.
 DR P-PSDB; AAW67471.
 XX
 PT New sunflower albumin 5' regulatory region - useful for directing
 PT altered lipid metabolism in plant seeds
 XX
 PS Example 2, Fig 1; 38pp; English.
 XX
 CC This sequence is the gene encoding the borage (Borage officinalis)
 CC delta-6 desaturase enzyme. The lipid metabolism gene is an example
 CC of a heterologous gene which can be expressed at high levels in a

CC seed-specific manner in transgenic plants, when placed under control
 of the sunflower albumin gene 5' regulatory region (AAV34397).

XX Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other:

Query Match 32.0%; Score 618.4; DB 19; Length 1684;

Best Local Similarity 66.5%; Pred. No. 1,1e-111; Mismatches 446; Indels 0; Gaps 0;

Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

326 AAGAAATCATTAACCTTCAAGAGAGCTGAAGGCTCAACAACAGAGGAGATTATGATC 385
 58 AAGAAATCATTAACCTTCAAGAGAGCTGAAGGCTCAACAACAGAGGAGATTATGATC 117
 386 TCAATTCAGAGTAAGGTGTACAAATGTCTCAGATTGGGTCAAGAGAGACCTGGTGGTAT 445
 118 TCGATTCAAGGGAAGAGCTTATGATGATGTTTGGATTTGGGAAAGAACATCCAGTGGACG 177
 446 GTTCCAAATCTCAAACTTGTGCGCAGAGATGTCACTGATGATTCATATCATATACATCCT 505
 178 TTTCCTTGAAGAGCTTGTGTGTCAAGAGTAATGATTCATTTGTTGCAATTCATCCT 237
 506 GGCACAGATGTGTACACCTTGAAGAAATTTTCACTGCTACACCTGAGACTTCAAG 565
 238 GCCTCTACATGGAAGAAATCTTGATTAAGTTTTCACCTGGGTATTTATCTTAAAGATTACTCT 297
 566 GTCTCTGAGTGTCCAAAGACTACAGAAAGCTGATCTGATCTCAAAATTTGGGTCTT 625
 298 GTTCTGAGTGTCTTAAAGATTATGAAAGCTTGTGTGAGTTTCTTAAATGAGGTTTG 357
 626 TTTGACACCAAGGAGCATGTCACTTCAGCAACCTTGCATCTGTGCTTATGTTCTCTC 685
 358 TATGACAAAAGAGCATATTAATGTTGCAACTTGTGCTTATGCAATGCTGTTGCT 417
 686 ATTGACTCTATGTTGTTCTGAGTGACATGATGTTGGGCTCATTTGGGTTCAAGCATG 745
 418 ATGAGTGTATGAGGTTTGTGTTGTAGAGGTTTGTGTAACATTTGTTCTGGGTGT 477
 746 CTCTTAAAGGTTGCTTGAATGCAAGTCTTAATGAGGCAATGATTTGGGCACTATG 805
 478 TTGATGGGTTTCTTGAATGCAAGTGTGATGATGATGATGATGATGATGATGATGATG 537
 806 GTTATGACAAACCAATGTTTCAACAGGTTGACAGATCTCTCTGAGAACTGCTTGACC 865
 538 GTAGTGTCTGATTCAGGCTTAATAGTTTATGAGTTTATGCTGCAAAATGTTCTTCA 597
 866 GGGATTAACATTTGTTGTTGAGAGTGAAGTCAATGCTCACCACATTTGCTGCAACAC 925
 598 GGAATTAATGATTTGTTGTTGAGAAATGGAACCATTAATGACATCACATTTGCTGTAATAGC 657
 926 CTGACCAATGACCTGATCTGACAGACATGCGGCTTTCGATTTGCGCGGCTTCTTC 985
 658 CTGAAATTAATGACCTGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 717
 986 AATTCATTAACCTTCAATTTCTATGAGGAGAGTGAAGTGAATTTGATTTGATTTGATTTG 1045
 718 GGTTAACCTCACTCTCAATTTCTATGAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 777
 1046 TTGATCTGACAGACATTTAATTTTAAACCGGTAATGTTGTTGTTGTTGTTGTTGTTG 1105
 778 TTTGTAATTAATCAATTTGACATTTTAACTTATTAATGTTGTTGTTGTTGTTGTTGTTG 837
 1106 TATCTGACAGCAATTTCTGATTTGTTTTCGAGGCAAAAGTGAAGTGAAGTGAAGTGAAG 1165
 838 TATGTAACATCTCTATTAATGTTGTTGACCAAGAAAGTGTCTATCTGACACTGAGGA 897
 1166 ATAATGGAGATCTTGTGTTTGAAGTGGTCCCTCTTATGATGCTTGTGCTGCAAT 1225
 898 CTCTTGGAGATGCTGATGTTCTGATTTGATGATGATGATGATGATGATGATGATGATG 957
 1226 TGGCTGAGAGGTTATGTTTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1285
 958 TGGGTTGAAGAAATTAATGTTTGTATGCAATTTATCATGATGATGATGATGATGATGATG 1017

OY 1286 CAGTCTGTTGTAATCACTTGTGCAATGATATGTCGGCCACCGAGTGGAAATGAC 1345
 DB 1018 CAGTCTGTTGTAATCACTTGTGCAATGATATGTCGGCCACCGAGTGGAAATGAC 1077
 OY 1346 TGGTTGAGAGACAGACAGTGTGATCTGTTGCTTGTGCTTGTGATGATGG 1405
 DB 1078 TGGTTGAGAGACAGACAGTGTGATCTGTTGCTTGTGCTTGTGATGATGG 1137
 OY 1406 TTTTGGTGGCTTGGAGTTTCACTTGTGATGATGATGATGATGATGATGATGATGATG 1465
 DB 1138 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
 OY 1466 CAATGAGAGAAATTTGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 1525
 DB 1198 AACTTGAAGAAATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1257
 OY 1526 AGAGCTTGTATTTGGAGGCTCAATGATGATGATGATGATGATGATGATGATGATG 1585
 DB 1258 AATATGATCTTCTTCAAGGCTCAATGATGATGATGATGATGATGATGATGATGATG 1317
 OY 1586 CTAACTTGGAGCTTAAACCAACCTGCTTAAAGATTTGTTGGGAACTGTTAT 1645
 DB 1318 TTGAGGCTAGGATTAATTAACCAACCTGCTTAAAGATTTGTTGGGAACTGTTAT 1377
 OY 1646 ACCCATGCTGA 1657
 DB 1378 ACTCATGTTTA 1389

RESULT 10
 AAX24917
 ID AAX24917 standard; cDNA; 1684 BP.
 XX
 AC AAX24917;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Borage delta-6 desaturase cDNA.
 XX
 KM Delta-6 desaturase; borage; oleosin; AtS21, promoter;
 KW transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 KM gamma-linolenic acid; octadecatrienoic acid; de.
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT 43..1389
 FT CDS /*tag= a
 XX
 PN MO9845461-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07179.
 XX
 PR 09-APR-1997; 97US-0831575.
 XX
 PA (RHON) RHON-POULENC AGROCHIMIE.
 XX
 PI Li Z, Thomas TL;
 XX
 DR WPI; 1999-180333/15.
 DR P-FSDB; AAM98130.
 XX
 PT Nucleic acid containing oleosin 5'-regulatory region - useful for
 PT modulating fatty acid synthesis and lipid metabolism in plants,
 PT particularly to increase content of gamma-linolenic acid
 XX
 PS Example 2; Page 59-61; 101pp; English.
 CC The present sequence encodes borage delta-6 desaturase (see
 CC AAM98130), an enzyme that catalyses the conversion of linoleic acid
 CC to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was

CC isolated from a borage membrane-bound polysomal cDNA library
 CC using a partial clone, obtained from an EST database search, as
 CC probe. The borage delta-6 desaturase nucleic acid can be
 CC operably linked to the seed-specific 5' regulatory region (see
 CC AX24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed
 CC expression cassettes of the invention. Transgenic plants, e.g.
 CC sunflower, soybean, maize, tobacco, cotton, peanut, oilseed
 CC rape or Arabidopsis are obtained that show increased levels of
 CC GLA or octadecatrienoic acid. The levels of desirable fatty
 CC acids in oilseed crops can be manipulated to provide seed
 CC oils of use in human health and industrial applications.

XX Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;

Query Match 32.0%; Score 618.4; DB 20; Length 1684;
 Best Local Similarity 66.5%; Pred. No. 1.1e-111;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AAGAATACATTAACCTCAGAGAGCTGAAGGCTCAACAACAAGAGAGATTATGATC 385
 Db AAGAATACATTAACCTCAGAGAGCTCAACAACAAGAGAGATTATGATC 117
 QY 386 TCAATTCAGAGTAAAGGTGACATCTCTCAATTGGGTCAAGAGACACCTGTGTGAT 445
 Db TCGATTCAAGGGAAGCCATATGATGTTTGGATTGGTGAAGAACATCCAGGTGGCAGC 177
 QY 446 GTTCCAACTCAAACTGTGCGCAGAGATGCACTGATGCAATTCATAGCATACCTCT 505
 Db TTTCCCTGAAGAGCTTGTGCTGCTCAAGAGTAACTGATGCAATTTGTCATCTCATCT 237
 QY 506 GGCAACAGCATGTCACACCTTGAAAATTTCTTCACTGCTACACCTCAGTACTTCAAG 565
 Db GCCTCTAATAGGAAGATCTTGATTAAGTTTTCATGCTGATTAATCTTAAAGATTACTCT 297
 QY 566 GTCTCTAGGTGTCGAAGACTACGAAGAACTTGATCTGAAGTTCTCAAAATTTGGCTT 625
 Db GTTCTCTAGGTGTCGAAGACTACGAAGAACTTGATCTGAAGTTCTCAAAATTTGGCTT 357
 QY 626 TTGACACCAAGGCGCATGTCATGCAACCTTGATCTGTGCTGATATGTTCTC 685
 Db TATGACCAAAAGGCGCATATTAATGTTGCAACTTTGCTTTAAGCAATCTGTTGCT 417
 QY 686 ATTGACTCTAATGCTGTTCTGAGTGCACTAGTGTGGGCTCATTTGGTTCAGGCATG 745
 Db ATGAGTGTATAGGGGTTTGTGTTGAGGGGTGTTTGTGATCATTTTTCGCGGT 477
 QY 746 CTCTTAAGGTTGCTTTGATGCAAAAGTCTTAATGTGGCCATGATTCGGCCACTATG 805
 Db TTGATGGGGTTCCTTGGATTCAGAGTGTGATGCAATGATGCTGGGCATTATATG 537
 QY 806 GTTATGACAAACCAATGTTTCAACAAGTTGCAACGATCCTCTGCGGAATGCTTGACC 865
 Db GTAGTGTGATTCAGGCTTAATTAAGTTTATGGGTATTTTTCGCAAAATTTGCTTCA 597
 QY 866 GGATTAACCATTTGCTTGGTGAAGTGACTCAACAATGCTCAACATGCGGGAACAGC 925
 Db GGAATTAATTTGCTTGGTGAAGTGAACCAATTAATGCAATCACTATGCTGTATATG 657
 QY 926 CTGACCAATGACCTGATCTGACGACATGCCGCTTTGCAAGTTTCGTGCGGTTCTTC 985
 Db CTGGAATATGACCTGATCTTAATAATATACCATTCCTGTTGTGTCTTCAAGTTTTC 717
 QY 986 AATTCATTAACCTGCTCATTTTCTAATGGAGAAAGTTGAGTTGATTCATGCTAGGTT 1045
 Db GGTTCACTCACCTCTCATTTCTATGAGAAAGGTTGACTTTTGACTCTTATCAAGATTC 777
 QY 1046 TTGATCTGCTACGACGACTTACTTTTACCAGGTAATGTTGTTGCCAGGCTCAACTG 1105
 Db TTTGTAAGTTATCAACATTTGACATTTTACCCTTATATGTTGCTGCTAGGCTCAATATG 837
 QY 1106 TATCTGACAGCAATTTCTGCTATGTTTTCGAGCCAAAGTGCAGATAGACCTTGATC 1165
 Db TATGTAATCTCTCATATGTTGTTGACCAAGAAATGTTGCTCTATGAGCTCAGGAA 897

QY 1166 ATAATGGAGATCTTGATGTTTGGACTTGGTCCCTCTTTAGTGTCTTGCCGCAAT 1225
 Db CTCTTGGAGATCCCTAGTGTCTTCAATTTGGTACCCGTTGCTGTTTCTTGTGCTTAT 957
 QY 1226 TGCGCTGAGAGGTTATGTTGTTGCTTGTGCTGCTGCTGTTTGTTCATCAGACAT 1285
 Db TGGGGTGAAGAAATTAATGTTGTTATGCAAGTTTATCAGTACGTGAATGCAACAGTT 1017
 QY 1286 CAGTTCTGTTGATTCATTTGCTGCAAAATGATATGTCGGGCCACGAGTGGGAATGAC 1345
 Db CAGTTCTCTTGAACCACTTCTTCAAGTTTATGTTGGAAGCCTTAAAGGGAATAT 1077
 QY 1346 TGGTTTGAAGACAGACAGATGATATGATATCTTGTGCTCTTGATGATGATG 1405
 Db TGGTTTGAAGAAACAGATGAGACACTGACATTTCTTGTCTCTTGATGATGATG 1137
 QY 1406 TTTTTCGCTGCTGCAATTTGCACTTGAAGCATTTGTTTCAAGGCTACCTCGGTG 1465
 Db TTTCATGTGATGATGCAATTCGAATTTGAGATCATTTGTTTCCAGATGCTTATG 1197
 QY 1466 CAATTGAGAAATTTGCTGCTTGTGTTAGTACCTTTGCAAGAACATATTTGCTTAT 1525
 Db AACCTTAGAAATCTGCGCTACGTGATGATGCAAGTATGCAAGAAACATATTTGCTTAC 1257
 QY 1526 AGAGCTTGTGATTTTGGAGGCGCAATCAGTGAACATTTGAGACCTCAGACTGCTGCC 1585
 Db AATTATGATCTTCTTCAAGGCGCAATGAATGACCTCAGAACATTTGAGGACACAGCA 1317
 QY 1586 CTACAGCTAGGACCTTAACAAACCTGCGCTTAAGATTTGTTGGGAAAGCTTTAT 1645
 Db TTGAGGCTAGGATATATACCAAGCCGCTCCGAAAGATTTGATGGAAGCTCTTAC 1377
 QY 1646 ACCCATGCTGA 1657
 Db ACTCATGTTAA 1389

RESULT 11

AT30395
 ID AT30395 standard; DNA, 1685 BP.

AC AT30395;

DT 15-SEP-1996 (first entry)

DE Borage delta-6-desaturase gene.

KW Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;

KW polyunsaturated fatty acid; octadecatrienoic acid;

KW chilling resistance; oilseed; ss; db.

OS Borage officinalis.

FT Key Location/Qualifiers

FT CDS 44..1390

FT CDS /*tag= a

PN MO9621022-A2.

PN 11-JUL-1996.

PD 28-DEC-1995; 95WO-IB01167.

PR 30-DEC-1994; 94US-0366779.

PA (RHON) RHONE POULENC AGROCHIMIE.

XX Freyresineb GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 XX WPI; 1996-333997/33.
 XX P-PSDB; AAR98455.


```

FT      /*tag= a
FT      /product= "Borage delta-6-desaturase #1"
FT      /transl_except= (pos:1151..1153, aa:Ser)
XX      US2002108147-A1.
XX      08-AUG-2002.
XX      21-DEC-2001; 2001US-0029756.
XX      13-OCT-1992; 92US-0953952.
XX      19-SEP-1997; 97US-0934254.
XX      10-OCT-1991; 91US-0774475.
XX      08-JAN-1992; 92US-0817919.
XX      14-SEP-1994; 94US-0307382.
XX      28-JAN-1997; 97US-078936.
XX      (THOM/) THOMAS T L.
XX      Thomas TL;
XX      WPI; 2003-066659/06.
XX      P-PSDB; ABG73095.
XX      Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
XX      for producing plant with increased gamma linolenic acid content, and
XX      for inducing octadecatrienoic acid production in plant
XX      Example 9; Fig 5A; 55pp; English.
XX      The invention relates to a nucleic acid encoding an evening primrose
XX      delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
XX      nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
XX      for producing a plant (such as sunflower, soybean, maize, tobacco,
XX      peanut, carrot or oil seed rape plant) with increased gamma-linolenic
XX      acid (GLA) content by transforming a plant cell with the nucleic acid or
XX      vector and regenerating a plant with increased GLA content from the plant
XX      cell, for inducing or increasing production of GLA in an organism lacking
XX      in or producing low levels of GLA and for inducing production of
XX      octadecatrienoic acid in at least one of a plant deficient or lacking
XX      in or producing low levels of octadecatrienoic acid, a bacterium which
XX      produces alpha-linolenic acid or a bacterium which exhibits a
XX      delta-15-desaturase activity on a GLA substrate. This sequence represents
XX      cDNA encoding a borage delta-6-desaturase polypeptide.
XX      Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other:
XX      Query Match      32.0%; Score 618.4; DB 25; Length 1685;
XX      Best Local Similarity 66.5%; Pred. No. 1.1e-111;
XX      Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

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Db      359 TATGACAAAAAGGTCATATATATATGTTGCAACTTTGCTTTATAGCAATGCTGTTGCT 418
Qy      686 ATTGTACTATATGTTGTTGAGGTGCACTAGTGTGTGGGCTATTTGGTTGAGGCATG 745
Db      419 ATGAGTGTATATGAGGTTTGTGTTGTTGAGGTTTGTGTTGTTGTTGTTGTTGTTGTTG 478
Qy      746 CTTTGAAGTTGCTTTTGAATGCAAAAGTCTTATGTGGGCAATGTTGCGCACTATGTG 805
Db      479 TGTATGGGGTTTCTTTGATTCAGAGTGTGTGATGTGATGATGATGATGATGATGATGATG 538
Qy      806 GTTATGACAAACCAATGTTTCAACAGTTGCAAGTCTCTCTGTGGGAATGCTTGACC 865
Db      539 GTATGTCTGATTCAGGCTTAATATGATTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 598
Qy      866 GGATATAGCAATGCTTGTGGGAGTGAAGTGAAGTCAATGCTCAATGCTCAATGCTCAATGCT 925
Db      599 GGAATATAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 658
Qy      926 CTTGACCATGACCTGTATCTGACAGACATGCGGCTCTTGCAGTTTGTGCGGGTTCTTC 985
Db      659 CTTGATATGACCTGTATCTGACATATATACATCTCTGTGTGTGTTGTTGTTGTTGTTGTTG 718
Qy      986 AATTCCATTAACCTCTCATTTCTATGAGGAGGAGTTGAGTTGATTTCTATGCTGATGCTC 1045
Db      719 GGTTCACCTCACTCTCATTTCTATGAGGAGGAGTTGAGTTGATTTCTATGCTGATGCTC 778
Qy      1046 TTGATCTGTACCAAGCACTTACTTTTACCGGTTATGTTGTTGTTGTTGTTGTTGTTGTTG 1105
Db      779 TTGTATGTTATCAACATTTGACATTTTACCTTATATATGTTGTTGTTGTTGTTGTTGTTG 838
Qy      1106 TATCTGACAAATTCATCTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1165
Db      839 TATGTACATCTCTCATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 898
Qy      1166 ATAAATGGGATCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1225
Db      899 CTTCTGGGATGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 958
Qy      1226 TGGCCTGAGAGGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1285
Db      959 TGGGATGAAATTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1018
Qy      1286 CAGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1345
Db      1019 CAGTTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1078
Qy      1346 TGTGTTGAGAGCAAGCAAGTGTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1405
Db      1079 TGTGTTGAGAGCAAGCAAGTGTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1138
Qy      1406 TTTTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1465
Db      1139 TTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1198
Qy      1466 CAATTGAGAAAGTTTGGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1525
Db      1199 AACCTTAGAGAAATCTGCGCTTACGTATGATGATGATGATGATGATGATGATGATGATG 1258
Qy      1526 AGAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1585
Db      1259 AATTATGATCTTTCTCCAGAGGCAATGAAATGACATGACATGAAATGATGAGAACACAGCA 1318
Qy      1586 CTACAGTTAGGACTTATACAAACCTGCGCTTAAAGATTTGTTGTTGTTGTTGTTGTTGTTG 1645
Db      1319 TTGCAAGGTTAGGATATATACCAAGCCCTCCGAAAGATTTGTTGTTGTTGTTGTTGTTG 1378
Qy      1646 ACCATGAGCTGA 1657
Db      1379 ACTCATGTTAA 1390

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RESULT 14
ABK49503

ID	ABK49503 standard; DNA; 1702 BP.
XX	ABK49503;
AC	15-JUL-2002 (first entry)
XX	
DT	DNA encoding Evening primrose delta6-desaturase.
XX	
DE	delta6-desaturase; sunflower; soybean; maize; tobacco;
XX	peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
KW	chilling tolerance; gene; ds; evening primrose.
XX	
OS	Oenothera biennis.
XX	
EH	Key
FT	Location/Qualifiers
FT	CDS
FT	48..1406
FT	/tag=a
XX	/product="delta6-desaturase"
PN	US6355861-B1.
XX	
PD	12-MAR-2002.
XX	
PF	19-SEP-1997; 97US-0934254.
XX	
PR	13-OCT-1992; 92US-09559952.
PR	10-OCT-1991; 91US-0774475.
PR	08-JAN-1992; 92US-0817919.
PR	14-SEP-1994; 94US-0307382.
PR	28-JAN-1997; 97US-078936.
XX	
PA	(RHON) RHONE-POULENC AGROCHIMIE.
PI	Thomas TL;
DR	WPI; 2002-380944/41.
DR	P-PSDB; AAU79851.
XX	
PT	Novel nucleic acid encoding evening primrose delta6-desaturase which
PT	converts linoleic acid to gamma linolenic acid useful for producing
PT	gamma linolenic acid in transgenic plant or bacteria
PS	Claim 2; Column 41-46; 53pp; English.
XX	
CC	The invention describes an isolated nucleic acid encoding an evening
CC	primrose Delta6-desaturase. The nucleic acid and a vector expressing the
CC	nucleic acid are useful for producing a plant such as sunflower, soybean,
CC	maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC	gamma linolenic acid (GLA) content, and also for inducing or increased
CC	production of GLA in a bacteria or plant deficient, lacking in or
CC	producing low levels of GLA. The nucleic acid is also useful for inducing
CC	chilling tolerance in plants. This sequence encodes the evening primrose
CC	delta6 desaturase involved in the production of gamma linolenic acid.
XX	
XX	Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
XX	
Query Match	28.7%; Score 555; DB 24; Length 1702;
Best Local Similarity	64.8%; Pred. No. 2.8e-99;
Matches	889; Conservative 0; Mismatches 470; Indels 12; Gaps 4
OY	321 AGGAGAAAGATGATCACTAACTCAGAGAGCTGAAGGTCACAAAGAGGAGATTAT 380
Db	58 AAGCTTAAAGATATATCAACGGCGGAGGAGACTTCGCGGCACAAAGTCCGGCATCTCT 117
OY	381 GGATTCGAATTCAGAGTAAGGTGATCAATGTTCTTCAGATTGGGTCAAGAGCACTTGGTG 440
Db	118 GGATTCATTCAGGCAAGGCTTACAGACTGCTTCGCGGGCGGAGAGCACTCCGGCG 177
OY	441 GTGATGTTCAATCTCAAACTTGTGGCGCAGAGATGTCATGATTCATTATGATGATACC 500
Db	178 GCGAGGTCCCGGTCTCTCAGTCTGGCGCGCAGAGATGACAGCGCTTATGCGTACC 237
OY	501 ATCTGGACACAGCATGTGTACACTTTGAAAAATTTCTTCACTGG--CTACACCTCAGTG 557

Db	238	ACC	GGG	GCA	CGG	CGT	GG	CGG	CAT	CTG	GA	AT	CCG	CTT	CA	CGG	CTA	CTA	CTT	CA	AG	297							
Qy	558	ACTT	CA	AGG	CT	CT	GAG	GTG	TC	CA	AA	GACT	CA	GA	AA	GCTT	GCA	CT	GAT	CT	GAT	CT	CA	AA	AT	617			
Db	298	ACTT	CGA	AGT	GT	CG	GA	AGT	CT	TC	CA	AG	AT	CC	GG	AGG	CTT	TG	AA	CGA	AGT	CG	CGT			357			
Qy	618	TGG	GT	CTT	TTT	TG	CA	CA	AA	GGG	CGT	CA	CTT	CA	TG	CA	AC	CTT	GCA	TC	TG	TG	CTT			677			
Db	358	CCG	GAT	CTT	CGA	GA	AA	GGG	CG	CA	CA	TC	AT	GT	GA	CG	TT	CG	CG	CTT	GG	CGT	CA			417			
Qy	678	TG	TT	CC	TAT	TG	TAC	TAT	TAT	GT	GT	CT	GAG	TG	CA	CTA	AGT	GT	GGG	CT	CA	TT	GGG	TT		737			
Db	418	TG	AT	GG	CGG	CA	AT	CT	CT	CA	CGG	CG	TG	CGG	CGT	CGA	GT	CGG	AT	TC	CA	AT	CGT			477			
Qy	738	CAG	GAT	CT	CT	TG	AGG	GTG	CTT	TG	AT	GAT	GCA	AA	GCT	TAT	TG	GGG	CG	AT	GA	TT	CT	GG	CC	797			
Db	478	GCG	GCG	CA	CT	CGT	GG	CTT	G	CT	G	AT	TC	CA	AG	CGG	CG	AT	AT	TG	GG	CC	AT	AT	CG	CG	537		
Qy	798	ACT	AT	GTG	GT	TAT	TG	CA	CA	CA	AT	GT	TT	CA	CA	AG	GT	TG	CA	CAG	AT	CCT	CT	TG	GG	AA	857		
Db	538	ATT	AC	AG	GT	AT	GT	CG	CA	AC	CGT	GG	AT	CA	CA	GA	AT	CA	CG	CA	AT	CT	CA	TAG	CA	GG	CA	597	
Qy	858	GCTT	GA	CCG	GG	AT	TA	AG	CA	TTG	CTT	GG	TG	GA	AGT	TG	CA	CT	CA	AA	T	CT	CA	CC	AT	TT	GG	917	
Db	598	TCTT	AA	CGG	GA	T	CA	GC	AT	CGG	TG	TG	GA	AGT	GA	CC	CA	CA	CG	CA	CA	CT	CG	CT			657		
Qy	918	GCA	AC	AG	CTT	TG	AC	AT	ACC	CT	GA	T	TC	GA	CA	CA	CT	CCG	GT	CTT	G	CA	TTT	GT	GT	CG	977		
Db	658	GCA	AC	AG	CTT	G	AT	CA	CA	CC	CG	CA	CTT	CA	CA	CA	AT	CC	CG	GT	AT	TC	CG	CT	CT	CA	CC	717	
Qy	978	GAT	T	CTT	CA	AT	TC	CA	TA	CC	T	CT	CA	AT	TT	CT	TA	TG	GA	GA	AG	TT	GA	TT	CA	TT	G	103	
Db	718	GAT	CTT	CA	CT	CA	CT	CA	CT	CG	CTT	CA	T	AT	TG	GG	CG	AGT	CCT	GA	AA	TT	CGA	CA	AG	TT	G	777	
Qy	1038	CTA	G	TT	CTT	T	AT	CT	G	T	CA	CC	AG	CA	CTT	ACTT	TTT	T	AC	CGG	T	AT	T	GT	GT	TC	CA	GG	109
Db	778	CAC	GGT	CT	CT	AT	GT	CA	G	T	CA	CG	CA	CA	CT	CA	CT	CA	CC	GG	AT	CA	TT	CTT	CG	CG	CA	G	837
Qy	1098	TCA	ACT	GT	AT	CT	G	AG	CA	CA	AT	TC	G	CT	AT	TT	T	G	AGG	CG	AA	AA	AT	G	CA	G	TA	AG	115
Db	838	TC	AA	CTT	AT	CA	T	CA	CA	G	CTT	TTT	AT	T	AT	CT	CT	CA	CA	GGG	CG	CA	CT	TC	G	CA	CG	897	
Qy	1158	CTT	GA	CA	T	AT	G	GG	AT	TC	CTT	GT	T	TG	GA	CTT	GG	AT	TC	CTT	TT	AT	GT	GT	TC			121	
Db	898	CT	TA	AA	CTT	AT	AT	G	GT	AT	TC	CG	GG	TTT	CT	G	A	CG	T	GGT	TC	CC	GT	CTT	CG	AT	TT		

DB 1318 GGATGCGCGCGTTACAGCGCGTGACCTTAATTCGCCGCCCTTAAGAACTGGGT 1377
QY 1629 TGTGGAGCTGTTAATACCATGCTGAGCATTTGAGTTTAAAGTT 1679
DB 1378 ATGGGAGCTTAATACCATGCTGATTTGTTGTTGGTT 1428

RESULT 15
ABX15367
ID ABX15367 standard; cDNA; 1702 BP.
XX
AC ABX15367;
XX
DT 16-APR-2003 (first entry)
XX
DE Evening primrose delta-6-desaturase #1 cDNA.
XX
KW Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KW octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
KW evening primrose.
XX
OS Oenothera biennis.
XX
FH Key Location/Qualifiers
FT CDS 48..1406
FT /tag=a
FT /product= "Evening primrose delta-6-desaturase #1"
XX
PN US2002108147-A1.
XX
PD 08-AUG-2002.
XX
PF 21-DEC-2001; 2001US-0029756.
XX
PR 13-OCT-1992; 92US-0959952.
PR 19-SEP-1997; 97US-0934254.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
PA (THOM/) THOMAS T L.
XX
FI Thomas TL;
XX
DR WPI; 2003-066659/06.
DR P-PSDB; ABG73416.
XX
PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
PT for producing plant with increased gamma linolenic acid content, and
PT for inducing octadecatrienoic acid production in plant
XX
PS Claim 2; Fig 10; 55pp; English.
XX
CC The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GLA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GLA content from the plant
CC cell, for inducing or increasing production of GLA in an organism lacking
CC in or producing low levels of GLA and for inducing production of
CC octadecatrienoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecatrienoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GLA substrate. This sequence represents
CC cDNA encoding an evening primrose delta-6-desaturase polypeptide.
XX
SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;

Query Match 28.7%; Score 555; DB 25; Length 1702;

Best Local Similarity 64.8%; Pred. No. 2,8e-99;
Matches: 889; Conservative 0; Mismatches 470; Indels 12; Gaps 4;
QY 321 AGAAGAAAGTATACATACCTCAGAGAGCTGAAGGTCAACAAGAGAGAGATTAT 380
DB 58 AAGCTAAGAAATATATACAGCGCGAGAGCTCCGCCCAACAACTCCGGCATCT 117
QY 381 GGATCTCAATTAAGGTAGGTGTACATGTCTCAGATTGGGTCAAGAGACACCTGGT 440
DB 118 GATCTTCATCCAGGCGAAGGTCTACGACTCTCGTGGGCGGAGACACCCGGCG 177
QY 441 GTGATGTTCAATCTCAAAACCTTGCGCGAGAGATGCTACTGATCATTAAGCATACC 500
DB 178 GCGAGTCCCGCTCTCAGTCTGGCCGCGCAGAGACGTCAGACGCTTATTCGTAACC 237
QY 501 ATCTGGCAGACATGTGTACACCTTGAAAATTTCTCACTGG---CTACACCTCAGT 557
DB 238 ACCCGGACACGGGTGGCGGATCTGTGATCCGCTTCACCGGCTACTACTCAAG 297
QY 558 ACTTCAAGTCTCTGAGGTGCCAAGACTACAGAAAGCTTGCATCTGATCTCAAAAT 617
DB 298 ACTTCAAGTCTCTGAGATCTCCAGAGACTACCGGAGCTTTGAAGAGATGTGGGCT 357
QY 618 TGGGCTTTTGAACCCAAAGGCGATGCACTTCAATGACACCTTGATCTGTTGTTA 677
DB 358 CCGGATCTTCAGAAAGAGGCGCACACATCATGTGACGTTCTGCGGCTTGGTCA 417
QY 678 TGTTCCTCATTTGACTTATGTGTGTGTGAGTGCTACTAGTGTGTGGCTCATTTGGGT 737
DB 418 TGATGGCGGCAATCGTCTACGGGTGTGCGGTGCGATCGGATCGGATTCATGCTCT 477
QY 738 CAGGCATGCTCTTAGGGTGTGCTTGTGATGCAAGTGTGTAATGTGGCATGATCTGGCC 797
DB 478 GCGGCGACTGTGGGCTTGTGTGATCAAGCGCGGTATGTGGCATGATCTCGGCC 537
QY 798 ACTATGTGTTATGACCAACCAATGTTTCAACAAGTTGACAGATCTCTGGGAACT 857
DB 538 ATTACAGAGTATGATCCAAACCGGTGATACAAAGATCAAGCACTATAGCAGGCAACA 597
QY 858 GCTTGACCGGATTAAGCATTTGTTGTGGAAGTGAATCACAATGCTCACCACATTGGCT 917
DB 598 TCCCTAACCGAATACAGATCGCGGTGTGGAAGTGAACCAACGCCACCACTCCGCT 657
QY 918 GCAACAGCTTGACCATGACCCGTGATGTGACGACATGCGCGTCTTGACGTTTGGTGGC 977
DB 658 GCAACAGCTTGATGATGACCCGACCTCCAGACATCCCGTATTCGCGTCTCCACC 717
QY 978 GGTTCCTCAATTCATTAACCTCTCATTTCTATGTGGAAGAAAGTTGAGTTGATTTCAATG 1037
DB 718 GACTCTTCACTCATCATCAGCTCGGTCTTATGCGCAGATCTGAATTCGACGAATGG 777
QY 1038 CTAGGTTCTGATGTGCTACGACATTTACTTTTACCCGGTATGTGTTCGAGG 1097
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QY 1098 TCACTGTATTCGACACAATCTGCTATTTGTTGAGCGGAAAGTGAGATAGAG 1157
DB 838 TCAACTCTTCAATCAAGACCTTTTATTTGCTCTCACCAGCGGAGCTCTACCGCG 897
QY 1158 CTTGAACATTAATGGGATCTTGTGTTTGAAGTTGATCTCTTTAATGTCTTGGC 1217
DB 898 CTCMAACTTAATGGGATGCGGTTTTCGAGATGTGTTCCGCTCTTGCTATCTTGTGTC 957
QY 1218 TGCCAAATGGCTGAGAGGTTATGTTTGTGCTGCTAGCTTGTGCTTGTTCATTC 1277
DB 958 TCCGGAATCGCTGAACGCTTCGCGTTCGCTCATCAGCTTTCGCGTCAACGCGATTC 1017
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DB 1018 AGCAGTTCAGTATACCTCAACCATCTTCGCGCAACATAGTGGGCCCCCAAG 1077
QY 1338 GGAATGACTGGTTGAGAGAGACAGATGTGATCATGTGATCTTGTGCTCTTTCGA 1397


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Db      1078 GCGACAACTGGTTCGAGAGCAGAGAAAGGACATCATATATACGTGCCACCGTGA 1137
QY      1398 TGGATTGGTTTTTGGTGGCTTGCAGTTTCAGTTGAGCATCATTTGTTCCAGGCTAC 1457
Db      1138 TGGACTGGTTCTTTGGTGGGCTGCAAGTTCCAGTTGAGACACACTTGTCCCTAGGCTGC 1197
QY      1458 CTCGGTCCCAATTGAGAGAGATTTGGCCTTTGTTAGTGACCTTTGCAAGAGCATTAAT 1517
Db      1198 CGCGTGGGCAAGCTTAGAGAGATTCGCCCTTGGCTCGGGACTTGTATAGAGACAGGGA 1257
QY      1518 TGCCTTATAGAGAGCTTGTCAATTTG---GAGGCCAATCAAGTGAACAATTAGAACCTCA 1574
Db      1258 TGCCTATAGAGAGCTTGGGGTTTGGGACGACGCTTAATGTCAGAGACAATTGGAAGCTGA 1317
QY      1575 GAACTGCTGCCCTTCAAGCTTAGGACTTAA---CAAACCTGCCCCCTAAGAA---TTGT 1628
Db      1318 GGGATGGGGCGGTTCAAGCGGCTGACCTTAATTCGGCCCCGCTTAAGAACTTGGGT 1377
QY      1629 TGTGGGAAGCTGTTAATACCCATGCTGAGGCATTGGAGTTTGTAGAGTT 1679
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:48:07 ; Search time 2947.44 Seconds
(without alignments)
15947.709 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	740	38.3	776	10	BE658198
2	571.4	29.5	579	9	AI748200
3	487.6	25.2	592	10	BE347857
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9	432.4	22.4	868	14	CB291094
10	395	20.3	588	12	BM143768
11	391.8	20.3	588	12	BM143768
12	389.4	20.1	571	12	BI787611
13	388.4	20.1	575	14	CA938317
14	388.2	20.1	741	13	BU028011
15	387.6	20.0	676	13	BQ402431
16	387	20.0	742	13	BU025031
17	385	19.9	673	13	BF003445
18	384.2	19.9	736	13	BU025987
19	383.6	19.8	721	14	CB972537
20	381.4	19.7	403	9	AI988466
21	381.4	19.7	722	13	BU024653
22	377	19.5	725	13	BU025380
23	373.8	19.3	737	13	BU025297
24	372.8	19.3	585	13	BU811579
25	372.6	19.3	702	13	BU025281
26	372.2	19.2	585	14	CB829088
27	361.8	18.7	717	13	BU028018
28	360.4	18.6	957	10	BF268631
29	359.2	18.6	826	14	CB972811
30	358.8	18.6	607	14	CD037696
31	355	18.4	823	28	BH687867
32	354.6	18.3	715	28	BH927841
33	352.4	18.2	692	13	BU025175
34	350.8	18.1	674	14	CB002504
35	350	18.1	744	13	BO281359
36	349.8	18.1	673	14	CB002410
37	349.8	18.1	696	13	BQ153475
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39	346.2	17.9	505	10	BG726179
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ALIGNMENTS

RESULT 1
LOCUS BE658198/c
DEFINITION GM700005A20G6 Gm-r1070 Glycine max cDNA clone Gm-r1070-1836 3',
mRNA sequence.
ACCESSION BE658198
VERSION BE658198.1 GI:9984146
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 776)
Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Corryell, V., Erpelting, J., Rapp, C., Shoop, E., Pardinna, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)
TITLE A Functional Genomics Program for Soybean (NSF 9872565)
JOURNAL Unpublished
COMMENT Other ESTs: AI748200 corresponding to Gm-cl011-238 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147

Fax: (217) 333-4582
 Email: l-vodkin@iuc.edu
 This clone is available through: Genome Systems, Inc. 4633 World
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 427-3324 or contact: clones@genomesystems.com or info@genome
 systems.com web site: www.genomesystems.com
 Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'.

FEATURES

Source

1. .776
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1070-1836"
 /clone_1b="Gm-r1070"
 /note="The library Gm-r1070 is a sequence-driven, rerecked
 set of 9,216 clones selected from cDNA libraries from
 various tissues and stages of development of soybean that
 represent 2,639 sequences from immature cotyledons, 1,770
 from immature seed coats, 3,938 from flowers, and 869
 from young pods. The 5' ESTs of the source clones from
 the different libraries were used to select singletons, or
 a representative of each contig, which were rerecked to
 form library Gm-r1070. The cDNA clones of the rerecked
 Gm-r1070 library were then sequenced at the 3' end. The
 contig analysis to select unique genes was performed by
 the laboratory of Ernest Rezel, Center for Computational
 Genomics and Bioinformatics, University of Minnesota,
 http://www.cbc.umn.edu/ResearchProjects/Soybean/Index.html
 . Rerecking was performed by Genome Systems, St. Louis,
 http://www.genomesystems.com, and 3' sequencing by the
 Keck Center for Comparative and Functional Genomics,
 University of Illinois,
 http://www.life.uiuc.edu/biotech/keck.html. Note: The
 corresponding 5' EST from each clone in the Gm-r1070
 library is listed in the 'OTHER EST' field. The detailed
 information on the source library for each clone can also
 be obtained by referring to the Genome Systems clone ID of
 the original cDNA library that is also listed under
 'OTHER EST'.

BASE COUNT 269 a 189 c 139 g 168 t 11 others
 ORIGIN

Query Match 38.3%; Score 740; DB 10; Length 776;
 Best Local Similarity 98.7%; Pred. No. 6.9e-61;
 Matches 762; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 1090 TGGCAGGGTCAACTGTATCTGCAGACAAATTCGTAATGTTTCGAGCGAAAGTCA 1149
 DB 775 TNNCAGGGTCAACTGTATCTGCAGACAAATTCGTAATGTTTCGAGCGAAAGTCA 716
 QY 1150 GGATAGAGCTTGAACATAATGGGATCTTGTGTTTGAAGTTCCTCTTTAGT 1209
 DB 715 GGATAGAGCTTGAACATAATGGGATCTTGTGTTTGAAGTTCCTCTTTAGT 656
 QY 1210 GTCTGCTGCGCAATATGGCTGAGAGGTTAGTGTGCTGCTGCTGCTGCTGCTG 1269
 DB 655 GTCTGCTGCGCAATATGGCTGAGAGGTTAGTGTGCTGCTGCTGCTGCTGCTG 596
 QY 1270 TTCCATTCAGACACATTCAGTTCGTTTGAATCACTTTGCGCAATATATGTCGGCC 1329
 DB 595 TTCCATTCAGACACATTCAGTTCGTTTGAATCACTTTGCGCAATATATGTCGGCC 536
 QY 1330 ACCGAGTGGGAATGACTGTTTGAAGACAGCAAGTGTAATGTAATCTCTGTGC 1389
 DB 535 ACCGAGTGGGAATGACTGTTTGAAGACAGCAAGTGTAATGTAATCTCTGTGC 476
 QY 1390 CTCTTCATGATGATGTTTTCGTTGCTGCACTTCAGTTGAGATCAATTTGTTCC 1449
 DB 475 CTCTTCATGATGATGTTTTCGTTGCTGCACTTCAGTTGAGATCAATTTGTTCC 416
 QY 1450 AAGGCTACCTCGGTGCAATTTGAGGAAGATTTGCTTTGTTAGTACCTTTGCAAGAA 1509

DB 415 AAGGCTACCTCGGTGCAATTTGAGGAAGATTTGCTTTGTTAGTACCTTTGCAAGAA 356
 QY 1510 GGATATTTGCTCTTATAGAGCTGTGTCATTTTGGAGGCGCATTCAGTGACATTAGAC 1569
 DB 355 GGATATTTGCTCTTATAGAGCTGTGTCATTTTGGAGGCGCATTCAGTGACATTAGAC 296
 QY 1570 CCTCAGAGCTGCTGCGCTTCAAGAGTGAAGGACTTAAACAAACCTGCCCCCTAGATTTGT 1629
 DB 295 CCTCAGAGCTGCTGCGCTTCAAGAGTGAAGGACTTAAACAAACCTGCCCCCTAGATTTGT 236
 QY 1630 GTGGGAAGCTGTATATACCATGCTGAGGCAATTTGAGATTGAGATTGTTG 1689
 DB 235 GTGGGAAGCTGTATATACCATGCTGAGGCAATTTGAGATTGAGATTGTTG 176
 QY 1690 TCAAGCTCTTTTCTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1749
 DB 175 TCAAGCTCTTTTCTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 117
 QY 1750 TGGTACCCCCCACTTTTCAGATTGGCTTTGTAATTTAATTTTGTAGTGTGCTGA 1809
 DB 116 TGGTACCCCCCACTTTTCAGATTGGCTTTGTAATTTAATTTTGTAGTGTGCTGA 57
 QY 1810 CAAATGATGTGATCCA-GATGTTACTGCAAGTTCAATGCTTTGATCAAT 1860
 DB 56 CAAATGATGTGATCCANNNTGTTACTGCAATGCTTTGCAANNAAT 5

RESULT 2
 A1748200 579 bp mRNA linear EST 30-NOV-2001
 LOCUS sb49d11.y1 Gm-c1011 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-c1011-238 5' similar to TR:082348 082348 PURATIVE CYTOCHROME B5.
 ; mRNA sequence.

ACCESSION A1748200
 VERSION A1748200.1 GI:5126464
 KEYWORDS
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 579)
 Shoemaker R., Keim P., Vodkin L., Erpelting J., Coryell V., Khanna
 A., Bolla B., Matra M., Hillier L., Kueba T., Martin J., Beck C.,
 Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers
 Y., Person B., Swaller T., Gibbons M., Page D., Harvey N., Schurk
 R., Richter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann
 R., Waterston R. and Wilson R.
 Public Soybean EST Project

TITLE

Public Soybean EST Project

JOURNAL

Unpublished

Contact: Shoemaker R./Public Soybean EST Project

Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@wustl.edu

Possible reversed clone: similarity on wrong strand This clone is
 available through: Resgen, Invitrogen Corp. 2130 South Memorial
 Parkway Huntsville, AL 35801 For further information call: (800)
 1-533-4363 or contact via email: cu@resgen.com
 Insert Length: 1134 Std Error: 0.00
 High quality sequence stop: 412.

FEATURES

Source

1. .579
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1011-238"
 /issue_type="Immature cotyledons of greenhouse grown
 plants"
 /lab_host="DH10B"

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/clone lib="Gm-cl011"
/notes="Vector: Bluescript II SK+, Site 1: EcoRI, Site 2:
XhoI. This cDNA library was constructed from mRNA isolated
from immature cotyledons (100-200mg) of greenhouse grown
plants. The cDNA library was prepared using the life
Technologies superscript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a poly
(dT) sequence with a Not I restriction site. Sal I
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-Sal I restriction
site of the pSPORT 1 vector. The ligated cDNA fragments
were transformed into E. coli Electromax DH10B host cells.
This library was constructed by Dr. Lila Vodkin and Dr.
Anu Khanna."
BASE COUNT      119 a      126 c      143 g      187 t      4 others
ORIGIN
Query Match      29.5%; Score 571.4; DB 9; Length 579;
Best Local Similarity 99.1%; Pred. No. 5.3e-45;
Matches 572; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY      826  CAAACAAGTTGACACAGATCTCTCTGGGAAGTGGTGAACCGGATTAAGATTGCTG 885
DB      3    CAGCAAGTTGACACAGATCTCTCTGGGAAGTGGTGAACCGGATTAAGATTGCTG 62
QY      886  GAATGGAATCACAATGCTCAGACATTTGGTGCAAGCGCTTGACCATGACCTGATCT 945
DB      63  GAATGGAATCACAATGCTCAGACATTTGGTGCAAGCGCTTGACCATGACCTGATCT 122
QY      946  GCAGCAGATGCGCGCTCTTTCAGTTTGTGCGCGTCTTCAATTCATCACTCTGATTT 1005
DB      123  GCAGCAGATGCGCGCTCTTTCAGTTTGTGCGCGTCTTCAATTCATCACTCTGATTT 182
QY      1006  CTATGGAGAGAGTTGAGATTGATTCATTTGCTAGGTTCTTGATCTGTACAGACACTT 1065
DB      183  CTATGGAGAGAGTTGAGATTGATTCATTTGCTAGGTTCTTGATCTGTACAGACACTT 242
QY      1066  TACTTTTACCGGTATGATGATGCTGCGAGGTCATCTGTATCTGACAGACTTGTCT 1125
DB      243  TACTTTTACCGGTATGATGATGCTGCGAGGTCATCTGTATCTGACAGACTTGTCT 302
QY      1126  ATTGTTTTCGAGCGCAAAAGTGCAGATAGAGCTTGAACATATAGGGATCTTGTT 1185
DB      303  ATTGTTTTCGAGCGCAAAAGTGCAGATAGAGCTTGAACATATAGGGATCTTGTT 362
QY      1186  TTGAGCTTGGTCTCTCTTTTATGTCCTTGCCTGCAAAATTTGCTGAGAGGTTATGTT 1245
DB      363  TTGAGCTTGGTCTCTCTTTTATGTCCTTGCCTGCAAAATTTGCTGAGAGGTTATGTT 422
QY      1246  TGTGCTTGTAGCTTTGCTGTTTGTTCATCCAGACATTCAGTTCTGTTGAATCACTT 1305
DB      423  TGTGCTTGTAGCTTTGCTGTTTGTTCATCCAGACATTCAGTTCTGTTGAATCACTT 482
QY      1306  TGTGCAAAATGATATGTCGGGCGCACCGAGTGGAAATGACTGTTTGAGAGAAGCAAG 1365
DB      483  TGTGCAAAATGATATGTCGGGCGCACCGAGTGGAAATGACTGTTTGAGAGAAGCAAG 542
QY      1366  TGTGATCATGATATCTCTTGTGCTCTTGTGATGAT 1402
DB      543  TGTGATCATGATATCTCTTGTGCTCTTGTGATGAT 579
RESULT 3
BE347857      592 bp      mRNA      linear      EST 04-DEC-2001
LOCUS      gp06107.y1 Gm-cl041 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION      Gm-cl041-2102 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
B5. i. mRNA sequence.
ACCESSION      BE347857
VERSION      BE347857.1 GI:9259710
KEYWORDS      EST.
SOURCE      Glycine max (soybean)

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ORGANISM      Glycine max
REFERENCE      Glycine max
AUTHORS      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; rosids
; eurosid1; Fabiales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 592)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Rheising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mccam
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Trace considered overall poor quality This clone is available
through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway
Huntsville, AL 35801 For further information call: (800)-533-4363
or contact via email: ccu@resgen.com
Insert Length: 149 Std Error: 0.00
High quality sequence stop: 1.
FEATURES
source
1..592
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl041-2102"
/cisue_type="Senescing leaves, mature plant, greenhouse
grown"
/lab_host="DH10B"
/clone_lib="Gm-cl041"
/notes="Vector: pTR73Pac (Pharmacia); Site 1: EcoRI;
Site 2: HindIII; This library was constructed from mRNA
isolated from senescing leaf tissue of mature greenhouse
grown plants of the cultivar Williams. Complementary DNA
was synthesized from mRNA using a 3' anchored poly(dT)
primer. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by digestion with EcoRI and
HindIII. The cDNA fragments were directionally cloned
into the EcoRI-HindIII restriction site of the pTR73-Pac
vector. The ligated cDNA fragments were transformed into
DH10B host cells. This library was constructed by Dr.
Randy Shoemaker."
BASE COUNT      132 a      124 c      139 g      197 t
ORIGIN
Query Match      25.2%; Score 487.6; DB 10; Length 592;
Best Local Similarity 89.2%; Pred. No. 3.7e-37;
Matches 526; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY      822  GTTTCACAAGTTGACACAGATCTCTCTGGGAATGCTTTAGCGGGAATGAGATTGCTT 881
DB      3    GTTTCACAAGTTGACACAGATCTCTCTGGGAATGCTTTAGCGGGAATGAGATTGCTT 62
QY      882  GGTGGAAGGAGCTACATGCTCAGACATTCGCGGCAACAGCGCTTGACCATGAGCCCTG 941
DB      63  GGTGGAAGGAGCTACATGCTCAGACATTCGCGGCAACAGCGCTTGACCATGAGCCCTG 122
QY      942  ATCTGACAGACATGCGGCTCTTTCAGTTTGTGCGGCTTCTTCAATTCATTAACCTCTC 1001
DB      123  ATCTGACAGACATGCGGCTCTTTCAGTTTGTGCGGCTTCTTCAATTCATTAACCTCTC 182
QY      1002  ATTTCTATGGAAGAGAGTTGAGATTGATTCATTTGCTAGTCTTCTTGAATCTGTACAGC 1061
DB      183  ATTTCTATGGAAGAGAGTTGAGATTGATTCATTTGCTAGTCTTCTTGAATCTGTACAGC 242
QY      1062  ACTTTACTTTTACCCGGTAATGATGTTGCCAGGGTCAACTTGTATCTGACAGACAATTC 1121

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Db 243 ACTTACTTTTACCCGTATGATGAGTTGCCAGGGTCACTGTATCTCAGACAAATTC 302
 QY 1122 TGTATTTTGTGAGGCGGAAAGTGAAGATAGAGCTTGAACATTAATGGGATCCTTG 1181
 Db 303 TGTATTTTGTGAGGCGGAAAGTGAAGATAGAGCTTGAACATTAATGGGATCCTTG 362
 QY 1182 TGTATTTGAGCTTGGTCCCTCTTTTGTGAGTGTGCTGCGCAAAATGGGCTGAGAGGTTA 1241
 Db 363 AGTTTGTGAGCTTGGTCCCTCTTTTGTGAGTGTGCTGCGCAAAATGGGCTGAGAGGTTA 422
 QY 1242 TGTATTTGAGCTTGGTCCCTCTTTTGTGAGTGTGCTGCGCAAAATGGGCTGAGAGGTTA 1301
 Db 423 TGTATTTGAGCTTGGTCCCTCTTTTGTGAGTGTGCTGCGCAAAATGGGCTGAGAGGTTA 482
 QY 1302 ACTTGTGCAATATGATATGATGAGGCGGCGGAGAGTGAAGTGAAGTGAAGAGAGA 1361
 Db 483 GCTATGATGAGATGATATGATGAGGCGGCGGAGAGTGAAGTGAAGTGAAGAGAGA 542
 QY 1362 CAAGTGTATGATGATATGATGAGGCGGCGGAGAGTGAAGTGAAGTGAAGAGAGA 1411
 Db 543 TCAGTGTATGATGATATGATGAGGCGGCGGAGAGTGAAGTGAAGTGAAGAGAGA 592
 RESULT 4
 LOCUS AY103762 1764 bp mRNA linear HTC 16-OCT-2002
 DEFINITION Zea mays P00087385 mRNA sequence.
 ACCESSION AY103762
 VERSION AY103762.1 GI:21206840
 KEYWORDS Zea mays
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1764)
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1764)
 Coe, E.H.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
 COMMENT
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
 location/Qualifiers
 1. 1764
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeDB:634923"
 /db_xref="taxon:4577"
 /clone_11b="Maize Mapping Project/Dupont Consensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
 BASE COUNT 310 a 602 c 456 g 396 t
 ORIGIN
 Query Match 24.8%; Score 479.8; DB 11; Length 1764;
 Best Local Similarity 60.9%; Pred. No. 9.2e-37;

Matches 816; Conservative 0; Mismatches 517; Indels 6; Gaps 2;
 QY 335 ATAACTCAGAGAGCTGAAGGCTCACAACAAGAGAGATTTATGATCTCAATTCAA 394
 Db 155 ATCTCTCCAGAGAGCTCCGCGCTTACGCTTCCGCGAGAGACTCTGATCTTCATCTCC 214
 QY 395 GGTAAAGTGAACATGCTCAAGTTGGGTCAAGAGACACCTGGTGGTATGTTCCAAATC 454
 Db 215 GCGAGCTGTAGAGAGCTCAAGCTTGGCTTCCCAACACCCGCGGCGGACCTCCGCTT 274
 QY 455 TCAAACTTGTGCGCGAGAGATGCTAGTATGATATGATATGATATGATATGATATG 514
 Db 275 CTCACCTTGTGCGCGAGAGAGCTCAAGCTTGGCTTCCCAACACCCGCGGCGGAG 334
 QY 515 TGTGACACCTTGAATAAATTTCTTCACTGCTACCACTGATGATCTCAAGCTCTGAG 574
 Db 335 CGCGCGCTCTCCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 391
 QY 575 GTGTCCAAAGACTACAGAAAGCTTGATCTGATCTGATCTGATCTGATCTGATCTGAT 634
 Db 392 GCGTCCGCGAGCTACCGCGCGCTCTCGCGAGCTATCTCGCGGCGCTCTTGAAGCG 451
 QY 635 AAGGCGATGTCACTTATGACACCTTGATCTGTTGCTGTTATGTTCTCATTTGATCTC 694
 Db 452 GTGCGCCCAACCCCAAGGTCCAGCTCTGATGCGGCTCTCTTCTTCAAGCGCGCTG 511
 QY 695 TATGCTGTCTGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 754
 Db 512 TACCTGCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 571
 QY 755 TTGCTTTGATGCAAGTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 814
 Db 572 TTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 631
 QY 815 ACCAATGTTTCAACAAGTTGCAAGATCTCTCTGGAATCTGCTGCAACCGGATTAAC 874
 Db 632 CATCCGCTCTGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
 QY 875 ATGCTTGTGAGAGGAGCTCAACATGCTCAACATGCTCAACATGCTCAACATGCTCAAC 934
 Db 692 ATGCTTGTGAGAGGAGCTCAACATGCTCAACATGCTCAACATGCTCAACATGCTCAAC 751
 QY 935 GACCTGATCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994
 Db 752 GACCTGATCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
 QY 995 ACCTGCTATTTATGAGAGAGAGTGAAGTGAATTTATTTATTTATTTATTTATTTAT 1054
 Db 812 TGTGCTTACTTCAACAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
 QY 1055 TACGACACTTAACTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1114
 Db 872 TACGACACTTAACTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
 QY 1115 ACAATCTGCTATTTGTTTCAAGAGCGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1174
 Db 932 TCGCGCTTGTGCTTCAAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 991
 QY 1175 ATCTTGTGTTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
 Db 992 GTGCGCAATTTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1051
 QY 1235 AGGCTATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1294
 Db 1052 AGGCTATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111
 QY 1295 TTGAATCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1354
 Db 1112 CTGAACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
 QY 1355 AAGCAGCAAGTGTATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1414
 Db 1172 AAGCAGCAAGTGTATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231

Qy	1415	GGCTTGCAGTTTCAGCTTGAGGATCATTTGTTTCCAAAGCTACCTGGGCGCAATTGAGG	1474
Db	1232	GGCTCGCAGTTCCAGATTGAGACACATCTGTTTCCCGCTACCTCGGTGCACCTTGGC	1291
Qy	1475	AAGATTTGCGCTTTGGTTAGTGACCTTTGGCAAGACATTAATTGGCTTAATGAGAGCTTG	1534
Db	1292	AAGGTTCACCGGCGCGTCCGGACCTTTGGCAAGACATGGGCTCACTTAATTTCGACACC	1351
Qy	1535	TCATTTTGGAGGGCCCATCAGTCGCAATTGAGACCTCAGGACCTGCGCCCTCAAGCT	1594
Db	1352	ACATTTCTGGGTCGCAATATGTCTTACAGAGAGACACTCAGGAGCTGCTGCATTGAGGCC	1411
Qy	1595	AGGGACTTAACAA--ACCTGCGCCCTAAGAAATTTGTTGGGAAGCTGTTAATCCCAT	1651
Db	1412	AGGACCGCTACAAGTGCTGTGCTCTCCGAAGAAATTTGATGGGAAGCTGTGMAACCCAT	1471
Qy	1652	GGCTGAGGCAATTTGGAGTT	1670
Db	1472	GGATTAATGGAGTGAAGAT	1490

RESULT 5	LOCUS	DEFINITION
BI311411	BI311411	772 bp mRNA linear EST 20-JUL-2001
	EST531316	GEDD Medicago truncatula cDNA clone GEDSD10F10 5' end, mRNA sequence

```

TIGR sequence name: MTPA129TK
More information is available at: www.medicago.org
Seq primer: Skm0d (CTA gaa CTA gtc gat cc).
Location/Qualifiers
1..772
source

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/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="pGESD10F10"
/tissue_type="Immature seeds"
/dev_stage="Immature seeds, 11 to 19 days after
pollination"
/clone_id="GESD"
/note="Vector: pBluescript SK-; Site_1: EcoRI, Site_2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA
enriched RNA. The cDNA was directionally ligated into
the Uniap XR vector from Stratagene and packaged using
Gibpack III Gold packaging extracts. Plasmids containing

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CDNA inserts were excised from the recombinant lambda-dag phage using Ex-assist helper phage and propagated in XL0LR cells."	
BASE COUNT	172 a 158 c 161 g 281 t
ORIGIN	

Query Match	24.7%	Score 478.4	DB 12	Length 772
Best Local Similarity	77.8%	Pred. No. 2.2e-36		
Matches 591, Conservative	0	Mismatches 166	Indels 3	Gaps 1

OY	902	GCTACACCAATTTGGGTGACAGGCTTGTACCATGACCTGTATCTGCAGACACATGCGCGTC	961
Db	6	GCTCATCATTTGCTGTCGATATAGCTCTGATTATGATCTGTATTTGCAGACATATCCCTGTT	65
OY	962	TTTGCAGTTTGGTGGCGGGTCTTGCATTTCCATTAACCTTCAATTTCTATGGAGGAATTG	1022
Db	66	TTGCGTGTCTCATGCGCATTTCTTTGGTTTCGATTAATCTTATTTCTATGATGACAGTTA	125
OY	1022	GAGTTTGAATTCATTTGCTAGGTTCTGTATCTGTACCAAGCATTTACTTTTAAACCGGTA	108
Db	126	AAGTTTATGCTTTGTGCMAAGTTTCTTATCAGTTACCGACATATCACCTTTTAAACCTGTTC	185
OY	1082	ATGTGTGTGCGAGGGTCAACTTGTATCTGAGACAAATTCGTATTTGTTTTCG---AGG	113
Db	186	TTTGTTTTCGAAGGCTTTAATCTTTGACTTCAACATTTTGTCTTTGTTTTCGCCATCA	245
OY	1139	CGAAAGTGCAGATATAGACCTTGACATPAATGGGGATCCTTGTGTTTGTGAATTGGTTTC	1199
Db	246	CGAATATGTTCTGATTAAGGCTTTAACAACATCATGAGGTATCGGTGTCTTCGACCTTGTTTC	305
OY	1199	CCTCTTTTAGTGTCTTGCTGTGCCAAATTTGGCTTGAGAGGCTTATGTTGTGCTGTAC	1255
Db	306	CCTGTGCTATATGTCAAGCCCTCCCAAGTTGGCGAGAAAGCTCATGTTGTGTTCTTGT	365
OY	1259	TTTGCCTGTTTTCATCCAGACAAATTCAGTCTCTGTTGAATCACTTTGCTGCAATATGA	1311
Db	366	TTTGTGTTTTCATCATTCAACATCTTCAATCTGTGTGAACATTTGCTGCAAACTGT	425
OY	1319	TATGTGGGGCACCGAGTGGGAATGACTGTGTTTGAAAGACAGACAAAGTGTACATTTGAT	1379
Db	426	TATCTGGGTCCAGCGAGGAAATGATTGGTTTGAAACAAACAGCTGGAAATTTGGAT	485
OY	1379	ATCTCTGTGCTCTTTCGATGGAATTTGTTTTCGTTGGCTTGCAGTTTCAGTTAGCAT	1433
Db	486	ATCATCTGTTTCMAATGATGATGATTGGTCTTGTGTGTTTGCAGTTTCAGTTTAAACAT	545
OY	1439	CATTTGTTTCCAAAGCTACCTCGGGGCCAATTTGAGGAATTTGGCCTTTGGTTTGTAC	1499
Db	546	CATTGTGTTCCAAAGCTCTTCAAGGCTCAATTTGAGGAAGTTTGCCTCATTTGGTATTTGAT	605
OY	1499	CTTTGCAAGAAAGCATTAATTTGCCCTTATATAGAGCTGTTCATTTTGGGAGGCCCATCAGTGG	1559
Db	606	CTATGCAAGAAAGCATTAATTTGCCCTTACGAAGTTTGTATATTGTTGAGAGGCATCTTTGG	665
OY	1559	ACAAATTAGACCTTCAGACTGTGCTGCCCTCAACAGCTTAGGAACTTAAACAAACCTTGCCCT	1619
Db	666	ACTCTCAAGACTTTAGGACTGTGCTGCAATTTGACAGCAAGGGAATTTTACCAACTCTCTTCA	725
OY	1619	AAGAATTTGTTGNGGAAGCTGTATATATCCATGCTTAG	1658
Db	726	CAGAACTTGTGTGGAACTTTTATATCTATGCTGAG	765

RESULT	6
LOCUS	BG647198
DEFINITION	BG647198 783 bp mRNA linear EST_24-APR-2001 EST508817 HOGA Medicago truncatula cDNA clone phoga-15P24 5' end,
ACCESSION	BG647198
VERSION	BG647198.1 GI:13782310
KEYWORDS	EST.
SOURCE	Medicago truncatula (barrel medic)
ORGANISM	Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 783)

Hahn, M.G., Ojansen-Reubs, T., Samac, D., Town, C.D., Van Aken, S., Utebach, T., Cho, J., and Fraser, C.M.
ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20

Unpublished
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu
G390804e TIGR sequence name: MTMBV96TK More information is available at: www.medicago.org
Seq primer: Skmod (CTA GAA CTA gtc gat cc).
Location/Qualifiers

FEATURES
Source
1..783
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="phOGA-15P24"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
/clone_11b="HOGA"
/note="Vector: pBluescript SK-; Site 1: EcoRI, Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."

BASE COUNT 173 a 142 c 169 g 299 t

ORIGIN

Query Match 24.4%; Score 471.2; DB 10; Length 783;
Best Local Similarity 76.8%; Pred. No. 1e-35;
Matches 602; Conservative 0; Mismatches 178; Indels 4; Gaps 2;

QY 696 ATGGTCTTCTAGAGTGCATAGTGTGGCTCATTTGGGTTGAGGATCTTTAGGCT 755
DB 1 ATGGT 60
QY 756 TGGCTTGGATGCAAGTCTTATGTGGGCGCATGATTTGGCGCATGATGTGTATGACA 815
DB 61 TGGTATGATGCAAGTCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 120
QY 816 CCAATGTTTCAAGTGTGACAGATCTCTCTGTGGAGCTGTGACGGGATTAAGCA 875
DB 121 GTGGAATTAACAATTAAGCAAAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 876 TTGCTTGGTGAAGTGTGACATCAATGCTACCAATTTGGGTGCAAGCCTTGACCAT 935
DB 181 TTGCTTGGTGAAGTGTGACATCAATGCTACATATGCTTGGCAATGATCTGTATATG 240
QY 936 ACCCTGATGTGACAGACATCCGGTCTTTGCAAGTTGTGTGGGTTTCAATTCATAA 995
DB 241 ATCTGATTTGACAGATATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 300
QY 996 CCTCTCATTTCTATGGAGAGATGTGAGTTTATTTCAATGCTAGTCTTGTATGCT 1055
DB 301 AATCTTATTTCTATGATGACAGTAAAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 1056 ACAGAGCTTACTTTTACCCGGTAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1115

DB 361 ACCAGATATCACTTTTACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 1116 CAATTCCTGCTATTTGTTGG---AGCGAAAGTGAGATTAAGCCTTGAACATATG 1172
DB 421 CATTTTGTCTGTTGTTTGGCCATCAGAAAGTTCTTATAGCTTTTCAACATCATGG 480
QY 1173 GGAATCTTGTGTTTGGACTGTGGTCCCTTTTATGTTGCTTGGCCCAATTTGGCCTG 1232
DB 481 GTATCGGT 540
QY 1233 AGAGGTTATGTTTGT 1292
DB 541 AAGGCTCATGTTTGT 600
QY 1293 GTTGAATCATTTTGT 1352
DB 601 GTTTGAACCATTTTGT 660
QY 1353 AGAAGCAGACAAAGTGTATGATGATATCTTGTGCTCTTGTGATGATGATGTTTTCG 1412
DB 661 AGAAACAAACAGCTGGAACATTTGATATCACTTTTCAACATGATGATGATGTTTTCG 720
QY 1413 GTGGCTTGAAGTTTCAAGCTTGTGACATCATTTTGTTCGAAAGCTTCTGCTGCAATTGA 1472
DB 721 GTGGTTTGCAGTTTCAAGTTTGAACATCATTTTGTTCGAA-GCTTCTTAGGGCTCAATTGA 779
QY 1473 GGAA 1476
DB 780 GGAA 783

RESULT 7
CA935212 449 bp mRNA linear EST 30-DEC-2002
LOCUS saus0d04.y1 Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1071-4376 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME B5. /, mRNA sequence.
CA935212
VERSION CA935212.1 GI:274235692
KEYWORDS EST.
ACCESSION CA935212
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
1 (bases 1 to 449)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Reggen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@reggen.com web site: www.reggen.com
Seq primer: -40RP from Gibco.

FEATURES
Source
1..449
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1071-4376"

/issue_type="Immature pods (~2cm long) of greenhouse grown plants"
 /lab_host="DH10B"
 /clone_lib="Gm-cl071"
 /note="Vector: pSPORT1, Site 1: NotI, Site 2: SalI; The cDNA library was constructed from mRNA isolated from Immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life Technologies superscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. email: l-vodkin@uiuc.edu"

BASE COUNT 86 a 86 c 115 g 162 t

Query Match 23.2%; Score 449; DB 14; Length 449;
 Best Local Similarity 100.0%; Pred. No. 1.9e-33;
 Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1015 GAAGTTGAGTTGATTTGATTCCTGCTGATCTGTACACACTTTACTTTTA 1074
 1 GAAGTTGAGTTGATTTGATTCCTGCTGATCTGTACACACTTTACTTTTA 60
 1075 CCCGGTAATGTGTGTGTCAGAGGCTCACTTGTATCTGCAGACAATCTGCTATTTTTC 1134
 61 CCCGGTAATGTGTGTGTCAGAGGCTCACTTGTATCTGCAGACAATCTGCTATTTTTC 120
 1135 GAGCGCAAAAGTCAGAGATGAGCTTGAACATTAATGGGAGCTCTTGTGTTTGAAGTTG 1194
 121 GAGCGCAAAAGTCAGAGATGAGCTTGAACATTAATGGGAGCTCTTGTGTTTGAAGTTG 180
 1195 GTTCCCTCTTTAGTGTCTTGTGCTGCAATTTGGCTGAGAGGTTATGTTGTGCTTGC 1254
 181 GTTCCCTCTTTAGTGTCTTGTGCTGCAATTTGGCTGAGAGGTTATGTTGTGCTTGC 240
 1255 TAGCTTGTGTTGTTGTTCCATCCAGACAATTCAGTTCTGTTGATCACTTTGCTGAAA 1314
 241 TAGCTTGTGTTGTTGTTCCATCCAGACAATTCAGTTCTGTTGATCACTTTGCTGAAA 300
 1315 TGTATATGTGCGGCCACCGAGTGGAAATGACTGTTTGAAGAAGCAGACAAGTGTACATT 1374
 301 TGTATATGTGCGGCCACCGAGTGGAAATGACTGTTTGAAGAAGCAGACAAGTGTACATT 360
 1375 GATATCTCTTGTGCTCTTTCATGATGATTTGTTTGGTGGCTTGCAGTTTCAGTTGA 1434
 361 GATATCTCTTGTGCTCTTTCATGATGATTTGTTTGGTGGCTTGCAGTTTCAGTTGA 420
 1435 GCATCATTTGTTTCCAAAGCTACCTCGGT 1463
 421 GCATCATTTGTTTCCAAAGCTACCTCGGT 449

RESULT 8
 CB291093/c 892 bp mRNA linear EST 28-FEB-2003
 LOCUS UCRCS01_02bd10 b1 Washington Navel orange cold acclimated flavedo &
 DEFINITION albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02bd10, mRNA
 sequence.
 ACCESSION CB291093
 VERSION CB291093.1 GI:28616550
 KEYWORDS EST.
 SOURCE Citrus sinensis
 ORGANISM Citrus sinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE 1 (bases 1 to 892)
 AUTHORS Close, R.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kim, H.R.,
 Kudrna, D., Manamaker, S., Ming, R., and Yu, Y.
 TITLE Development of EST Resources and New Genetic Markers for California
 Citrus
 JOURNAL Unpublished
 COMMENT Contact: Timothy Close
 Department of Botany & Plant Sciences, University of California
 Riverside, CA, 92521-0124
 Tel: 9097873318
 Fax: 9097874437
 Email: timothy.close@ucr.edu
 Seq primer: 17.

FEATURES

source 1. 892
 Location/Qualifiers
 /organism="Citrus sinensis"
 /mol_type="mRNA"
 /cultivar="Washington Navel"
 /db_xref="taxon:2711"
 /clone_lib="UCRCS01_02bd10"
 /issue_type="Rind containing flavedo and albedo"
 /dev_stage="Mature fruit"
 /lab_host="E. coli T0C121"
 /clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"
 /note="Vector: lambda uni-zap XR, excised phagemid; Site 1: EcoRI, Site 2: XhoI; plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified. A cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of phagescript SK(-) phagemide. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemide were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI350 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Ming, Yu). Chromatogram files were transmitted to UC Riverside (by Yu). Then processed at UC Riverside (by Manamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 306 a 194 c 167 g 225 t

Query Match 22.9%; Score 443.4; DB 14; Length 892;
 Best Local Similarity 79.4%; Pred. No. 3.8e-33;
 Matches 525; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

1013 AGAAGTTGAGTTGATTTGATTCATGCTGATCTGTACACACTTTACTTTT 1072
 891 AAAAAATTGATTTGATTCCTGCTGATTCCTGTGAGTTACAGAGATTTGACATTT 832
 1073 TACCGGTAATGTGTGTGTCAGAGGCTCACTTGTATCTGCAGACAATTCGCTATTTT 1132
 831 TACCGGTAATGTGTGTGTCAGAGGCTCACTTGTATCTGCAGACAATTCGCTATTTT 772
 1133 TCGAGCGCAAAAGTCAGAGATGAGCTTGAACATTAATGGGAGCTCTGTGTTTGGACT 1192
 771 TCMAAGCGTAAGTCCAGATGAGCTTGAACATTAATGGGAGCTCTGTGTTTGGACT 712
 1193 TGGTCCCTCTTTAGTGTCTTGTGCTGCAATTTGGCTGAGAGGTTATGTTTGTGCTT 1252


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Db      711 TGGTCCCACTTCAAGTTATCTACCAACAGGCGCTTAAGGGGATGTTTGATG 652
Qy      1253 GCTAGCTTCTGTTGTTGCTTCATCCAGCAATTCAGTTCTGTTGAATCCTTTGTCGA 1312
Db      651 GCAAGTTTACTGTCAAGGCGCTCAACACATTCAGTTTGTAAACCACTTGTGCGCA 592
Qy      1313 AATGATATGTGGGCGCAGGAGTGGAATGATCGGTTTGAAGAGCAGCAAGGAGTACA 1372
Db      591 AAGCTGATTTTGTGCTCCGCTTAAGGAGATGATGTTTGAAGACAAAGTGGAGCA 532
Qy      1373 TTGGATATCTCTGTGCTCTTCATGATGATGTTTTCGATGCTTGAAGTTCAAGCTT 1432
Db      531 TTGGATATCTCTGTGCTCTTCATGATGATGTTTTCGATGCTTGAAGTTCAAGCTT 472
Qy      1433 GAGCATATTTGTTTCCAGGCTACCTCGGTGCCAATTGAGAAAGATTGGCTTGGTT 1492
Db      471 GAGCATATTTGTTTCCAGGCTACCTCGGTGCCAATTGAGAAAGATTGGCTTGGTTG 412
Qy      1493 AGTGACCTTGGCAAGACATTAATTTGCTTATAGAGCTGTGATTTTGGAGGCGCAAT 1552
Db      411 AGGATTTTGGCAAGACATTAATTTGCTTATAGAGCTGTGATTTTGGAGGCGCAAT 352
Qy      1553 CAGTGCATATTTAGACCTCAGGACTGTGCTTCAAGCTAGGAGCTTAACAAACCTT 1612
Db      351 GTGTGACCTTTAGACCTCAGGAGGTGCTGCTTCAAGCTCGGAGCTCAACAAACCTT 232
Qy      1613 GCCCTTAAGATTTGTTGGGAAAGCTGTTAATCCATGCTGAGGCAATTTGAGTTT 1672
Db      291 GTCCCAAGATTTGCTTGGGAAAGCTTAAATCATGCTGATGTTGTTTCTTT 232
Qy      1673 T 1673
Db      231 T 231

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RESULT 9
LOCUS   CB291094/1 868 bp mRNA linear EST 28-FEB-2003
DEFINITION
UCRCS01_02bd10.g1 Washington Navel orange cold acclimated Flavado &
albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02bd10, mRNA
sequence.
ACCESSION
CB291094
VERSION
CB291094.1 GI:28616551
KEYWORDS
EST.
SOURCE
Citrus sinensis
ORGANISM
Citrus sinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eustosids II; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 868)
Close,T.J., Collura,K., Fenton,R.D., Feuerbacher,O., Kim,H.R.,
Kudrna,D., Wamamaker,S., Wing,R. and Yu,Y.
Development of EST Resources and New Genetic Markers for California
Citrus
JOURNAL
Unpublished
COMMENT
Contact: Timothy Close
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124
Tel: 9097873318
Fax: 9097874437
Email: timothy.close@ucr.edu
Seq primer: T3.
Location/Qualifiers
source
1..868
/organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Washington Navel"
/db_xref="taxon:2711"
/clone="UCRCS01_02bd10"
/tissue_type="Rind containing flavado and albedo"
/dev_stage="Mature fruit"
/lab_host="B. coli TUC121"

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```

/clone lib="Washington Navel orange cold acclimated
flavado & albedo cDNA library"
/note="Vector: lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
field at University of California, Riverside Agricultural
Operations since 1983. The action was Washington Navel
orange and the rootstock Carizzo Citrange. Tissue from
mature fruit was harvested at mid-day in January 2002
during a cold spell, when pre-dawn temperatures were
approximately -2 to 2 degree C. Approximately 2 cm median
sections of the rind were excised in the field from
several fruits, then wrapped in aluminum foil and frozen
quickly in dry ice. Total RNA was extracted using a phenol
extraction procedure described in J. Japanese Soc. Hort.
Sci. (1996) 64:809-814. Poly(A) RNA was purified. A cDNA
library was made, and 1 million primary lambda cDNA clones
were in vivo excised to give a population of plasmids
SK(-) phagemids. All steps to this point were performed in
the TJ Close lab at the University of California,
Riverside (Fenton). Phagemids were plated, plasmid DNA
purified, cDNA clones archived, and DNA sequences
determined bi-directionally using an ABI350 at the
Arizona Genomics Institute, University of Arizona (Collura
, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files
were transmitted to UC Riverside (by Yu), then processed
at UC Riverside (by Wamamaker) using the HareEST pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a pruned 17
region of at least 100 bases were deposited to GenBank."
BASE COUNT
296 a 190 c 161 g 221 t
ORIGIN
Query Match 22.4%; Score 432.4; DB 14; Length 868;
Best Local Similarity 80.1%; Pred. No. 4.2e-32;
Matches 508; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
Qy 1040 AGGTTTATGTCGACACGACCTTACTTTTACCGGTATGTTGTCAGAGGTC 1099
Db 868 AGATTCTCTTGAGTTACACGACATTTGACATTTTACCTGTTATGTTGTCAGAGTA 809
Qy 1100 AACTTGTATCTGACAGCAATTCGTATGTTTTCAGGCGAAGATGAGATAGAGCC 1159
Db 808 AATTATATTTACAGACATTTTGTATTGTTTAAACGTAAGGTCCAGATAGAGCC 749
Qy 1160 TTGAACATATGAGGATCCTTGTGTTTGAAGTTGCTTCTTTTATGTTGCTTGC 1219
Db 748 TTGAACATATGAGGATCCTTGTGTTTGAAGTTGCTTCTTTTATGTTTATCTTA 689
Qy 1220 CCAATTTGCGGAGAGGTTATGTTTGTGCTTGTGCTTGTGTTGTTGTCATCCAG 1279
Db 688 CCAATTTGCGGAGAGGTTATGTTTGTGCTTGTGCTTGTGTTGTTGTCATCCAA 629
Qy 1280 CACATTCAGTTCTGTTGATCATCTTGTGCAATATGATGTCGGGCGACGAGTGGG 1339
Db 628 CACATTCAGTTCTGTTGATCATCTTGTGCAATATGATGTCGGGCGACGAGTGGG 569
Qy 1340 AATGACTGTTGAGAGCAGACAGTGTATCTCTTGTGCTTGTGCTTGTGATG 1399
Db 568 AATGACTGTTGAGAGCAGACAGTGTATCTCTTGTGCTTGTGCTTGTGATG 509
Qy 1400 GATTGTTTTTGGTGTGCTGATGTTGCTGAGCATATTTGTTTCAAGGCTACCT 1459
Db 508 GATTGTTTTTGGTGTGCTGATGTTGCTGAGCATATTTGTTTCAAGGCTACCT 449
Qy 1460 CGGTGCAATTTGAGAGATTTGCTTGTGTTAGTATGCTTGTGCAAGAGCATATTTG 1519
Db 448 AGGTGCAATTTGAGAGATTTGCTTGTGTTAGTATGCTTGTGCAAGAGCATATTTG 389
Qy 1520 CTTTATAGAGCTTGTATTTTGGAGGCGCAATCACTGACATTTAGACCTCAGAGCT 1579
Db 388 CTTTATAGAGCTTGTATTTTGGAGGCGCAATCACTGACATTTAGACCTCAGAGGCT 329

```

QY 1580 GCTGCCCTCAACAGCTAGGAGCTTAACAAACCTCCCTCAAGATTGTTGGGAAGCT 1639
 DB 328 GCTGCTCTGCAAGCTCGGAGCCTCACAAACCTCTGTCCCCAAGATTGCTTGGGAAGCT 269
 QY 1640 GTTAATACCATGGCTGAGGACATTTGGAGTTT 1673
 DB 268 CTTAATATCATGCTGAGATTGTTTCTTTT 235

RESULT 10
 CB893839 817 bp mRNA linear EST 24-APR-2003
 LOCUS EST46631 HOGA Medicago truncatula cDNA clone HOGA-29M7, mRNA
 DEFINITION
 ACCESSION CB893839
 VERSION CB893839.1 GI:30101008
 KEYWORDS
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 817)
 Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,
 Utecherback, T., Cho, J., and Fraser, C.M.
 ESTs from roots of Medicago truncatula treated with
 oligogalacturonides of DP 6-20
 Unpublished
 Contact: Michael G. Hahn
 Complex Carbohydrate Research Center
 University of Georgia
 220 Riverbend Road, Athens, GA 30602-4712, USA
 Tel: 706-542-4457
 Fax: 706-542-4412
 Email: hahn@ccrc.uga.edu
 TIGR sequence name: MTMDK767K
 More information is available at: www.medicago.org
 Seq primer: SKmod (CTA GAA CTA gtc gat CC).
 Location/Qualifiers
 1. 817
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /cultivar="A17"
 /db_xref="taxon:3880"
 /clone="HOGA-29M7"
 /issue_type="3 day old seedling roots"
 /dev_stage="24 hours after treatment in the dark at 26 C
 with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
 presence of 100 ug/ml Gentamicin"
 /lab_host="XLOLR"
 /clone_1lb="HOGA"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unipat XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-aseIst
 helper phage and propagated in SOLR cells."

BASE COUNT 217 a 110 c 183 g 307 t
 ORIGIN
 Query Match 20.4%; Score 395; DB 14; Length 817;
 Best Local Similarity 72.9%; Pred. No. 1.4e-28;
 Matches 520; Conservative 0; Mismatches 191; Indels 2; Gaps 1;

QY 244 TATYAGTTCATGTCGATTCAGTATTCAGTATTCGTTGTTGTTGTTAACAAGC 303
 DB 107 TTTTGTAATTTCTCTGTTTTCATCTGGGTTTGTGTTGTTGGCTGGCA--T 164
 QY 304 AATGAGGTTGTTGAGAGAGAGAGATCATTAACCTCAGAGAGCTGAGGTCACAA 363
 DB 165 TATTACATGAGGTTGAGAGAGAGAGATCATTAACCTCAGAGAGCTGAGAGATGA 224

QY 364 CAAGAGGAGATTATGATCTCAATTCAAGTAAGTGTACAAATGTCTCAGATTGGGT 423
 DB 225 CAAGAAGAGGAGATCTATGATCTCAATTCAAGGTAAAGTTTACAAATGTTTCAGATTGGC 284
 QY 424 CAAGAGCACCTGTGTGTATGTTCCAACTCAACCTTGTGCGCAGAGATGCACTGA 483
 DB 285 TAAAAAACAATCCGTGGAGAGAGTTGTTTGTGAATCTTGGCTGGCAGAGATGA 344
 QY 484 TGCAATTCATAGCATTCATTCCTGCGACAGCATGTCACACCTTGAATAATCTTCACTGG 543
 DB 345 TGCAATTCATAGCATTCATTCCTGCGACAGCATGTAACCTTGAACAGATTGTTCACTGG 404
 QY 544 CTACACCTCAGTGACTTCAAGGCTCTGAGGTCGCAAGACTACAGAAAGCTGATC 603
 DB 405 CTAATTCCTGAGAGATTTTAAGTATCTGAAGTTCTTAAGATTAAGAGACTGTTTC 464
 QY 604 TGAATTCGAAAATTGGCTCTTTTGACACCAAGGAGCATTCATTCATGACCTTGC 663
 DB 465 TGAGTTTGTCAAAATGGGTTGTTGAAAAGAAAGAAAGATGTTTATTCACATTAA 524
 QY 664 ATCTGTGCTGTATGTTCTCTATTTACTCTATGTTCTTGTGAGGTGCACTAGTGTG 723
 DB 525 ATCTGTGCTATTAATGCTTGTATTTGTTTATGTTGTTGTTGTTGTTGTTGTTG 584
 QY 724 GGCTCATTTGGGTTGAGGATGCTCTAGGTTGCTTGGATGCAAGGCTTATGTTGG 783
 DB 585 GGCTCATTTAGGTTTGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 644
 QY 784 CCATGATTCCTGCACTATGATGTTATGACAACTATGTTTCAACAGTTGTCACAGAT 843
 DB 645 TCATGATTTCTGTCATTTAGAGATTAATGTCAGTGAAGTTTAAACAAATTAGCACAAAT 704
 QY 844 CCTCTCTGGAACTGTTGACCGGATTAAGCAATGCTTGTGTGAAGTGAATGCAATGC 903
 DB 705 TCTTTGTGTTATTTGATGACTGTATTAAGTATGCTTGTGTGAAGTGAATGCAATGATGC 764
 QY 904 TCACCACTTGGTGCACAGCTTGCACATGACCTGATCTGCGACATGC 956
 DB 765 TCATCATTTGCTTGCATTAATGCTTGTATGATGATCTGATTTGACGATATTC 817

RESULT 11
 BM143768 588 bp mRNA linear EST 29-NOV-2001
 LOCUS saj38e09.y1 Gm-c1072 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-c1072-2921 5' similar to TR:082348 O82348 PUTATIVE CYTOCHROME
 B5.; mRNA sequence.
 ACCESSION BM143768
 VERSION BM143768.1 GI:17153835
 KEYWORDS
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 588)
 Shoemaker, R., Kelm, P., Voklin, L., Erpelting, J., Corvelli, V., Khanna
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk
 R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R., and Wilson, R.
 Public Soybean EST Project
 Unpublished
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com

Seq primer: -40RP from Gibco
High quality sequence stop: 426.
Location/Qualifiers

FEATURES

source

1. 588
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1072-2921"
/tissue_type="seedlings induced for symptoms of SDS (Sudden Death Syndrome) disease"
/dev_stage="2-3 weeks old"
/lab_host="DH10B"
/clone_lib="Gm-c1072"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 2-3 week old seedlings that were induced for symptoms of SDS (Sudden Death Syndrome) disease by the translocation of culture filtrate of Fusarium solani f. sp. glycinis (Plant Cell Report 18:375-380). Cultivar PI 567374 is partially resistant to the disease SDS. Plant tissue (expanded leaves, folded leaves, and new shoots) were collected at 1, 6, 24, and 48 hrs. after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E. coli Electromax DH10B host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois)."

BASE COUNT 124 a 120 c 138 g 205 t 1 others
ORIGIN

Query Match 20.3%; Score 391.8; DB 12; Length 588;
Best Local Similarity 79.1%; Pred. No. 3.5e-28;
Matches 465; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

677 ATGTTCTCTATGCTATGCTGAGTGCATGATGAGGCTCATTTGGGT 736
1 ATGTTCTCTATGCTATGCTGAGTGCATGATGAGGCTCATTTGGGT 60
737 TCAGGATGCTCTTGAAGGCTTTGGAGTCAAAAGTCTTATGAGGCTCATTTGGC 796
61 GTCGCCCTTTGTTGGCTTGTGATGCAAGCACTTACGTGGGTCACTGCGC 120
797 CATATGCTGTTATGACAAACCAATGTTTCAACAGAGTTCACATCTCTCTGGGAC 856
121 CACTATGAGGTTTATGCTACCCCTGGCTACAAACAAATTTGGCAAAATCTTTGTGGCAAT 180
857 TCGTTGACCGGATTAAGCATTTGCTGGTGAAGTGAATGATCAATGCTCACCATTTGGC 916
181 TGCATGATCTGGATTAATCATTTGATGAGGAGTGAAGTGAATGCTCACCATTTGCA 240
917 TGCAGACGCTTGAACCATGACCTGATCTGAGACAGACATGCGGCTTTGGAGTTTGGTCG 976
241 TGCATGATCTGGATTAATCATTTGATGAGGAGTGAAGTGAATGCTCACCATTTGCA 300
977 CGGTTCTCAATTCATCACTCTCATTTCTATGAGGAGGAGTGAAGTGAATTTCAAT 1036
301 CGGTTCTCAATTCATCACTCTCTCATTTCTATGAGGAGGAGTGAAGTGAATTTCAAT 360
1037 GCTAGGTTCTGATGCTGCTACGAGCACTTACTTTTACCCTGGATGCTGTTGGCAGG 1096

|||||
Db 361 TCAGGTTCTCTATGCTATGCTGAGTGCATGATGAGGCTCATTTGGGT 420
Qy 1097 GTCATCTTGTATCTGACGACATTCCTGCTATTTGTTTCCAGCGGAAAAGTGCAGATAGA 1156
Db 421 GTCATTTGATCTCCAGACTTGTGCTGTTTCTTCAAGGAAAGTGCAGATAGA 480
Qy 1157 GCCTTACATATATGAGGATCCCTGCTTTGGAGTGGTCCCTTTAGTCTTGC 1216
Db 481 GCCTTACATATATGAGGATCCCTGCTTTGGAGTGGTCCCTTTAGTCTTGC 540
Qy 1217 CTCGCAATTTGGCTGAGAGGCTTATGTTGCTTGTAGCTTTGCT 1264
Db 541 CTCGCAATTTGGGAGAGGCTTATGTTGCTTGTAGCTTTGCT 588

RESULT 12
B1787611 571 bp mRNA linear EST 30-NOV-2001
LOCUS sa147f09.y1 Gm-c1065 Glycine max cDNA CLONE GENOME SYSTEMS CLONE
DEFINITION ID: Gm-c1065-6425 5', similar to TR:082348 082348 PUTATIVE
CYTOCHROME B5.;, mRNA sequence.

ACCESSION B1787611 GI:15815336
VERSION B1787611
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max (soybean)

REFERENCE 1 (bases 1 to 571)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuck,R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project

TITLE Unpublished
JOURNAL Contact: Shoemaker R/Public Soybean EST Project
COMMENT Public Soybean EST Project
4444 Forrest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watscon.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
Location/Qualifiers

FEATURES

source

1. 571
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1065-6425"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/clone_lib="Gm-c1065"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library

was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 126 a 122 c 131 g 192 t
 Query Match 20.1%; Score 389.4; DB 12; Length 571;
 Best Local Similarity 80.4%; Pred. No. 66-28;
 Matches 456; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1024 GTTGTATTCATGTCAGTCTTGTGATCTGCTACCGACCACTTACTTATCCCGGTAAAT 1083
 DB 1 GTTGTATTCATGTCAGTCTTGTGATCTGCTACCGACCACTTACTTATCCCGGTAAAT 60
 QY 1084 GTGTGTTCAGGAGCACTTGTATCTGACAGCAATTCCTATGTTTTCAGAGGAGAA 1143
 DB 61 GTGCTTTCAGAGGAGCACTTGTATCTGACCACTTGTGCTTGTCTTACCGACCACTT 120
 QY 1144 AGTCAGATAGACCTTGAACTAAATGAGGATCTTGTGTTTGAATGTTTCCCTCT 1203
 DB 121 GGTGCAAGATAGACCTTAACTAAATGAGGATCTTGTGTTTGAATGTTTCCCTCT 180
 QY 1204 TTATGCTCTGCTGCTGCAATTCGCTGAGAGGTTATGTTGCTGCTGCTTGGC 1263
 DB 181 GTTGATCTCTGCTGCTGCAATTCGCTGAGAGGTTATGTTGCTGCTGCTTGGC 240
 QY 1264 TGTGTTTCATGTCAGCACTTGTGTTTGAATTCCTTGTGCAATGATATATG 1323
 DB 241 TGTGTTTCATGTCAGCACTTGTGTTTGAATTCCTTGTGCAATGATATATG 300
 QY 1324 CGGCGCACCGAGTGGAGATGCTGTTTGAAGACAGCAAGTGTACATGTTGATATCTC 1383
 DB 301 GGGCCACCAAGATGGAGATGCTGTTTGAAGACAGCAAGTGTACATGTTGATATCTC 360
 QY 1384 TTGTGCTCTGCTGCTGCAATTCGCTGAGTGTGCTGCTGCTGCTGCTGCTGCT 1443
 DB 361 TTGTGCTCTGCTGCTGCAATTCGCTGAGTGTGCTGCTGCTGCTGCTGCTGCT 420
 QY 1444 GTTTCAGGCTGCTGCTGCAATTCGCTGAGTGTGCTGCTGCTGCTGCTGCTGCT 1503
 DB 421 GTTTCAGGCTGCTGCAAGGCTGCAATTCGCTGAGTGTGCTGCTGCTGCTGCTGCT 480
 QY 1504 CAGAAGCATTAATTCCTTATAGAGCTGTCATTTTGGAGGCAATCAGTGACAAAT 1563
 DB 481 CAGAAGCATTAATTCCTTATAGAGCTGTCATTTTGGAGGCAATCAGTGACAAAT 540
 QY 1564 TAGGACCTCAGAGCTGCTGCTTACA 1590
 DB 541 TAGGACCTCAGAGCTGCTGCTTACA 567

RESULT 13
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 LOCUS sav30g08.y1 Gm-cl048 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-cl048-7215 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
 B5.;; mRNA sequence.
 ACCESSION CA938317 GI:27426797
 VERSION CA938317.1
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 575)
 Shoemaker R., Keim P., Vodkin L., Erpellding J., Corvelli V., Khanna
 A., Bolla B., Matra M., Hillier L., Kucaba T., Martin J., Beck C.,
 Wylie T., Underwood K., Stepien M., Theising B., Allen M., Boers
 Y., Peterson B., Swaller T., Gibbons M., Page D., Harvey N., Schuck
 R., Riter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann
 R., Waterston R. and Wilson R.
 Public Soybean EST Project

JOURNAL Unpublished
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available through: Reggen, Invitrogen Corp, 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact: cdu@reggen.com web site:
 www.reggen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 422.

FEATURES
 source location/Qualifiers
 1..575
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-cl048-7215"
 /tissue_type="whole seedlings of greenhouse grown plants"
 /dev_stage="1 week old"
 /lab_host="DH10B"
 /clone_1b="Gm-cl048"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI. The Clark NIL was constructed and seed was provided
 by Dr. J. Specht, University of Nebraska (Shoemaker and
 Specht, 1995). The cDNA library was constructed from mRNA
 isolated from whole seedlings of 1 week old greenhouse
 grown plants. Complementary DNA was synthesized from mRNA
 using a primer consisting of a poly(dT) sequence with a
 XhoI restriction site and a 3' anchor. EcoRI adapters were
 ligated to the blunt-ended cDNA fragments followed by XhoI
 digestion. The cDNA fragments were directionally cloned
 into the EcoRI-XhoI restriction site of the pBluescript
 vector. The ligated cDNA fragments were transformed into
 DH10 host cells (GibcoBRL). The library was constructed
 in cooperation with Dr. Paul Keim's laboratory at Northern
 Arizona University."

BASE COUNT 129 a 127 c 131 g 188 t
 ORIGIN
 Query Match 20.1%; Score 389.4; DB 14; Length 575;
 Best Local Similarity 79.8%; Pred. No. 66-28;
 Matches 459; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1038 CTAGGTTCTGATCTGCTACGACACTTACTTATCCCGGTAAATGTTGTTCCAGAG 1097
 DB 1 CAAGTTTCTGATCTGCTACGACACTTACTTATCCCGGTAAATGTTGTTCCAGAG 60
 QY 1098 TCAATCTGATCTGACAGCAATTCGCTATGTTTGAAGCGAAGTGCAGAGATAGAG 1157
 DB 61 TCAATCTGATCTGACAGCAATTCGCTATGTTTGAAGCGAAGTGCAGAGATAGAG 120
 QY 1158 CCTGAAACATATGGGAGATCTGCTGTTTGAAGCTGCTGCTGCTGCTGCTGCTGCT 1217
 DB 121 CCTTAAACATATGGGAGATCTGCTGTTTGAAGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 1218 TGCAGAAATGGGCTGAGAGGTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1277
 DB 181 TACCAATATGGGAGAGAAAGGCTATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 1278 AGCAATCTGATCTGTTGAAATCACTTGTGCAATGTATATGTGGGCGCAGAGTG 1337
 DB 241 AGCACTCTCAATTTGTTGAAACCAATTTCTCAGCAGATGTATAGAGGCGCCCAAAATG 300
 QY 1338 GGAATGACGTGTTTGAAGACAGACAGTGTATATGATATCTGCTGCTGCTGCTGCT 1397
 DB 301 GGAATGACGTGTTTGAAGACAGACAGTGTATATGATATCTGCTGCTGCTGCTGCT 360
 QY 1398 TGGATGTTGTTTGGTGGCTGCAAGTTTCACTTGTGAGCATATTTGTTTCCAGAGCTAC 1457
 DB 361 TGGATGTTGTTTGGTGGCTGCAAGTTTCACTTGTGAGCATATTTGTTTCCAGAGCTTC 420

QY 1458 CTCGTCGCAATGAGGAAGATTCGCTTGTAGTACCTTGTGCAAGACATTAAT 1517
 DB 421 CAAGGCAACATTTGAGGAATAATCTCACCTTGTGATGATCTTTCGAAGACACAT 480
 QY 1518 TGCCTTATAGAGACTTGTCACTTTTGGAGGCCAATGACGACATTTAGACCTTGGA 1577
 DB 481 TGCCTTACAGACATTTGACATTTGTTGAGGCCAATCTTGTGACTTTAGACCTCAGA 540
 QY 1578 CTGCTGCTCTTACAGGAGCTTACCAACCT 1612
 DB 541 CTGCTGCTCTTACAGGAGCTTACCAACCT 575
 RESULT 14
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 LOCUS QHG9G05.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA
 DEFINITION: clone QHG9G05, mRNA sequence.
 ACCESSION BU028011
 VERSION BU028011.1 GI:22463531
 KEYWORDS EST.
 SOURCE Helianthus annuus (common sunflower)
 ORGANISM Helianthus annuus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.
 1 (bases 1 to 741)
 Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
 Lin,H., van Damme,M., Lavelle,D., Chevaller,P., Ziegler,J., Ellison,
 P., Kojkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
 Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Composite Genome Project
 http://compgenomics.ucdavis.edu/
 Unpublished
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmudson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmoreveg@ucdavis.edu]
 belongs to config QH_Config742, see http://cspdb.ucdavis.edu/
 for details.
 Place: QHG9 row: G column: 05.
 Location/Qualifiers
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 /organism="Helianthus annuus"
 /mol_type="mRNA"
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 /db_xref="taxon:4232"
 /clone="QH9G05"
 /lab_host="E.coli"
 /note="Vector: pBRCDNA5flab; The library was constructed
 from 11 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cspdb.ucdavis.edu/
 TAG_LIB=QH_EFGHJ sunflower RHA280
 TAG_TISSUE=roots environmental stress
 TAG_SEQ=ATCTCGCGCG"
 BASE COUNT 181 a 180 c 157 g 223 t
 ORIGIN
 Query Match 20.1%; Score 388.2; DB 13; Length 741;
 Best Local Similarity 70.4%; Pred. No. 6.5e-28;
 Matches 519; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 827 AACAGGTTGACAGATCCCTCTGCGGAACCTGTTACCCGGATTAAGCATTTGCTGGTG 886
 DB 4 AACAACTGGCCGGAAATCTTTATTTGGGAATTTGATTAACCGATATACGATCGGTGTG 63
 QY 887 AAGTGACTACAAATGCTACCAACATTTGGCTGCAACAGCTTGACCATGACCTGATCTG 946
 DB 64 AAGTGACCCATATATACATCATCATTTGCTGCAACAGCTGCAATATATGACCCCGATCTT 123
 QY 947 CAGCAATCCGGCTCTTTCAGATTCGTGCGCGCTTCTTAATTCATACCTCTCATTTTC 1006
 DB 124 CAACATTTACCAATGTTTACCCGATCTTTCGAAACCTTTCAACCTGTTGACCTGCTTTC 183
 QY 1007 TATGGAGAGAGTTGAGATTTGATTTTCACTTGATGTTTCTTATGCTTACACGACTTT 1066
 DB 184 TATGGAGAGAGTTGATTTGATTTTCACTTGATGTTTCTTATGCTTACACGACTTTAC 243
 QY 1067 ACTTTTACCCGGATATGTTGTTGGCAGGTTCAACTTGTATCTGACAAATTTGCTTA 1126
 DB 244 AGTATTTACCCGATCATGTTGCGTGGCCGTTCAACCTTTACTTACAAACATATTTGCTA 303
 QY 1127 TTGTTTTCAGAGCGAAAGATGACAGATATAGCTTGAACATATATGGGATCTTGTGTTT 1186
 DB 304 CTACTTTCAAAACGAAAGATCCCGACCGCGTTTAAACATATATGGAACCTGATCTTC 363
 QY 1187 TGGACTTGGTCCCTCTTTTATGTTCTTCCCTGCAATTTGGCTGAGAGGTTATGTTT 1246
 DB 364 TGGACGTGTTTCCGTTACTCGTTCCTGCTTACCACTGCGCCGAAAGCGGTGCTTT 423
 QY 1247 GTGCTTGTAGCTTGTGCTGTTTGTTCATTCAGACATTCAGTCTGTTTGAATCACTTT 1306
 DB 424 GTGCTGTAGCTTGTGTTGTACGGGTATTCACAAATGTTCAATTCCTTAAACCACTTTT 483
 QY 1307 GCTGCAATGATATATGTCGGGCAACGAGTGGAAATGACTGTTTGAAGACGAAAT 1366
 DB 484 GCGCCCAATGATATATGTCGGGCAACGAGTGGAAATGACTGTTTGAAGACGAAAT 543
 QY 1367 GGTACATGATATATCTTGTGCTGCTTGTGATGATTTGCTTGGCTGAGTTT 1426
 DB 544 GGGACCATGACATTCGTTGTTCTTATCATATGATTTGTTTGGCGGTTTACAGTTT 603
 QY 1427 CAGCTTGAACATATTTTTCGAAGCTACCTGCTGCAATTTGAGAAAGATTTGGCT 1486
 DB 604 CAACGTGACACACATTTGTTCTAGTTGCGCGGTGTCACCTTGAAGTTCATCTCCC 663
 QY 1487 TTGCTTATGATCTTGTGCAAGACATATTTGCTTATAGAGCTTGTGATTTGGAG 1546
 DB 664 ATGTTTGGGAACCTTTCGAAGAAACATTAACCTTATATAGTATTTCAATTTAGAT 723
 QY 1547 GCCAATCAGTGACAAT 1563
 DB 724 GCTAATGTATGACT 740
 RESULT 15
 BQ402431 576 bp mRNA linear EST 22-MAY-2002
 LOCUS GA_Ed0049E09f Gossypium arboreum 7-10 dpa fiber library Gossypium
 DEFINITION: Arabidopsis cDNA clone GA_Ed0049E09f, mRNA sequence.
 ACCESSION BQ402431
 VERSION BQ402431.1 GI:21090118
 KEYWORDS EST.
 SOURCE Gossypium arboreum
 ORGANISM Gossypium arboreum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 576)
 Wing,R.A., Friesch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,
 D., Wood,T.C., Leslie,A. and Wilkins,T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 Unpublished
 JOURNAL

COMMENT

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu

Total High Quality bases = 565
Seq primer: TAATACACTACTACTAGGG
High quality sequence start: 5
High quality sequence stop: 641.
Location/Qualifiers

FEATURES

source

1..676

/organism="Gossypium arboreum"

/mol_type="mRNA"

/strain="AKA"

/cultivar="8400"

/db_xref="taxon:29729"

/clone="GA_Ed0049B09f"

/issue_type="Fibers isolated from bolls harvested 7-10 dpa"

/lab_host="E. coli"

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT

151 a

149 c

150 g

226 t

ORIGIN

Query Match

20.0%; Score 387.6; DB 13; Length 676;

Best Local Similarity 76.6%; Pred. No. 7.9e-28;

Matches 513; Conservative 0; Mismatches 154; Indels 3; Gaps 3;

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QY 629 GACACCAAGGGGATGTCATTCATGACCCCTGACCTGATGCTGTATGTTCCATTT 688
DB 2 GAACACCAAGGGGATGTCATTCATGACCTGATGCTGTATGTTCCATTT 61
QY 689 GTAATCTATGCTGTTGAGTGCACATGCTGAGGCTCATTTGGGATTCAGGATGCTC 748
DB 62 GTTCTTTAGCGTGTCTTGAGATGCGATGAGTGTGGGCTCATCTGGGTGCGCATGCTG 121
QY 749 TTAGGCTGCTTGGATGCAAGTGTATGTTGGGCTCATTTGCGCATGTTGCGCATGTT 808
DB 122 TTGGGATGCTTGGATGCAAGTGTATGTTGGGCTCATTTGCGCATGTTGCGCATGTT 181
QY 809 ATGACACCAAGGGGATGTCATTCATGACCCCTGACCTGATGCTGTATGTTCCATTT 868
DB 182 ATGACACCAAGGGGATGTCATTCATGACCCCTGACCTGATGCTGTATGTTCCATTT 241
QY 869 ATGACATGCTTGTGTAAGTGAAGTCAATGCTCAACATGCTCAACATGCTCAACATGCT 928
DB 242 ATGACATGCTTGTGTAAGTGAAGTCAATGCTCAACATGCTCAACATGCTCAACATGCT 301
QY 929 GACCATGACCTGATGTCAGCAATGCGGCTTTGCAAGTTCGTGCGGTTCTCAAT 988
DB 302 GATTATGACCTGACCTGACCAATGCTTCTTTTGGAGTCTTCAAGTTCCTCAAT 361
QY 989 TCCATTAACCTGATTTCTATGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1048
DB 362 TCAATTACGCTTGTGTTAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 421
QY 1049 ATCTGCTACAGACTTTACTTTTACCCGATATGCTGTTGCTGCAAGGCTCAACTGTAT 1108
DB 422 ATGAGTTACAGACTTTAGCTTTTATCCGTATGCTGCTGAGGAGGAGGAGGAGGAGGAG 481
QY 1109 CTGACAGACAATTTGCTATTTGTTGAGGCGAAAGTGCAGATAGAGCTTGAACATA 1168
DB 482 TTACAGACAATTTGCTATTTGTTGAGGCGAAAGTGCAGATAGAGCTTGAACATA 541
QY 1169 ATGGGATCCTTGTGTTGAGTGTGCTGCTTTTATGCTGCTGCTGCTGCTGCTGCTGCT 1228
DB 542 ATGGGATCCTTGTGTTGAGTGTGCTGCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY 1229 CCTGAGAGGCTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1288
```

DB

602 CCAGA-AAGTTCATGTTGTTCTTAAC-ACCTTGGCTGTTACATTCATTCGA-CATATCCAG 658

QY

1289 TTCTGTTGA 1298

DB

659 GTCTGTTGA 668

Search completed: December 31, 2003, 23:59:24
Job time : 2950.44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:49:12 : Search time 95.9683 Seconds
(without alignments)
8894.970 Million cell updates/sec

Title: US-09-857-524B-7
Perfect score: 1934
Sequence: 1 gcacgagcacaagaftaaaa.....aaaaaaaaaaaaaaaaaa 1934

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	618.4	32.0	1684	2 US-08-831-570-1	Sequence 1, Appl1
2	618.4	32.0	1684	2 US-08-831-575-1	Sequence 1, Appl1
3	618.4	32.0	1685	1 US-08-366-779-4	Sequence 4, Appl1
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7	153	7.9	291	4 US-09-313-294A-1966	Sequence 1966, Ap
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9	67	3.5	1443	4 US-09-904-615-21	Sequence 21, Appl1
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11	64.6	3.3	931	4 US-08-482-273-31	Sequence 31, Appl1
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13	64.2	3.3	2186	4 US-09-360-545-66	Sequence 66, Appl1
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18	63.4	3.3	289	1 US-08-341-568-3	Sequence 3, Appl1
19	63.4	3.3	289	4 US-08-911-020-3	Sequence 3, Appl1
20	63.4	3.3	485	4 US-09-996-243-245	Sequence 245, App
21	63.4	3.3	2406	4 US-09-594-506-37	Sequence 37, Appl1
22	62.6	3.2	1037	4 US-09-489-847-112	Sequence 112, App
23	62.4	3.2	4072	3 US-09-245-041-16	Sequence 16, Appl1
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37	61	3.2	1201	4	US-09-461-325-36	Sequence 36, Appl1
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45	60.6	3.1	888	3	US-09-188-930-13	Sequence 13, Appl1

ALIGNMENTS

RESULT 1
US-08-831-570-1
: Sequence 1, Application US/08831570
: Patent No. 5959175
: GENERAL INFORMATION:
: APPLICANT: Thomas, Terry L.
: APPLICANT: Number, Andrew N.
: APPLICANT: Beremand, Phillip D.
: TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
: TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Scully, Scott, Murphy & Presser
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: New York
: COUNTRY: USA
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/831,570
: FILING DATE: 09-APR-1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: DiGiglio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 10545
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 743-4366
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1684 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 43..1387
: US-08-831-570-1
: Query Match 32.0%; Score 618.4; DB 2; Length 1684;
: Best Local Similarity 66.5%; Pred. No. 26-128;
: Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;


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Qy 626 TTTGACACAAAGGCGATGTCACTTCATGCAACCTTCATCTGTGCTGTATGTTCTC 685
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Qy 866 GGAATAGCATTTGCTGGTGGAGAGGACTCAACATGCTCAACATTTGGGTCAGGCAAGC 925
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Db 778 TTGTAAGTTATCAACATTTGACATTTTAACTTATATGTTGCTGCTAGGCTCAATATG 837
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Db 1018 CAGTTCTCTTGAACCACTTCTCTTCAAGTGTATGTTGAAAGCTTAAAGGGAATAT 1077
Qy 1346 TGGTTTGAAGCAACAGATGTAATGATGATATCTTGTGCTCTTTCATGATGATGG 1405
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Qy 1526 AGAGCTTTCATTTTGGAGGCGCAATCAGTGAACAATTTGGAAGCTCAGAGCTGTGCG 1585
Db 1258 AATTATGATCTTTTCTCAAGGCGCAATGATGATGATGATGATGATGATGATGATGAT 1317
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Db 1318 TTGAGGCTAGGAGTAAATACCAAGCGCTCCGGAAGATTTGATGGAAGCTTCTCAC 1377
Qy 1646 ACCCATGCTGA 1657
Db 1378 ACTCATGTTAA 1389

RESULT 2
US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 5977436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,575
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4363
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
; US-08-831-575-1

Query Match 32.0%; Score 618.4; DB 2; Length 1684;
Best Local Similarity 66.5%; Pred. No. 2e-128;
Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;
Qy 326 AAGAAATACATTAACCTCAGAGAGCTGAAAGGGTCACAAACAGAGAGGAGATTATGATC 385
Db 58 AAGAAATACATTAACCTCAGAGAGCTGAAAGGGTCACAAACAGAGAGGAGATTATGATC 117

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 QY 1646 ACCCATGCTGA 1657
 Db 1378 ACTCATGCTTA 1389
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 ; Sequence 4, Application US/08366779
 ; Patent No. 5614393
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/366,779
 ; FILING DATE: 30-DEC-1994
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-366-779-4
 Query Match 32.0%; Score 618.4; DB 1; Length 1685;
 Best Local Similarity 66.5%; Pred. No. 2e-128;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;
 QY 326 AAGAATACCTAATCTCAGAGAGCTGAAGGCTCAACAAGAGGAGATTTATGATC 385
 Db 59 AAGAATACCTAATCTCAGAGAGCTGAAGGCTCAACAAGAGGAGATTTATGATC 118
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Qy      566 GTCTCTGAGGTGTCAGAAAGCTACAGAAAGCTTGACATGAGTCTCAAAATGGGTCT 625
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RESULT 4
US-08-789-936-4

; Sequence 4, Application US/08789936
; Patent No. 5789220

; GENERAL INFORMATION:

; APPLICANT: Thomas, Terry L.

; APPLICANT: Reddy, Avutu S.

; APPLICANT: Nuccio, Michael

; APPLICANT: Freysinet, Georges L.

; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

; TITLE OF INVENTION: DELTA 6-DESATURASE

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: United States

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/789,936

; FILING DATE: 28-JAN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/366,779

; FILING DATE: 30-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Presser, Leopold

; REGISTRATION NUMBER: 19,827

; REFERENCE/DOCKET NUMBER: 83832YXW

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; TELETYPE: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1685 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-789-936-4

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Qy      326 AAGAAGTACATAACCTGAGAGAGCTGAGGTCACAACAAGAGGAGATTATGATC 385
Db      59 AAGAATAACATTAACCTGAGATGAACTCAAGAAACCAAGATTAACCCGAGATCTATGATC 118
Qy      386 TCAATTAAGGTAAGTGTCAATGTCTCAGATTGGCTCAAGAGACCCCTGATGAT 445

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Db 119 TCGATTCAGGGAAGGCTATGATGTTGCGATGGGTGAAGACATCCAGTGGAGC 178
 Qy 446 GTTCCATTCGAACCTTGTGGCCAGGATGCTCATGATTCATAGCATACCATCT 505
 Db 179 TTTCCTTGAAGACTCTTGTGCTCAAGAGGTAACATGATGATTTGTCATTCCT 238
 Qy 506 GGCACAGATGTCACACCTTGAAGAAATCTTCACTGGCTACCACTCAGTACTCAAG 565
 Db 239 GCGCTCATGAGGAAGATCTTGATAGTTTTCATGGGTATATCTTAAAGATTACTCT 298
 Qy 566 GTCTGTGAGTGTCCAAAGACTACAGAAAGTTGCATGTAGTTCTCAAAATGGGTCT 625
 Db 299 GTTCTGAGGTTCTAAAGATTATAGAACCTTGATGTTGATTTCTAAATGGGTTTG 358
 Qy 626 TTGACACCAAGGAGATGCTCATTCATGCAACCTTGATCTGTGCTGATGTTCTC 685
 Db 359 TATACCAAAAGGTCATATATGTTTGCACCTTGTCTTATAGCAATGCTTTGCT 418
 Qy 686 ATTGACTCTATGTTGTTGAGGTGCACTAGTGTGGGCTCATTTGGGTTGAGCATG 745
 Db 419 ATGAGTGTATAGGGTTTGTGTTGAGAGGTGTTTGTGATCATTTGTTTCTGGGT 478
 Qy 746 CTCTAAGGTTGCTTTGAGTCAAGTGTATGTTGGCCATGATCTGGCCATATGTG 805
 Db 479 TTGATGGGTTCTTTGATTCAGAGTGTGATGATGATGATGATGATGATGATG 538
 Qy 806 GTTATGACCAATGTTTCAAGATGTCACAGATCTCTCTGGGAATGCTTGACC 865
 Db 539 GTAGTGTGATGATCAAGGCTTAAATGATTAAGGATTTTGTGCAAAATGCTTTCA 598
 Qy 866 GGGATAGCATTTGCTGGTGAAGTGAAGTCAATGCTGACCATTTGCGTGAACAGC 925
 Db 599 GGAATAGATGTTGTTGTTGAGTAATGAAACATATGACATTCATTCCTGTAATAGC 658
 Qy 926 CTGACCATGACCTGATCTGACAGACATGCGGTCTTTGAGTTCGTGCGGTCTTC 985
 Db 659 CTGAAATATGACCTGATTTACAAATATATACATTCCTGTTGTTGTTCCAAATTTT 718
 Qy 986 AATTCATTAACCTCTCATTTTCTATGAGGAAGTGAAGTTGATTCATTTGCTAGTTC 1045
 Db 719 GGTTCACCTCACCCTCATTTCTATGAGAAAGGTTGACTTTTGAATCTTTATCAAGATTC 778
 Qy 1046 TTGATCTGCTACGACCTTACTTTTACCCTGTAATGTTGCTGAGGCTCAACTG 1105
 Db 779 TTGTAATGATCAACATTTGACATTTTACCCTTATATGTTGCTGAGGCTCAATATG 838
 Qy 1106 TATCTGACAGCAATCTGCTATGTTTTCGAGGCAAAAGTGAAGATGAGACCTTGAC 1165
 Db 839 TATGTACAAATCTCATATGTTGTTGACCAAGAAATGTTGCTATGAGCTCAGGA 898
 Qy 1166 ATATAGGAGATCTTGTGTTTGAATGCTTCCCTCTTTAGTGTCTGCTGCCAAT 1225
 Db 899 CTCTGGAGATGCTGAGTGTCTCATTTGTTGATCCGTTGCTGTTGTTGCTCTAAT 958
 Qy 1226 TGGCTGAGAGGTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1285
 Db 959 TGGGCTGAAGAAATATGTTGTTGATGCAAGTTATAGTACATGAGATCAACAGTT 1018
 Qy 1286 CAGTCTGTTGATTCATTTGCTGCAATATATATGCGGGCACCAGTGGGAATGAC 1345
 Db 1019 CAGTCTCTTGAACCACTTCTCTCAAGTGTATATGTTGGAAGGCTTAAAGGAATAT 1078
 Qy 1346 TGGTTTGAAGACAGACATGTTGATCATGATATCTCTGCTCTCTGAGATTTGG 1405
 Db 1079 TGGTTTGAAGAAACAGATGAGGACATTCATCTCTCTCTCTGAGATTTGG 1138
 Qy 1406 TTTTTCGCTGCTGAGTTTCACTGAGATCATTTGTTTCAAGGCTACCTCGGTGC 1465
 Db 1139 TTTCAATGATGATGCAATTCGAATGAGATCATATTTGTTTCCAGATGCTGAGATGC 1198
 Qy 1466 CAATGAGAGATTTGCTCTTGTGTTAGTACCTTTGCAAGAAAGATATTTGCTTAT 1525
 Db 1199 AACCTTAGGAATATCTGCTCTAGCTGATGAGATTTATGCAAGAAATATTTGCTTAC 1258

Qy 1526 AGAGCTTGTCAATTTGGAGGCCAATCAGTGCATTAAGAACCTCAGGACTGTGCC 1585
 Db 1259 AATTATGATCTTTCTTCCAGAGCCCATGAAATGACATCTGAAATTTGAGAACACGCA 1318
 Qy 1586 CTACAACTTGAAGGACTTAACAAACCTGCGCCCTAAGATTTGTTGGGAAGCTGTTAAT 1645
 Db 1319 TTGAGGCTAGGATATTAACCAAGCCGCTCCGAAGAAATTTGGTATGGAAGCTTTCAC 1378
 Qy 1646 ACCATGCTGA 1657
 Db 1379 ACTCATGTTTAA 1390

RESULT 5
 US-08-934-254-4
 ; Sequence 4, Application US/08934254
 ; Patent No. 6355861
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE.
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,254
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-934-254-4

Query Match 32.0%; Score 618.4; DB 4; Length 1685;
 Best Local Similarity 66.5%; Pred. No. 2e-128;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

Qy 326 AAGAAGTACCTAATCTTCAAGAGGCTGAAAGGCTCACAAACAAGAGAGATTTATGATC 385
 Db 59 AAGAATATCAATTAACCTTCAAGTGAATCAAGAACCAAGATTAACCCGAGATCTATGATC 118
 Qy 386 TCAATTCAGAGTGAAGTGTATGATGTTGATGTTGGTCAAGAGCACCTGTTGAT 445
 Db 119 TCAATTCAGAGGAAAGCTTATGATGTTGGATTTGGTGAAGACATTCAGATGGCAGC 178
 Qy 446 GTTCCATTCGAACCTTGTGCTGCGCAGAGATGCTATGATGATTCATGATACCATCT 505
 Db 179 TTTCCTTGAAGAGTCTTGTGCTGATCAAGAGTAACTGATGATTTGTTGATTCATCT 238
 Qy 506 GGCACAGATGTCACACCTTGAAGAAATCTTCACTGGCTACCACTCAGTACTCAAG 565

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Db      239 GCCTCTACATGAGAAATCTGTATAGTTTCTACCTGGGTATATCTTAAGATTACTCT 298
Qy      566 GTCTCTAGAGTGTCCAAAGACTACAGAAAGCTTGATGTAGTCTCAAAATGGGCTT 625
Db      299 GTTCTGAGGTTTCTAAAGATTATAGAAAGCTGTGTGAGTTTCTAAATGGGTTG 358
Qy      626 TTGACACCAAAAGGCAATGTCATTCATGCAACCCCTGCACTGTGTGCTGTAATGTCTC 685
Db      359 TATACAAAAGGCTATATATATGTTGCAACTTGTGCTTATAGCAATCTGTGCT 418
Qy      686 ATGTACTATATGTTCTGAGTGCACTAGTGTGGCTCAATTTGGGTTCAAGCAGC 745
Db      419 ATGAGTGTATAGGGGTTTGTGTGAGGGTGTGTGTGATATTTGTTTCTGGGGT 478
Qy      746 CTCTTAGGGTCTTTGGATGCAAAAGTCTTATGTGGCCATGATTCGGCCATATGT 805
Db      479 TTGATGGGTTTCTTTGATTCAGAGTGTGATGACATGATGCTGGCCATTTATATG 538
Qy      806 GTTATGACCAACAAATGTTTCAACAGGTTGACAGATCTCTGCGGACGTGGTAC 865
Db      539 GTAGTGTCTATTAAGGCTTAATAGTTTATGGGTATTTTGTGCTCAATTTCTTTCA 598
Qy      866 GGATTAAGCATTTGCTGTGGAAGTGAATGACATGCTCAACATTCGCTGCAACAGC 925
Db      599 GGAATTAAGTATTTGGTGTGAAATGAAACATATATGACATTCATTCCTGTAATAGC 658
Qy      926 CTTAACCATGACCTGATCTGACAGCATGCCGGTCTTTGCAATTTCTGGCGTTCTC 985
Db      659 CTTAATATGACCTGATTTAATATATATATATATATATATATATATATATATAT 718
Qy      986 AATTCATTAACCTCTATTTCTATGAGGAGAAATGAGTTGATTTGATTTGCTAGTTC 1045
Db      719 GCTTCACTCACTCTCTATTTCTATGAGAAAGGTTGACTTTTATCTTTATCAAGATTC 778
Qy      1046 TTGATCTGCTACAGACATTTACTTTTACCCTGATATGTGTGTCAGGATCAACTTG 1105
Db      779 TTGTAAGTTATCAACATTTGACATTTTACCTATATATGTGTGCTAGGCTCAATATG 838
Qy      1106 TATCTGACAGCAATTTCTCTATTTGTTTTCGAGCGAAAGTGCAGATAGACCTTGAC 1165
Db      839 TATGTACATCTCTCATATGTGTGTGACCAAGAAATGTGCTATCGAGCTCAGAA 898
Qy      1166 AATAAGGGGATCTTGTGTTTGTGACTGTGCTCTTTAGTGTCTGTGCTGCAAT 1225
Db      899 CTCTTGGATGCTTAGTGTCTCTGATTTGTTGTAACCTGCTGTGTTCTGTGCTTAT 958
Qy      1226 TGCCCTGAGAGGTTATGTTGTGCTGCTAGCTTGTGCTGTTTCCATCAGACAT 1285
Db      959 TGGGGTGAAGAAATTAATGTTGTTATGCAAGTTTATCAGTGAATGCAACAAGTT 1018
Qy      1286 CAGTTCTGTTGAATCACTTGTGCAAAATATATATGTGGGCCACGAGTGGATGAC 1345
Db      1019 CAGTTCTCTTGAACCACTTCTCTTCAAGTTTATATGTGAAAGCCCTAAAGGGGATAT 1078
Qy      1346 TGTGTTGAGGACAGCAAGTGTATCATTTGATATCTGTGCTCTGTGATGATGG 1405
Db      1079 TGTGTTGAGGACAAACGAGTGGACCTTACATTTCTGTCTCTTGTGATGATGG 1138
Qy      1406 TTTTTCGTGCTGCAATTCAGCTTGAAGCATTTTGTTCAGAGCTACCTCGGTGC 1465
Db      1139 TTTTATGATGATGATGCAATTCGAATGAGCATATTTGTTTCCAAATATGCTAGATGC 1198
Qy      1466 CAATTAAGAAATTTGCTCTTGTGATGACCTTTGCAAGAAAGCATATTTGCTTAT 1555
Db      1199 AACCTTAGAAATCTCGCTCAGCTGATCGAGTTATCAAGAAACATATTTGCTTAC 1258
Qy      1526 AGAGCTTGTATTTTGGAGGCAATGAGTGAACATTAAGACCTTAGAGCTGCTGCC 1585
Db      1259 AATTAATGATTTCTCCAAAGCCAAATAAATGACATCAAGAACTTGAAGAAACAGCA 1318
Qy      1586 CTACAGCTAGGAGCTTAACAAACCTGCTCCCTAAGATTTGTTGTGGAGCTGTTAT 1645

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Db      1319 TTGAGGCTAGGATATATACCAAGCCGCTCCGAAAGATTGTATGGAAGCTTTAC 1378
Qy      1646 ACCCATGGCTGA 1657
Db      1379 ACTCATGTTAA 1390

RESULT 6
US-08-934-254-26
; Sequence 26, Application US/08934254
; Patent No. 635861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; NAME/KEY: CDS
; LOCATION: 48..1406
; US-08-934-254-26

Query Match      28.7%; Score 555; DB 4; Length 1702;
Best Local Similarity 64.8%; Pred. No. 2,5e-114; Indels 12; Gaps 4;
Matches 889; Conservative 0; Mismatches 470;

Qy      321 AGGAGAAAGATACATTAACCTCAGAGAGCTGAAGGCTCAACAAGAGGAGATTAT 380
Db      58 AAGCTAAGAGTATATATACAGCGGAGGAGACCTCCGCGCCCAACAATCGGCGATCTCT 117
Qy      381 GGATCTCAATTCAGAGTATAGTGTATCATATGTCTCAATTTGGGTCAAGAGACCTCTGTG 440
Db      118 GGATCTCATATCAGAGGAGGAGTATACATGCTCTCGGTGGCGCGAGAGACCCCGGCG 177
Qy      441 GTGATGTCAATCTCAACCTTGTGCGCAGATGTCATGATGATATATATATATATATATAT 500
Db      178 GCGAGGTCCGCTCTCAATGTGCGCGCGAGAGCTTACCGAGCGCTTATTCGTAAC 237
Qy      501 ATCTGACAGCATGCTGACACCTTGAAAAAATTTCTCACTGG---CTACCACTCAAGTG 557

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Db 238 ACCGGGACGGCGCTGGCGGACATCGATCCGCTTTCACGGCTACTACTCAAGG 297
 Qy 558 ACTTCAAGGTCTGAGGTGTCCAAAGACTACAGAAAGCTTGACTGAGTTCTCAAAAT 617
 Db 298 ACTTCGAAGTGTCCGAAGATCTCCAAAGACTACCGAAGCTTTTGAACGAATGTCCGGT 357
 Qy 618 TGGGCTTTTGTACACCAAGGAGATGCTACTTACATGACCCCTTGACTGCTGTGA 677
 Db 358 CCGGGATCTTGAGAGAAAGGCGCACCATCATGTGAGCGTTGCTGGCGTTCCGGTCA 417
 Qy 678 TGTTCCTCATTTGACTCTATGTGTCTGAGGTGCTACATGTGTGGCTCATTTGGGTT 737
 Db 418 TGAATGGCGCAATGCTTACCGCGTGTGGGTGGAGTCCGTGGAGTTTCACTGTCTCT 477
 Qy 738 CAGGATGCTCTTGAAGGTGCTTGTGATGCAAGAGTGTATGTGGGCGCATGTTGGCC 797
 Db 478 GCGGCGACCTGTGGCTTGTGTGATCCAAAGCGGTATGTGGCGCATGCTCCGGCC 537
 Qy 798 ACTATGTGTTATGACCAACCAATGTTTCAAGGTTGACAGATCTCTCTGGGAAT 857
 Db 538 ATTACAGGTGATCCAAACCGGTGATACAAACAGATCAGCACTCATAGCAGGCAACA 597
 Qy 858 GCTTGACCGGATGACATGCTTGTGTGGAAGTGAATCAGATGCTCACCAATGGCT 917
 Db 598 TCCTAACCGAATGACATCGCTGTGTGGAAGTGAATCAGCAACCGCCACCACTCGCT 657
 Qy 918 GCAACAGCTTGACATGACCTGATCTGACGACATGCGGCTTGTGCAAGTTTCTGCTGC 977
 Db 658 GCAACAGCTTGACATGACCTGATCTGACGACATGCGGCTTGTGCAAGTTTCTGCTGC 977
 Qy 978 GGTTCCTCAATTCATTAACCTCTCATTTCTATGGAAGGAGTGTGAGTTGATTTCAATG 1037
 Db 718 GACTCTTCACTCATACCTCGGCTTCTATGCGCAGTCTCAAAATGACCAAGTGG 777
 Qy 1038 CTAGGTTCTGATGCTCTACGACATTTACTTTTACCGGTAATGTGTGTCCAGG 1097
 Db 778 CACGTTCTCAGTACGCTACGACATGACCTTACCGGTCATGATCTTCCGCGAG 837
 Qy 1098 TCACCTGTATCTGACGACATTCGCTATGTTTGTGAGCGGAAAGTGAAGATAG 1157
 Db 838 TCACCTGTATCTGACGACATTCGCTATGTTTGTGAGCGGAAAGTGAAGATAG 1157
 Qy 1158 CTTGACATTAATGAGGATCTTGTGTGTTGACATTTGCTCTTTTATGTTGCTTGC 1217
 Db 898 CTCTAACTTAATGAGGATCTTGTGTGTTGACATTTGCTCTTTTATGTTGCTTGC 1217
 Qy 1218 TGCCAAATGAGCTGAGAGGTTATGTTGTGCTTGTGCTTGTGCTTGTGCTTGC 1277
 Db 958 TCCGAACTGAGCTGAGAGGTTATGTTGTGCTTGTGCTTGTGCTTGTGCTTGC 1277
 Qy 1278 AGCATTGCTGTTGTTGATCTTGTGCTGCAATGTAATGTGCGGCGACGAGTG 1337
 Db 1018 AGCATTGCTGTTGTTGATCTTGTGCTGCAATGTAATGTGCGGCGACGAGTG 1337
 Qy 1338 GAAATGACTGTTGAGAGGACAGATGTTGATGATGATCTTGTGCTTGC 1397
 Db 1078 GCGAACAATGTTGAGAGGACAGATGTTGATGATGATCTTGTGCTTGC 1397
 Qy 1398 TGAATGTTTGTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 1457
 Db 1138 TGAATGTTTGTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 1457
 Qy 1458 CTGGTGTCCAAATGAGAGATTTGCGCTTGTGTTAGTGTGATGATGATGATGATGAT 1517
 Db 1198 CCGGTGTCCAAATGAGAGATTTGCGCTTGTGTTAGTGTGATGATGATGATGATGAT 1517
 Qy 1518 TGCTTATGAGAGCTTGTGATTTTGG---GAGGCAATGATGAGCAATTAGAGCTTCA 1574
 Db 1258 TGCTTATGAGAGCTTGTGATTTTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1628
 Qy 1575 GAGATGCTGCTTCAAGACTTAA---CAAACTGCTGCTTCAAGAA---TTTGT 1628
 Db 1318 GGGATGCGGGGTTCAAGCGGTGACCTTAATTTGGCCCGGTGCTTAAGAACTTGGT 1377

Qy 1629 TGTGGAAGCTGTATATACCATGCTGAGGCAATTTGAGTTTATAGATT 1679
 Db 1378 ATGGGAAGCTTATATACCAATGTTGATTTGTTGTGTTGGTT 1428
 RESULT 7
 US-09-313-294A-1966
 : Sequence 1966, Application US/09313294A
 : Patent No. 6476212
 : GENERAL INFORMATION:
 : APPLICANT: Laljudi, Raghunath V.
 : APPLICANT: Ico, Laura Y.
 : TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 : FILE REFERENCE: PL-0017 US
 : CURRENT APPLICATION NUMBER: US/09/313, 294A
 : NUMBER OF SEQ ID NOS: 7600
 : SOFTWARE: PERL Program
 : SEQ ID NO 1966
 : LENGTH: 291
 : TYPE: DNA
 : ORGANISM: Zea mays
 : FEATURE:
 : NAME/KEY: misc feature
 : OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
 : LOCATION: 256
 : OTHER INFORMATION: a, c, g, or other
 US-09-313-294A-1966
 Query Match 7.9%; Score 153; DB 4; Length 291;
 Best Local Similarity 71.3%; Pred. No. 3e-25;
 Matches 201; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
 Qy 1198 CCGCTTTTATGTTGCTTGTGCTGCTGCAATTTGCGGAGAGGTTATGTTGCTGCTAG 1257
 Db 2 CCGCTTGTGTTGCTTGTGCTGCTGCAATTTGCGGAGAGGTTATGTTGCTGCTAG 61
 Qy 1258 CTTGCTGTTTGTTCATCCAGACATTCAGTTCTGTTTGAATCACTTTGCTGCAATGT 1317
 Db 62 CTTCACATCTGGGGATTCAGACGTCATTCCTGCTGCAATTCCTGCTGCAATTCCTGCTGCA 121
 Qy 1318 ATATGTGCGGCCACCGAGTGGAAATGATGTTGTTGAGAACAGAACAGTGTACATTGGA 1377
 Db 122 GTATGTGCGGCCACCGAGTGGAAATGATGTTGTTGAGAACAGAACAGTGTACATTGGA 181
 Qy 1378 TATCTGTGCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
 Db 182 CATCTGTGCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATG 241
 Qy 1438 TCATTTGTTTCAAGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1479
 Db 242 CCATCTGTTTCCCNCTACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283
 RESULT 8
 US-09-313-294A-3256
 : Sequence 3256, Application US/09313294A
 : Patent No. 6476212
 : GENERAL INFORMATION:
 : APPLICANT: Laljudi, Raghunath V.
 : APPLICANT: Ico, Laura Y.
 : APPLICANT: Sherman, Bradley K.
 : TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 : FILE REFERENCE: PL-0017 US
 : CURRENT APPLICATION NUMBER: US/09/313, 294A
 : NUMBER OF SEQ ID NOS: 7600
 : SOFTWARE: PERL Program
 : SEQ ID NO 3256
 : LENGTH: 266

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Query Match      3.4%; Score 65.4; DB 5; Length 1813;
Best Local Similarity 78.8%; Pred. No. 1.5e-05;
Matches 78; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      1836 TGCAGTTCATGTGCTTGATGCATCAATACAAATCATCATCATGATGCCAAAAAAAAAAAAA 1895
        ||| |||| |
Db       1706 TCCTCTTCTCTGCTTTATTATTAATAAAAACAGAAAAAAAAAAAAAAAAAA 1765

Qy      1896 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1934
        |||||
Db       1766 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1804

RESULT 11
US-09-482-273-31
; Sequence 31, Application US/09482273
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? Patent No. 6534631
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: 71 Human Secreted Proteins
? FILE REFERENCE: P2030P1
? CURRENT APPLICATION NUMBER: US/09/482,273
? CURRENT FILING DATE: 2000-01-13
? EARLIER APPLICATION NUMBER: PCT/US99/15849
? EARLIER FILING DATE: 1999-07-14
? EARLIER APPLICATION NUMBER: 60/092,921
? EARLIER FILING DATE: 1998-07-15
? EARLIER APPLICATION NUMBER: 60/092,922
? EARLIER FILING DATE: 1998-07-15
? EARLIER APPLICATION NUMBER: 60/092,956
? EARLIER FILING DATE: 1998-07-15
? NUMBER OF SEQ ID NOS: 267
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 31
? LENGTH: 931
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-482-273-31

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OPERATING SYSTEM: DOS
 SOFTWARE: WORDPERFECT 6.1
 CURRENT APPLICATION DATA: 6.1
 APPLICATION NUMBER: US/08/451.405A
 FILING DATE: 26-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/965,273
 FILING DATE: 15-JAN-1993
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 731
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: UNKNOWN
 US-08-451-405A-2

Query Match 3.3%; Score 64; DB 1; Length 731;
 Best Local Similarity 55.6%; Pred. No. 2.3e-05;
 Matches 148; Conservative 0; Mismatches 110; Indels 8; Gaps 1;
 Oy 1669 TTTTGAAGTTAGGATTTTGTCAAGTCTTTTGTGTTTCTTTTAAAGAA 1728
 Db 51 TTGATAGTATGTTTCTTTTCTTTTATTTTATTTTATTTTAAAAA 110
 Oy 1729 AAAAAATCTCATGTGATTTTGTCTAGCCCACTTTCCAGATTGGGCTTGAATTAA 1788
 Db 111 TAAAAATTAAGATTAATAATTTT-----CTATTGAAGAGTTTATTATTGATTTAA 162
 Oy 1789 CTTTGTAGGTGTGTGTACAAATGATGATGATGATGATGATGATGATGATG 1848
 Db 163 AATTATATTAAACATAGTAACCTAAATAGATTGTGACGATATATGATAGAAATT 222
 Oy 1849 CTTTGCAATACAAATTCATATCATGTATGCCAAAAAATTTTAAAAA 1908
 Db 223 CTAATAAAAAAATTCAGATTAATTTTGGATTGGAACAACAAAAAATTTTAAAAA 282
 Oy 1909 AAAAAAATTTTAAAAAATTTTAAAAA 1934
 Db 283 AAAAAAATTCAAAAAATTTTAAAAA 308

RESULT 15
 US-09-073-569-1
 Sequence 1, Application US/09073569
 Patent No. 6084088
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Grossmann, Angelika
 TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/073,569
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sawiak, Deborah A
 REGISTRATION NUMBER: 37,438

REFERENCE/DOCKET NUMBER: 97-14
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6672
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1733 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 34..1344
 OTHER INFORMATION:
 US-09-073-569-1

Query Match 3.3%; Score 64; DB 3; Length 1733;
 Best Local Similarity 73.2%; Pred. No. 3e-05;
 Matches 82; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Oy 1823 ATCCAGATGTTACTGCACTTCATGTGCTTGATCATACAAATTCATATCATGTATGCC 1882
 Db 1573 ATGTATCTGATTAATACAGACCTGTCTTCTCCAAAAAATTTTAAAAA 1632
 Oy 1883 AAAAAAATTTTAAAAAATTTTAAAAA 1934
 Db 1633 AAAAAAATTTTAAAAAATTTTAAAAA 1684

Search completed: January 1, 2004, 00:05:29
 Job time : 98.9683 secs

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 21:04:45 ; Search time 482.374 Seconds
(without alignments)
13877.414 Million cell updates/sec

Title: US-09-857-524B-7
Perfect score: 1934
Sequence: 1 gcagcagcacacagtaaaaa.....aaaaaaaaaaaaaaaaa 1934

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 452686

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639.2	33.1	1350	US-09-938-842A-558	Sequence 558, App
2	618.4	32.0	1685	US-10-029-756-4	Sequence 4, Appl
3	555	28.7	1702	US-10-029-756-26	Sequence 26, Appl
4	269.4	13.9	657	US-09-770-149-494	Sequence 494, App
5	255	13.2	267	US-09-878-574-15653	Sequence 15653, A
6	206.4	10.7	476	US-09-770-444-39	Sequence 39, Appl
7	188.4	9.7	287	US-09-878-574-3260	Sequence 3260, App
8	166.2	8.6	480	US-09-924-035A-370	Sequence 370, App
9	156.2	8.1	263	US-09-878-574-9255	Sequence 9255, Ad
10	94.8	4.9	265	US-09-923-876-5116	Sequence 5116, Ap
11	89.6	4.6	1098	US-10-369-493-27824	Sequence 27824, A
12	78.6	4.1	406	US-09-814-353-17782	Sequence 17782, A
13	74.6	3.9	299	US-09-814-353-4844	Sequence 4844, Ap
14	74.6	3.9	299	US-09-814-353-1141	Sequence 1141, A
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C 16	74.2	3.8	393	15	US-10-198-846-7182	Sequence 7182, Ap
C 17	73.4	3.8	286	10	US-09-960-352-8161	Sequence 8161, Ap
C 18	73.4	3.8	419	13	US-09-814-353-5099	Sequence 5099, Ap
C 19	73.4	3.8	419	13	US-09-814-353-11391	Sequence 11391, A
C 20	72.8	3.8	388	13	US-09-814-353-17525	Sequence 17525, A
C 21	72	3.7	424	15	US-10-198-846-2929	Sequence 2929, Ap
C 22	71	3.7	383	13	US-09-814-353-18006	Sequence 18006, A
C 23	71	3.7	416	10	US-09-960-352-4584	Sequence 4584, Ap
C 24	70.6	3.7	390	13	US-09-814-353-17808	Sequence 17808, A
C 25	70.6	3.7	425	13	US-09-814-353-5498	Sequence 5498, Ap
C 26	70.6	3.7	425	13	US-09-814-353-11785	Sequence 11785, A
C 27	69.6	3.6	467	13	US-09-814-353-4848	Sequence 4848, Ap
C 28	69.6	3.6	467	13	US-09-814-353-11145	Sequence 11145, A
C 29	69.6	3.6	579	13	US-09-814-353-5569	Sequence 5569, Ap
C 30	69.6	3.6	579	13	US-09-814-353-11856	Sequence 11856, A
C 31	69.4	3.6	406	13	US-09-814-353-4900	Sequence 4900, Ap
C 32	69.4	3.6	406	13	US-09-814-353-11195	Sequence 11195, A
C 33	69.2	3.6	510	13	US-09-814-353-6245	Sequence 6245, Ap
C 34	69.2	3.6	510	13	US-09-814-353-12523	Sequence 12523, A
C 35	68.8	3.6	317	13	US-10-125-968-1260	Sequence 1260, Ap
C 36	68.8	3.6	880	15	US-09-814-353-7060	Sequence 7060, Ap
C 37	68.6	3.5	349	13	US-09-814-353-18039	Sequence 18039, A
C 38	68.4	3.5	247	13	US-09-814-353-4819	Sequence 4819, Ap
C 39	68.4	3.5	247	13	US-09-814-353-11116	Sequence 11116, A
C 40	68.4	3.5	403	13	US-09-814-353-17949	Sequence 17949, A
C 41	68.2	3.5	1475	14	US-10-114-893-317	Sequence 317, App
C 42	68	3.5	294	13	US-09-814-353-5106	Sequence 5106, Ap
C 43	68	3.5	294	13	US-09-814-353-11398	Sequence 11398, A
C 44	67.8	3.5	723	13	US-09-814-353-4726	Sequence 4726, Ap
C 45	67.8	3.5	723	13	US-09-814-353-11024	Sequence 11024, A

ALIGNMENTS

RESULT 1
US-09-938-842A-558
; Sequence 558, Application US/09938842A
; Patent No. US20020160378A1
GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepe, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 558
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-558

Query Match 33.1%; Score 639.2; DB 10; Length 1350;
Best Local Similarity 67.1%; Pred. No. 2.9e-141;
Matches 905; Conservative 0; Mismatches 443; Indels 0; Gaps 0;

Qy	310	CGTTGTTGAAGGAGAGATACATTAACCTCAGAGGCTGAGGTCACAAAGCA	369
Db	3	GCGGGAAGAGACGAGAAAAGTACATTACGAGAGAGATCTTAAACAAACAATC	62
Qy	370	GGAGAGTTATGAGTCTCAATTCAGGTAGGTATGTCAGATTGGTCAAGCA	429
Db	63	TGAGATCTATGATGCGGATTACAGGCAAGCTTCAACGCTCCGATTGATTAAAC	122

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 DB 123 TCATCCCGAGGCGACACGGGTGATTCATCTCGTTGGTCAGACGTCAACGATGCTTT 182
 QY 490 CATAGCATCACTCTGGACACAGCAGTGTGACACCTTTGAAAATTTCTTCACTGTGCA 549
 DB 183 CATGCAATTCATCCCGAACCGCTTGGACACATCTGACCATCTTCAACCGGTTACCA 242
 QY 550 CCTCAGTCACTTCAAGGTCTCTAGGTGTCCAAAGATACAGAAAGTTTCATCTGATG 609
 DB 243 CATCAGAGATTTCCAAAGTCTCCGAAGTCTACCGGATTTACCGTGTGATGCGAGTT 302
 QY 610 CTGAAATTTGGTCTTTTGAACAACCAAGGAGATGTCATCTTCACTGACCTTGTGAT 669
 DB 303 TCGTAAACTGGTCTCTTCAAAAACAAAGGTACAGTACTCTACACTTACGCTTCTGT 362
 QY 670 TGTGTATGTTCTCTCATTTGACTCTATGATGTTCTGAGGTGCACTAGTGTGGCTCA 729
 DB 363 CGCGCGCATGTTCTCGGAGTGTCTAGGGTGTGTTGGCTGTGATCTCCGCTTCCGCTCA 422
 QY 730 TTTGGGTTACGGCATGCTCTTAGGGTGTCTTGGATGCAAAAGTCTTATGTGGCCATGA 789
 DB 423 CCAAAATCGCGCGCGCTTCTCGGTCTCTCTGTGATCAGAGCGCTTACATAGGTCA 482
 QY 790 TTTGGGCACTATGTGTGATGCAACAAAGGTTTCAACAAGGTTGCAAGATCTCTC 849
 DB 483 TTTCTGTCATTTAGTATCATGTGCAACAAATCTTAAACAGATTCGCTACGCTTCTC 542
 QY 850 TGGGAATCTGCTTGAACCGGATTAAGCATTTGTTGTGAGAGTGAAGTCAACATGCTCA 909
 DB 543 CGGTAACTGTCTACCGGAATCTCAATCGGTGTGAAATGAGCTCAATGCTCATCA 602
 QY 910 CATTGGGTGAACAGCTTGAACCATGACCTGATCTGACAGACATGCGGCTTTTGAGT 969
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 DB 663 CTCACCAAAATCTTCTCTCTCATTTAGCTTGAAGATTTTACGATCGAAATCACTGTTGA 722
 QY 1030 TTTCAATGTAGTGTCTTGAATCTGCTCAACAGCATTTACTTTTACCAGGTAATGTGT 1089
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 QY 1090 TGCAGGGTCAACTGTGATCTGACAGCAATTTGCTATTTGTTTTCAGGGGAAAGTGA 1149
 DB 783 TGGAAAGATCAATCTCTTCAATTCAAAGGTTCTCTGCTCTTCCAAAGTGAAGTACC 842
 QY 1150 GGATAGAGCTTGAACATTAAGGGGATCTTGTGTTTGTGACCTTGTCTCTTGTAGT 1209
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 QY 1270 TTTCAATCCAGACATTTGATTTGTTGAATCACTTGTCTGCAATGTATATGTGCGGCC 1329
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 DB 1023 ACCACCGGAGAGAGCTGTTTGAAGAGAGAGCGCGGGAACATGATATCTTGTAG 1082
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 DB 1143 TCGCTTACTGTTGCTGATCTCGGAAGTTCCTCGGTGTGTTCAAGAGCTTTGCAAGAA 1202

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 DB 1203 GCATTAATCTTCCGTATAGAGATGTGTGTTTGAAGCAAAATGTGTGACATTAACAC 1262
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 DB 1263 TTTGAAGACAGCAGCTTATCACTAGCTGAGACGTTGATTCGTTGATTAAGAACTTGT 1322
 QY 1630 GTGGAAGCTGTATATACCATGCTGA 1657
 DB 1323 TTGGAGCTTTCAATCTCATGCTTA 1350

RESULT 2

US-10-029-756-4

Sequence 4, Application US/10029756

Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029,756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 4:

LENGTH: 1685 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-029-756-4

Query Match

Best local Similarity 66.5%; Pred. No. 2,9e-136;

Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AAGAAGTACATACTCTCAGAGAGCTGAAAGGTCACACAGAGAGGAGATTTATGATC 385
 DB 59 AAGAATATACATTTCTCAGATGAACCTCAAGAACCAAGATTAACCCGAGATCTATGATC 118
 QY 386 TCAATTCAGAGTATGATGATATGCTGATTTGATGATGATGATGATGATGATGATGAT 445
 DB 119 TCATTCAGAGGAAACCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 178
 QY 446 GTTCCATCTCAAACTTGTGCGCAGAGATGTCATGATGATGATGATGATGATGATGAT 505

Db 179 TTTCCTTGAAAGAGCTTGTGCTCAAGAGTAAGTATGATTTGTCATTCCT 238
 QY 506 GGCACAGCATGTCACACCTTGAAATTTCTTCACTGCTACCACTCATGCTTCAAG 565
 Db 239 GCTCTACATGGAAGATCTTGATTAAGTTTTCACCTGGGATTAATCTTAAAGTTACTCT 298
 QY 566 GTCTCTGAGGTGTCAGAAAGCTACAGAAAGCTTGATCTGAGTTCTCAAAATGGGTCTT 625
 Db 299 GTTCTGAGGTTCTTAAAGATTAAGAGAGCTGTGTGAGTTTCTAAATGGGTG 358
 QY 626 TTGGAACCAAGAGGATGTCATTCATGACCCCTTGACCTGTGTATGTTCTTC 685
 Db 359 TATGACAAAAAGATATATTAATGTTGCAACTTTGTCTTATGACAAAGCTGTGTGCT 418
 QY 686 ATGTACTATGATGTTCTGAGTGCACACTAGTGTGGGCTGATTTGGGTGAGGAG 745
 Db 419 ATGAGGTTTAAAGGTTTGTGTTGAGGGGTTTGGTACATTTGTTCTGGGTGT 478
 QY 746 CTCTTAAGGTTGCTTGAATGCAAGTGTATGTGGCCATGATTCGGCCACTATGTG 805
 Db 479 TGATGGGGTTCTTGGATTCAGAGTGGTGGATTGACATGATGCTGGGCAATTATAG 538
 QY 806 GTTATCAACAACATGTTTCAACAAGTTGCAAGATCTCTCTGGGAAGCTGTTGAC 865
 Db 539 GTAGTGTCTGATTCAGGCTTAATTAAGTTATGGTATTTGCTGCAAAATGCTTTGA 598
 QY 866 GGGATAGCATGCTGTTGGAGAGTGGAGTCAACATGCTCAGCAATGCGTGCACAGC 925
 Db 599 GGAATTAAGTATGTTGGTGGAAATGAAACATTAAGCAATGACATGCTGTATAGC 658
 QY 926 CTTGACCATGACCTGATCTGACACATGCGCGTCTTGGCACTTTCGTGCGGTTCTTC 985
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 Db 719 GGTTCACTACCTCTCAATTTCTATGGAAAGGTTTACCTTTGACTTTATCAAAATTC 778
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 Db 839 TATGTACATCTCTCATATATGTTGTGACCAAGAAATGTCTTATGAGCTCAGAA 898
 QY 1166 ATTAATGGAGATCTGTGTGTTTGAAGTCTGCTCTCTTTTATGTGTCTGCTGCAAT 1225
 Db 899 CTCTTGGAGATGCTAGTGTCTGATTTGGTACCGTGTGCTTCTTGTGCTTAAT 958
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 QY 1346 TGGTTTGAAGAGCAAGAGTGTATGATGATCTCTTGTGCTCTTGTGATGATGAG 1405
 Db 1079 TGGTTTGAAGAAACAAAGATGGGACATTTGATCTCTCTCTGATGATGATGAG 1138
 QY 1406 TTTTTCGGTGGCTGAGTTTCAAGCTTGAGCATTTTGTTCAGAGGCTACTCGGTGC 1465
 Db 1139 TTTTCAATGAGTATGCAATTTCAATTTGAGCATATTTGTTCCAAAGATCCATGATG 1198
 QY 1466 CAATTGAGAAAGATTTGACCTTGTGTAAGACCTTTCAGAAAGATATATTTGCTTAAT 1525
 Db 1199 AACCTTAAGAAATCTCGCCCTTACGTGATGATGATTAAGCAAGAAATATATTTGCTTAC 1258
 QY 1526 AGGAGCTGTGATTTTGGAGGCAATCACTGACAAATAGAACCTCTCAGAGCTGTGTC 1585
 Db 1259 AATTATGATCTTTCTTCCAAAGGCAATGAATGACACTGAGAACATTTAGGAACACAGCA 1318

QY 1586 CTACAGCTAGGAGACTTAACAACCTGCCCCCTAAGAAATTTGTGGAGCTGTTAT 1645
 Db 1319 TTGCAGGCTAGGAGATTAACAAGCCGCTCCGAAATTTGATAGGAGCTTTCAC 1378
 QY 1646 ACCCATGCTGA 1657
 Db 1379 ACTCATGTTAA 1390
 RESULT 3
 US-10-029-756-26
 ; Sequence 26, Application US/10029756
 ; Publication No. US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/029,756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1702 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 48..1406
 ; NAME/KEY: CDS
 ; LOCATION: 48..1406
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-10-029-756-26
 Query Match 28.7%; Score 555; DB 14; Length 1702;
 Best Local Similarity 64.8%; Pred. No. 3,3e-121;
 Matches 889; Conservative 0; Mismatches 470; Indels 12; Gaps 4;

QY 321 AGAGAGAAGATCACTAAGCTGAGAGCTGAGAGGTCAACAAGAGAGGAGATTAT 380
 Db 58 AAGCTAAGAGATATCAAGCGAGAGACCTCCGCCCAACAAGTCCGGGAGATCTCT 117
 QY 381 GGAATCAATTAAGTATAGTATCAATGTCTCAGATTGGGTCAAGAGCAACCTGTG 440
 Db 118 GGAATCAATCAAGGCAAGGTCTACGACTGCTCTGAGGGGCGGAGACCCCGGG 177

QY	441	GTGATGTTCCAAATCTCAAAACCTGTGGCGAGAAATGTCATCGATGATCATTAATGATAC	500
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QY	501	ATCTGGCAGACAGATGTGTCAACCTTGA AAAATTTCTCACTGG---CTACACCTCACTG	557
Db	238	ACCGGGGACACGGCGGGCGGACATGTGATCCGCTCTTACCGGGCTACTACTACCTCAGG	297
QY	558	ACTTCAGAGCTCTGAGAGGTGCCAAGAAGCTACAGAAACCTTGATCTGATGTTCCAAAT	617
Db	298	ACTTCAGAGTGTCCGAGATCTTCAAGAGCTACCGAGGCTTTTGAACAGAGTGTGGCT	357
QY	618	TGGGCTTTTTCACACCAAGGGGCACTGTCACTTCATGACCCCTTGATCTGTGCTGTGA	677
Db	358	CCGGGATCTTCAGAGAAAGAGGCCACACATCATGTGACGTTGTCGGGGTGGGTGCA	417
QY	678	TGTTCTCATTTGTACTCTATGTGTCTTGAGAGTGCATAGTGTGTGGCTCATTTGGGTT	737
Db	418	TGATGGCGGCAATCGTCTTACGGCGGTCTGGGGCTCGGAGTCCGTCGGAATTCACATGCT	477
QY	738	CAGCATGCTCTTAAAGGTTGCTTTGGATGCAAAAGTCTTATGTGGGCGCATGTTGGCC	797
Db	478	GGCGGCACTGCTGGGCTTGTCTGTGATTCAGCCGCGTATGTGGGCATGACTCCGGC	537
QY	798	ACTATGTGTTATGACCAACCAATGTGTTCAACAAAGTTGCAACAGTCTCTTGGAACT	857
Db	538	ATTACAGAGTATGCAACCCGGTGATTCACACAGATCACGCACTCATACAGGACACA	597
QY	858	GCTTACCGGGATTAAGCAATGCTTGGTGGAAAGTGCATCAAGTCTACACACATTTGGCT	917
Db	598	TCTTCAACCGGATTCAGATCGGTGTGTGAAGTGAACCCACACGCCACACCTCTGGCT	657
QY	918	GCAACAGCTTGACCATGATCCCTGATCTGCAGACATGACCGGTCCTTTCAGTTTGTGCG	977
Db	658	GCAACAGCTCTGACATACGACCCCGACCTTCAGCATCCCGGTATGGCCGTCTCACCC	717
QY	978	GGTCTTCAATTTCCATACTCTCATTTCTATGGAGAAAGTTGGAATTTGATTTCAATG	1037
Db	718	GACTCTTCACTCAATCACTACCTGTGCTTCTATGGCCGAGCTGTAAATTCAGCAAGATGG	777
QY	1038	CTAGGTTCTTATCTGCTACAGACACTTTTACTTTTACCCGGTATGTGTGTGTCAGAG	1097
Db	778	CACGGTTCGTAGTACGATCACAGCACTGACCTACTACCCGATGATCTTCCGGCGAG	837
QY	1098	TCAACTGTATCTGCAGCAATCTCTGATTTGTTTCGAGCGCAAAAGTGCAGATAGAG	1157
Db	838	TCAACCTCTTATCATCAGACCTTTTATGTCTCTACCAAGGGCGACACTCCCTGACCCGG	897
QY	1158	CCTTGAACATPATGGGAGATCCCTGTGTTTGGACATGTGTCCTCTTATGATGCTTGGC	1217
Db	898	CTCTTAACCTTAATGGGATTCGGCGTTTCTGSACTGTGGTTCCCGCTCTTCTGATTTGTTC	957
QY	1218	TGCCAAATTTGACCTGAGAGGGTTATGTTGTGCTTGTACGCTTGGCTTGTTCATATCC	1277
Db	958	TCCGGAATGACCTGAGACGATTCGGGTTCTGCTCATGACCTTTCGGTACAGGGATCC	1017
QY	1278	AGCATTCTCACTCTGTTTGAATCACTTGTCTGCAAAATGATATATGTGGGCGACCGAGTG	1337
Db	1018	AGCAGTCTCAATTCACGCTCAACCTTCTCCGGGACACATACGTGGGCCCCCCCAAGG	1077
QY	1338	GGAAATGACTGTGTTGAGAGACAGACAAATGTGATATCTCTTGTGCTCTTTCGA	1397
Db	1078	GGCAGCACTGTTTCGAGAGACAGACAGAAAGGACGATGATATCACGTGCCACCTGTGA	1137
QY	1398	TGATTTGTTTTGGGTGGCTTGACGTTTCACTTGAACATCATTTGTTTCCAAAGCTAC	1457
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QY	1458	CTCGGTGCATATGAGAGAAATTTGCTTTGGTTAATGACCTTTCGACAAAGCAATATT	1517
Db	1198	CGCGTGGGCACTTAGAAGATGTGGCTTGTGCTGTGGAACTTGTGTAAAGACAGGGA	1257

Oy	1518	TGCGTTTAAAGAGCTTTCATTTGG---CAGGCGCATTCAGTGGACATTAGACCCCTCA	1574
Db	1358	TGCCGTTTAAAGAGCTTTGGGTTTTTGGGACGACGCTTAATGTCAGGACAAATTCGACGCTGA	1317
Oy	1575	GGACTGCTGCCTCAAGACTAGGGACTTAA---CAAACTGCCCCCTAAGAA---TTTGT	1628
Db	1318	GGGATGCGGCGGCTTCAGGCGGCGTACCTTAAATTGGCCCCGTGCTTAAGAAACTTGGGT	1377
Oy	1629	TGTGGGAAGCTGTTAATATCCCATGCTGAGGCATTTGGAGTTTAAAGATT	1679
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RESULT 4
US-09-770-149-494/c
; Sequence 494, Application US/09770149

```

GENERAL INFORMATION:
PATENT NO. US2002005963A1
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameeka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Iedford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker, Marja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurlban, Patrick
TITLE OF INVENTION: Expressed sequences of Arabidopsis thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIORITY APPLICATION NUMBER: 60/118,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 494
LENGTH: 657
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-149-494
```

Query Match	13.9%	Score 269.4	DB 9	Length 657
Best Local Similarly	67.2%	Pred. NC 1.2e-53		
Matches 381	Conservative 0	Mismatches 186	Indels 0	Gaps 0

Oy	1152	TTTAAAGCCTTGAACATATAATGAGGATCCTTATGCTTTGGACATGGTGTCCCTTTTAAATGT	1211
Db	657	ATCGTGTCTTAACTTGCGCGAATCTTAGCTCTTGAGCTGGTCTCCACTTAACTCT	598
Oy	1212	CTTGCCCTGCGAATAATGGCTGAGAGGGTATAGTTTGGCTGTGACCTTGTCTGTGTGT	1271
Db	597	CATGTCTACCAAACTGGCTGAGAGATTTCTTCTTGCTTACAAAGCTTCACCGTCAAG	536
Oy	1272	CCATCCAGCACATTCAGTTCTGTTTAATCATCTTGTGCAATGTATATGTGGGGCCAC	1331
Db	537	CGCTTCAACACATTCAAATCAACGGTTACCATATTCGTGCTGATGTCATGAGTGGTGCAC	478
Oy	1332	CGAGTGGGAATGACATGCTTTGAGAGACAGACAAGATGTGATCATTTGGATATCTCTGTGCTT	1391
Db	477	CCACCGGTAGACATGCTTTGAGAGACAGACGGGGGAACATCATGATATCTCTGTGTGAT	418
Oy	1392	CTTCGATGATGTGTTTTTCGGTGGCTTGACATTTCACTTGACATCATTTGTTCGAA	1451

Db 417 CATACATGATGGTGTCTTTGGATGATTAAGATTGAGCTTGAACATCATTTGTCCTC 358
Qy 1452 GGCTACTGCTGCTCCATTTAGAGAAATTTCCCTTTGTTAGTACCTTTGCAAGAAC 1511
Db 357 GCTTACTGCTGCTCCATTTAGAGAAATTTCCCTTTGTTAGTACCTTTGCAAGAAC 298
Qy 1512 ATAATTGCTTATAGAGAGCTTGTATTTGGAGAGCCATTCAGTGAATTAGAACCC 1571
Db 297 ATATCTCTCCCTATAGAGAGATGTCGTGTTAGAGAAATGTCGTGACATTTAGCTT 238
Qy 1572 TCAGAGCTGCTGCTCAAGAGCTTAACAAACCTGCTCCCTAGAAATTTGTTG 1631
Db 237 TGAAGACAGAGCTTATCAAGAGCTTAAGAGAGCTGCTTAACGAGTGAAGACTGTT 178
Qy 1632 GGAAGCTGTTATACCAAGCTGAGAGCTTTGAGTTTATGAGTTTATGCT 1691
Db 177 GGAAGCTTGAATACCTAGCTTAATGATTTTAAACAAATATGCTTTGTTT 118
Qy 1692 AAGCTTTTCTTTTCTCT 1718
Db 117 GGGTAAATTTGATGCTGTTTAT 91

RESULT 5

US-09-878-574-15653
; Sequence 15653, Application US/09878574
; Patent No. US2002010548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21 (15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 15653
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701070356H1
US-09-878-574-15653

Query Match 13.2%; Score 256; DB 10; Length 267;
Best Local Similarity 99.6%; Pred. No. 1,1e-50;
Matches 267; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 50 GGGTAAAGGGATTTAGATCTTGAACAGATCAATCAAAATCTGCTATGAGG 109
Db 1 GGGTAAAGGGATTTAGATCTTGAACAGATCAATCAAAATCTGCTATGAGG 60
Qy 110 TTGTGAAAAAACAATACATTTGTTGCTGTAAGAGGAGTTCTTATGCTAGATTG 169
Db 61 TTGTGAAAAAACAATACATTTGTTGCTGTAAGAGGAGTTCTTATGCTAGATTG 120
Qy 170 TTGTCATGAGAGAAACAGATACCCCATTTATTTCTTATCTATCTGCTATAT 229
Db 121 TTGTCATGAGAGAA-ACACGATACCCCATTTATTTCTTATCTATCTGCTATAT 179
Qy 230 TCTATTTATCTTATTTAGTTAGTTCTGATTTGCTGATTTCAAGTATTTGTTGTTT 289
Db 180 TCTATTTATCTTATTTAGTTAGTTCTGATTTGCTGATTTCAAGTATTTGTTGTTT 239
Qy 290 TGGTTAACAAAGATGAGGTTGTTG 317
Db 240 TGGTTAACAAAGATGAGGTTGTTG 267

RESULT 6

US-09-770-444-39
; Sequence 39, Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maya
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-39

Query Match 10.7%; Score 206.4; DB 9; Length 476;
Best Local Similarity 65.5%; Pred. No. 9,1e-39;
Matches 300; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

Qy 458 AACCTGCTGCGCCAGATGCTAGTATGATTCATGATACCATCTGACAGATGG 517
Db 18 AACCTGCTGCTGCAAGACGTCAGATGCTTATGATTCATGATTCGCGAAGCGTTGG 77
Qy 518 TCACACCTTGAATAATTCTTCACTGCTACACCTCAGTACTTCAAGTCTTGAAGTG 577
Db 78 CACCATCTGACCATCTTCAACCGGTTACCATCAGATTTCCAAAGTCTCGAAGTC 137
Qy 578 TCAGAGCTACAGAAAGCTGATGATGCTCAAAATTTGGCTTTTGAACCAAA 637
Db 138 TCAGAGATTAACCGTGTATGCTGCGAGTTGCTGAACCTCGGCTCTTGAACCAAA 197
Qy 638 GGGCATGCTCATTCATGACACCTTGCATGCTGTTATGTTCTCATTTACTTAT 697
Db 198 GGTCAAGTATCTCTACACTGAGCTTGTGCGCCATGTTCTCGAGAGTTCTCTAC 257
Qy 698 GGTGTTCTGAGGTGACATGATGTTGGGCTCATTTGGGTTCAAGCATGCTTAAAGGTTG 757
Db 258 GGTGTTTGGCTTGTACTCCGCTTCGCTCAACAAATGCGCCGCGCTTCTCGGCTTC 317
Qy 758 CTTTGAAGCAAGTCTATGAGGCAATGCTTGGCCATGATGTTATGATGACAAC 817
Db 318 CTTTGAATCAGAGCTTATAGTACAGATTTGTCATTTACGTTATCATGATGAGAC 377
Qy 818 AATGTTTCAACAAGTTGACAGATCTCTCTGGAAGTCTTGAACCGGATTAACATT 877
Db 378 AATCTTATACAGATTCGCTGAGCTTCTCTNNGTAACTGCTCAACCGGAATCTCAATC 437

Qy 878 GCTTGTGAGAGTCACTCACAATGTCACCACTTGC 915
 Db 438 GCGGTGTGAATGACTCACAATGCTCATCATCTAGC 475

RESULT 7
 US-09-878-574-3260

; Sequence 3260, Application US/09878574
 ; Patent No. US20020110548A1

; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878, 574

; PRIOR FILING DATE: 2001-12-21

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 3260

; LENGTH: 287

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(287)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: LIB028-013-Q1-B1-H6

US-09-878-574-3260

Query Match 9.7%; Score 188.4; DB 10; Length 287;
 Best Local Similarity 78.4%; Pred. No. 1.3e-34;

Matches 225; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1183 GTTTGACCTGTTCCCTCTTTAGTGTCTTGTGCTGCAGCAATGGCCTGAGAGGTTAT 1242

Db 1 GTTTGATTTGTTCCCTCTCTATGATCTCATCCCTGCCAATTTGGGAGAAAGGTCAT 60

Qy 1243 GTTTGCTGCTAGCTTTGCTGTTGTTCCATCAGACATTCATGTTGTTGAATCA 1302

Db 61 GTTTGTTTGGCGAGTTTGTGTTGCTGCTCATCAACCTCAATTTGTTGAACCA 120

Qy 1303 CTTTGTGCAATATATATGTCGCGCCACCAAGTGGGAATATCTGTTTGAAGCAGAC 1362

Db 121 TTTGCGACGATGTATGAGGCGCCACCAAAATGGCAATGCTGTTTGAAGCAAC 180

Qy 1363 AAGTGTACATTTGATATCTCTTGTGCTCTTGCATGATGATGTTTTCGGTGGCTTGA 1422

Db 181 TGTGTGCACTTGGACATCTCTTGTCTCTACATGATGATGATGTTTCTTTGGCGCTTGA 240

Qy 1423 GTTTACCTTGACGATCATTTGTTTCCAAAGGCTACCTCGTGCCAAAT 1469

Db 241 ATTCAACTTGACGACCATTTGTTCCCTTANGCTCCCAAGCACAAT 287

RESULT 8
 US-09-924-035A-370/c

; Sequence 370, Application US/09924035A
 ; Patent No. US20020142319A1

; GENERAL INFORMATION:
 ; APPLICANT: Grlach, Jm

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; FILE REFERENCE: 2011US

; CURRENT APPLICATION NUMBER: US/09/924, 035A

; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: US 60/148, 784
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 370
 ; LENGTH: 480
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-924-035A-370

Query Match 8.6%; Score 166.2; DB 10; Length 480;
 Best Local Similarity 67.4%; Pred. No. 3.2e-29;

Matches 234; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Qy 1372 ATTGATATCTCTTGTGCTCTCTGATGATGATGTTTTCGGTCTGACGTTACGT 1431

Db 480 AATCGATCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421

Qy 1432 TGAGCATATCTTTTCCAAAGGCTACCTGCTGCTCAATGAGGAATTTGCTTGTG 1491

Db 420 TGAGCATATCTTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361

Qy 1492 TAGTACCTTTGCAAGAGCATATTTGCTTATAGAGCTTGTCAATTTGGAGGCCAA 1551

Db 360 TCAAGAGCTTTGCAAGAGCATATTTGCTTATAGAGCTTGTCAATTTGGAGGCCAA 301

Qy 1552 TCAAGAGCATATTTGCAAGAGCATATTTGCTTATAGAGCTTGTCAATTTGGAGGCCAA 1611

Db 300 TGTGTGACCATTTACATTTGCAAGAGCATATTTGCTTATAGAGCTTGTCAATTTGGAGGCCAA 241

Qy 1612 TGCCCTTACAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1671

Db 240 GGTGTTTACAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 181

Qy 1672 TTAGAGTTTACAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1718

Db 180 AACAAATATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 134

RESULT 9
 US-09-878-574-9255

; Sequence 9255, Application US/09878574
 ; Patent No. US20020110548A1

; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878, 574

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/333, 535

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 9255

; LENGTH: 263

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: 701102270H1

US-09-878-574-9255

Query Match 8.1%; Score 156.2; DB 10; Length 263;
 Best Local Similarity 78.7%; Pred. No. 5.4e-27;

Matches 199; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

Qy 825 TCAACAAAGTTGACAGATCTCTCTGCGGAAGCTTTGACCGGAGTATAGCATTTGCTGT 884

Db 12 TCAGCGCGCTGAGCAATCTTTGTGCAATGATGATGATGATGATGATGATGATGATGATGAT 71

Qy 885 GGAAGTGAATCAATATGCTTACCAATGCTGCAAGCTTGAACCATGACCTGATC 944

Db 72 GGAAGTGAATCAATATGCTTACCAATGCTGCAAGCTTGAACCATGACCTGATC 130

Qy 945 TGAGCATATGCGGCTTTGCAAGTTGCTGCGGCTTTCAATTTCAATCAATCAATCTTCAT 1004

Db 131 TCAGCATATGCTGCTTTGCGGCTGCGGCTTTCAATTTCAATCAATCAATCTTCAT 190


```

QY      810 TGACAAACCAATGGTTTCACAGAGTTGCGACAGATCTCTCGGGAACTGCTGACCGGGA 869
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      230 CGACACATTTTCATGTCATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 289
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      870 TAAGATTTGCTTGTGAGAGTGTGACATGCTGACATGCTGACATGCTGACATGCTG 929
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      290 TCAGTCTAGAGTTGTGAGAGCGGACCAACAGTTGACATGCTGACATGCTGACATGCT 349
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      930 ACCATGACCTGATGCTGACAGATGCGGCTTTTGTGAGTTGTGCTGCGGCTTCTCAAT 989
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      350 AGACAGATTCGACATAGAACACCTCCCTTCTTCCGACATTTCCATGCTTCTTCACTA 409
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      990 CCATTAACCTCTCATTTCTATGAGAGAGAGTTGAGTTGATTTGATTTGATTTGATTTGA 1049
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      410 ATCTGCGGTCCACATGATGACCGGTGTGATGAGTACGACATCTTTGCAAAATTTCTTG 469
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1050 TCTGCTACGACACTTACTTTTACCCGGTAATGTGTGTCGACGGGTCACTTGTATC 1109
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      470 TCTCCCTCCAGCACTACCTCTACTACATCATGATGTTCCGCCGCTGACCTTACC 529
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 13

```

US-09-814-353-17782/c
; Sequence 17782, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17782
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 225..226, 227, 228
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-17782

```

```

Query Match      4.1%; Score 78.6; DB 13; Length 406;
Best Local Similarity 56.0%; Pred. No. 1.8e-08;
Matches 144; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

```

```

QY      1678 TTATGATTTTGTCAAGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1737
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      400 TTATATTTTTCCTCCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 341
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1738 TCATGTGATTTTGTGAGAGTGTGACATGCTGACATGCTGACATGCTGACATGCTG 1797
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      340 TTTTGGGGGTGTGAGAGATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 281
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1798 AGGTGTGTGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATC 1857
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

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DB      280 TTATTTTTTTTTTAAATAATTTTGGCCCAATAATTAATTTTTTTTTTTTTNNNNAAAA 221
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1858 AATACAAATTCATATATGATGACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1917
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      220 AAAAAAAAAAAAAAAAAATTTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 161
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1918 AAAAAAAAAAAAAAAAAAAAA 1934
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      160 AAAAAAAAAAAAAAAAAAAAA 144
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 14

```

US-09-814-353-4844/c
; Sequence 4844, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4844
; LENGTH: 299
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 146, 163, 175, 190, 191, 192, 195, 198, 199, 201, 202, 203,
; LOCATION: 206, 213, 214, 217, 222, 224, 225, 226, 229, 232, 233, 239,
; LOCATION: 246, 247, 249, 254, 255, 256, 264, 268, 274, 284, 286
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4844

```

```

Query Match      3.9%; Score 74.6; DB 13; Length 299;
Best Local Similarity 52.2%; Pred. No. 1.4e-07;
Matches 119; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

```

```

QY      1707 TTGTTTCTCTTAAAGAAAGAAATTCATGATGATTTTGTAGCCCACTTTT 1766
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      299 TTTTCTTTTAAAGAAAGAAATTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 240
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1767 CCAGATTTGGCTTTGAATTTAACTTTTGTAGTGTGATGACAAATGATGATGATCC 1826
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      239 NAAAAAANGNTNNNTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 180
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1827 AGATGTACTGACATGCTGATGCTTGTGATCAATCAATCAATCAATCAATCAATCAAT 1886
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      179 TTTTNAAAAAAAAAAGGNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 120
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      1887 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1934
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      119 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 72
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 15

```
US-09-814-353-11141/c
; Sequence 11141, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-0068
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11141
; LENGTH: 299
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 146, 163, 175, 190, 191, 192, 195, 198, 199, 201, 202, 203,
; LOCATION: 206, 213, 218, 217, 222, 224, 225, 226, 229, 232, 233, 239,
; LOCATION: 246, 247, 249, 254, 255, 256, 264, 268, 274, 284, 286
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11141

Query Match          3.9%; Score 74.6; DB 13; Length 299;
Best Local Similarity 52.2%; Pred. No. 1.4e-07;
Matches 119; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1707 TTGTTTCCTCTTAAGAAAAAATTCATGTTGCTAGCCCCACCTTT 1766
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 299 TTTTTCCTTTTNNAAAAAATTTTNCCTTTTNNNTTTTNNNGAATTT 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1767 CCAGATTGGCTTGAATTTTGTAGTGTGTACAATGATGATCC 1826
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 239 NAAAAAANCGNTTNNNTTTTNTTNNTTTNNAAANNNGNATNANNNTTTT 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1827 AGATGTTACTGCATGTCATGCTTGCATCAATACAAATTCATATCATGATGCCAAA 1886
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 179 TTTTNNAAAAAAGGATTTTNTTTTNTTTTNNAAAAAATTTTNNAAAAA 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1887 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1934
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 119 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 72
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

Search completed: January 1, 2004, 05:19:34
Job time : 484.374 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 16.9369 Seconds
(without alignments)
2555.128 Million cell updates/sec

Title: US-09-857-524B-8
Perfect score: 2449
Sequence: 1 MEVVEKEKKYITSEELKGNH.....RDLTNPAKNIILMEAVNTHG 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1943	79.3	449	2 A84900	hypotheical prote
2	1902	77.7	449	2 T47950	delta-8 sphingolip
3	1887	77.1	449	2 T50355	delta-8 sphingolip
4	1801	73.5	458	2 S68358	Delta8 sphingolip
5	684.5	28.0	523	2 JC7556	linoeloyl-CoA desa
6	451.5	18.4	444	2 JG0180	Deltae fatty acid
7	441.5	18.0	444	2 T13155	linoeloyl-CoA desa
8	401	16.4	472	1 T26280	linoeloyl-CoA desa
9	373.5	15.7	447	1 T43319	Deltae fatty acid
10	361	14.7	454	2 H88791	proteain T13f2.1 [i
11	221.5	9.3	345	2 T36617	probable Deltae fa
12	202.5	8.3	359	2 S3157	Deltae fatty acid
13	189.5	7.7	368	2 S54809	linoeloyl-CoA desa
14	180	7.3	135	2 A86380	hypotheical prote
15	179	7.3	427	2 G70530	probable dea33 pro
16	159	6.5	982	1 S16292	nitrate reductase
17	156.5	6.4	137	2 S46307	cytochrome b5 - r1
18	154.5	6.3	134	2 T14454	cytochrome b5 - w1
19	152.5	6.2	134	2 T52469	cytochrome b5 [imp
20	151.5	6.2	573	1 S06600	L-lactate dehydrot
21	149.5	6.1	121	2 T00766	probable Cytochrom
22	149.5	6.1	134	2 H96631	cytochrome b5 At2g
23	146.5	6.0	147	2 S67453	probable heme bind
24	146	6.0	905	1 JN0803	nitrate reductase
25	144.5	5.9	139	2 S46306	cytochrome b5 - co
26	144	5.9	134	1 CBRB5	cytochrome b5, mic
27	143.5	5.9	541	2 T27107	hypotheical prote
28	143	5.8	120	2 S63052	cytochrome b5 - ye
29	143	5.8	133	1 CBH05	cytochrome b5, mic

30	142.5	5.8	135	2 S49200	cytochrome b5 - co
31	140.5	5.7	140	2 T52468	cytochrome b5 [imp
32	140	5.7	370	2 B83034	conserved hypobet
33	139	5.7	141	2 T15210	probable cytochrom
34	137	5.6	112	2 S71324	cytochrome b5 - p1
35	137	5.6	926	1 RDSPNH	nitrate reductase
36	136.5	5.6	98	1 JN0316	cytochrome b5, ery
37	136.5	5.6	139	2 T41083	probable cytochrom
38	136	5.6	384	1 S54484	probable fatty aci
39	136	5.6	894	2 S52857	nitrate reductase
40	134	5.5	864	1 UC1422	nitrate reductase
41	133.5	5.5	134	1 CBR05	cytochrome b5, mic
42	133	5.4	134	1 CBPG5	cytochrome b5, mic
43	133	5.4	211	2 T49930	hypotheical prote
44	132.5	5.4	135	1 CBR75M	cytochrome b5, out
45	131	5.3	134	1 CBR75	cytochrome b5, mic

ALIGNMENTS

RESULT 1									
A84900									
hypotheical protein At2g46210 [imported] - Arabidopsis thaliana									
C/Species: Arabidopsis thaliana (mouse-ear cress)									
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001									
C/Accession: A84900									
R/lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N									
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;									
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.									
Nature 402, 761-768, 1999									
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.									
A/Reference number: A84420; MUID:20083487; PMID:10617197									
A/Accession: A84900									
A/Status: preliminary									
A/Molecule type: DNA									
A/Residues: 1-449 <STO>									
A/Cross-references: GB:AB002093; NID:G3702328; PIDD:AA062885.1; GSPDB:GN00139									
C/Genetics:									
A/Gene: At2g46210									
A/Map position: 2									
Query Match									
Best Local Similarity 79.3%; Score 1943; DB 2; Length 449;									
Matches 346; Conservative 41; Mismatches 59; Indels 0; Gaps 0;									
QY	5	EKEKKYITSEELKGNKSGDLWISIQKYNVSDWKEHPCGDPVJSNLAGDVTDAFIA	64						
DB	4	QTKKRYVTSEDLKKHNKPGDLWISIQKYNVSDWKEHPCGDPVJSNLAGDVTDAFIA	63						
QY	65	YHGTAMSHLEKFFTGHLSDPKYSESKDRKLASFSLGLPDTKGYTSCILASVAV	124						
DB	64	YHGTAMSHLEKHLNGHYVDHVSVDYRDLAEFSRGGLFDKKGHTTLVTLTCGV	123						
QY	125	MPFLIVYGVLRCTSVMAHLGSGMLGLIMQASVYVGHDSGHVYVMTNGFNKVAQILSGN	184						
DB	124	MLAAVLXGVLACTIRNAHLISAVLISLWIOSAVYGHDSGHVYVTSKPKNKLQILSGN	183						
QY	185	CLTGISIAWKKWTHNAHIAICNSLDHDPDLQHPVPVASSRFPNSITSHPYGRKLSEDFI	244						
DB	184	CLTGISIAWKKWTHNAHIAICNSLDHDPDLQHPVPVASSRFPNSITSHPYGRKLSEDFI	243						
QY	245	ARFLICYQHFTFFPWCVCVAVNLYLQTLILLPSRRKQDPAALIMGLVMTWTFPLLVSC	304						
DB	244	ARFLISYQHMTFFPWCVCGRINLPQTLLPSKSHVPRALINAGILVMTWTFPLLVSF	303						
QY	305	LPMWPERVMPVLASPAVCSIOHIOFCINHPAAVYVGPSPGNDMPKOTSGTLDISCASS	364						
DB	304	LPMWPERVMPVLASPAVCSIOHIOFCINHPAAVYVGPSPGNDMPKOTSGTLDISCASF	363						
QY	365	MDWFFGGLQOLBHHLPRLPRCOLRKISPLVSLDCKKNLPRYSLSFPMWANOITRTLR	424						
DB	364	MDWFFGGLQOLBHHLPRLPRCHLRVSPVVKELCKKNLPRYSLSFPMWANOITRTLR	423						

[illegible]

RESULT 3

T50555
delta-8 sphingolipid desaturase (imported) - rape
C:Species: Brassica napus (rape)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #ext_change 15-Sep-2000
A:Accession: T50555
R:Sperling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A>Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome
P450 gene family.
A:Reference number: Z22986; MUID:99003197; PMID:9786850
A:Accession: F50555
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-449 <SPES>
A:Cross-references: EMBL:NJ224160; PIDN:CAI1857.1
A:Experimental source: cultivar Drakkar
C:Genetics:
A:Gene: sld1

Query Match 77.1% Score 1887; DB 2; Length 449;

Best Local Similarity 74.7%; Pred. No. 7.7e-156; Matches 333; Conservative 52; Mismatches 61; Indels 0; Gaps 0;

Dd	424	TAAGADVAPNVKVLWEALNTHG 449
Oy	5	EKEKYITSEBELKGHNKBGDLWISIQGYVNVDWKYEHFGDVPISNLGGDVTDAFIA 64
Dd	4	QTKKRPISSDDLKKNNQPGLDWISIQQKVYDVSHMKSHPGGBAILNLGGDVTDAFIA 63
Oy	65	YHPTAMGHLEKFPPCYHLSDPKVSEVSQDYRKLSPEFKLGIPTDKGVTSCTLASAV 124
Dd	64	YHPGTAMRHLENLNHYVKDHVVDSRDYRLAAEFGRKLFDCKGHVTLTYLTICVA 123
Oy	125	MELLYLVCLTSTSWAHNGSGMLLGILMMOSAYVGHDSCGYVMTTGNKNYAQLISGN 184
Dd	124	MLAAVYGVACTSIWAHLISAVALIGLMTIQSAYVCHDSGYVTVTSKPCKLKQLISGN 183
Oy	185	CITGISIAMMKTTHANHHIACNSLDHPDLQHMPVEPAVSRRFPENSITSHEFYGRKLEDFI 244
Dd	184	CITGISIAMMWMTHTNAHHISCNSLDHPDLQIHPLVALANSKPFKSMTSRFYGRKLTEDFL 243
Oy	245	ARFLICYOHFFPYPMVCARVNYLIOTILLHSRRKQVRDALIMGLIVWTWPPLLVS 304
Dd	244	ARFLSYOHWSEYPIMCVGRINLFQTLLFSRRYYPRPALNIAGILVFWTFPLLVS 303
Oy	305	LPNWERWVFVASFAVCSIOHIQCINFHAANYVYGPPSNDMPFEKOTSGTIDISCASS 364
Dd	304	LPNQERILEFSLMAVTRAIQHVQFCLNHFADDVYTGPFRGNMFEEKQTGTIDISCASY 363
Oy	365	MDWFEGLOFOLEENLPRLPCPOLRKISPVSIDLCKKNLPYRSISFWEANOWTIFTRL 424
Dd	364	MDWFEGLOFOLEENLPRLPCPHLRGVSPVOELCKKNLPYSISSWEAWNWTLATLRL 423
Oy	425	TAALQARDLTNPARPKNLLMEAVNTHG 450
Dd	424	KAAVARDDVINPVLENLLMEALNTHG 449

RESULT 4

S68358
Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower
C:Species: Helianthus annuus (common sunflower)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #ext_change 21-Jul-2000
A:Accession: S68358
R:Sperling, P.; Schmidt, H.; Heinz, E.
Eur. J. Biochem. 232, 798-805, 1995
A>Title: A cytochrome-b(5)-containing fusion protein similar to plant acyl lipid desaturases
A:Reference number: S68358; MUID:96028121; PMID:7588718
A:Accession: S68358
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-458 <SEB>
 A:Cross-references: EMBL:X87143; NID:G1040728; PIDN:CAA60621.1; PID:G1040729
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase
 F:16-90/Domain: cytochrome b5 core homology <CBS>
 F:51.74/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 73.5%; Score 1801; DB 2; Length 458;
 Best Local Similarity 71.6%; Pred. No. 2.3e-148;
 Matches 317; Conservative 55; Mismatches 71; Indels 0; Gaps 0;

QY 8 KKVTSEELKHNKGGDMISIQKVVYVSDWKVKEHPEGDPVPSNLAGQVDTAFIAYHP 67
 D 16 KKVTSEELKHNKGNPNNDIMISILKVVYVTEMAKHPGSDAPLINALGQVDTAFIAYHP 75
 QY 68 GTANSHLEKPFYVHLSDFKYSVSVKDRKLASEPSKGLPDTGHTVSCILASAVAMFL 127
 D 76 GTANKHLDKLFYTHLNDYQVSDISRDYRKLAISEPAKAMEKKGHVYISLCVSLILS 135
 QY 128 ILYGVLRCTSVMAHLGSGMLGLLMQSAVYVGHSDGHVYVMTTNGFNKVAQILSGNCLT 187
 D 136 ACYGVLYSGSFVTHMLSGALGLAMQIAYLGHDAHYOMATRGMKAFGIFIGNCIT 195
 QY 188 GISIAMKWTNNAHIAACNSLDHDPDLOHMPVAVSSRFNSITSHFYGRKLEDFIARF 247
 D 196 GISIAMKWTNNAHIAACNSLDYDPDLOHLPMAVSSKLFNSITSVFYGRQTFEDPLARF 255
 QY 248 LICVHFTFVYVWCVARNVLYOTILLFSRRKQODRALNMGILFVFTWPRPLVSCLPN 307
 D 256 FVSYOHLYYPRVPCVARNVLYOTILLFSRRKIPDRGLNLTGLTFWTPRPLVSRLPN 315
 QY 308 WPERVMEVLASFVACSIOHIOFCINHFANVYVPGSGNDWFEKQTSGLTDISCASSMDW 367
 D 316 WPERVAVLVVSFCYTGIOHIOFTLNHPSGDVYVGRPKDMMFEKQGTITDIACSSMDW 375
 QY 368 FFGGLQFQLEHNLPRPLRCQKRIISPLVSDCKKHLPYRSLPWEANQVITRLRTAA 427
 D 376 FFGGLQFQLEHNLPRPLRCHLRISIPICRELCKYVNLPLYSLFYDANVTTLKTLRTAA 435
 QY 428 LQARDLTNPAPKLLMEAVNTHG 450
 D 436 LQARDLTNPAPKLLMEAVNTHG 458

RESULT 5

JC7556
 Lineoeyl-CoA desaturase (EC 1.14.19.3) - Mucor rouxii
 N:Alternate names: delta6-desaturase
 C:Species: Mucor rouxii
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
 C:Accession: JC7556
 R:Biochem. K.; Mammontarac, R.; Tanticaroen, M.; Cheevadhanarak, S.
 Biochem. Biophys. Res. Commun. 279, 17-22, 2000
 A:Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desaturase
 A:Reference number: JC7556; MUID: 20563795; PMID:11112411
 A:Accession: JC7556
 A:Molecule type: DNA
 A:Residues: 1-523 <LAO>
 A:Cross-references: GB:AF290983
 A:Experimental source: strain ATCC 24905
 C:Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformati
 C:Keywords: oxidoreductase; transformation

Query Match 28.0%; Score 684.5; DB 2; Length 523;
 Best Local Similarity 28.5%; Pred. No. 2.1e-51;
 Matches 147; Conservative 86; Mismatches 200; Indels 83; Gaps 7;

QY 6 KEKKYISEELKHNKGGDMISIQKVVYVSDWKVKEHPEGDPVPSNLAGQVDTAFIAY 65
 D 17 RSSNIVIEKQELIKQSDSVFTEQKVVYVNNFPAKAPGGAALRSLGRDVTDEIRTM 76
 QY 66 HPGTAMVLEKFTGYHLSDF----- 86

D 77 HPPQVY---EKLINLYCIGDYMEDVIRPASMKQOHTFPEKDKPVLTAWEGGFTVOAY 133
 QY 87 -----KVSEVSKD-----YRKLAISEPSKGLPDTGHTVSCILAS 121
 D 134 DDAIQDLKHKSHDLIDAVLQKDLNDQIRNAYRKLEAEIYAKGLF-----KCYWK 186
 QY 122 VA-----VMFLVLYGVLRCTSVMAHLGSGMLGLLMQSAVYVGHSDGHVYVMTTNGF 174
 D 187 YARGCYRVTLLIFLSLWPTLKGTETHTYMAAAMFAMFWQLVPTADAGNEITGSEI 246
 QY 175 NKVAQILSGNCLTGISIAMKWTNNAHIAACNSLDHDPDLOHMPVAVSSRFNSITSHF 234
 D 247 DHVGIYANFPIGGLSLGMMKDNVNHIVTNEHEDPDLOHMPFMAITTKFFNNISTY 306
 QY 235 YGRLEDFIARFLICYOHFTFVYVWCVARNVLYOTILLFSRRKQODRALNMGILVF 294
 D 307 YKRVLPDAASRFVRRHQLVLYLISFGFPMRLRSLFVALLCKAVRTTLELVGTFP 366
 QY 295 WTPFRLVSCLPWPERVMEVLASFVACSIOHIOFCINHFANVYVPGSGNDWFEKQTS 354
 D 367 FVWFGSLSTLPTWNRIRIAYIMVSYMLTFPLHQITLSHFGMSTEDRGPD-EPPAKMLR 425
 QY 355 GTLDISCASSMDWFFGGLQFQLEHNLPRPLRCQKRIISPLVSDCKKHLPYRSLPWE 414
 D 426 TTMDVDCPEWHDMFHGGLQYQAVVHILPRPLRPHNLRCVPLVKKFCDEVGILHYVYVNST 485
 QY 415 ANQWITRLTALALQARDLTNPAPKLLMEAVNTH 449
 D 486 GNGVLIQTLKSVADQVGFNMEVAKSNAEIWANDKEH 521

RESULT 6

JG0180
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
 C:Accession: JG0180
 R:Aki, T.; Shimaeda, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeata, S.; Ono, K.;
 Biochem. Biophys. Res. Commun. 255, 575-579, 1999
 A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desat
 A:Reference number: JG0180; MUID:99160394; PMID:10049752
 A:Accession: JG0180
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-444 <AKI>
 A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BA075496.1; PID:94514722
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
 F:18-94/Domain: cytochrome b5 core homology <CBS>
 F:53.76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 18.4%; Score 451.5; DB 2; Length 444;
 Best Local Similarity 28.5%; Pred. No. 2.9e-31;
 Matches 126; Conservative 62; Mismatches 157; Indels 97; Gaps 15;

QY 14 BELKGNKGGDMISIQKVVYVSDWKVKEHPEGDPVPSNLAGQVDTAFIAYHGTAMSH 73
 D 24 BEIQKHNLRTRDMLVIDRKVVNTKWSQRHPGGHVRVIGHVSGEDATAPFAF-----H 76
 QY 74 LEKFTGYHLSDF-----KVSEVSKDVKRLASEPSKGLPDTGHTVSCIT 118
 D 77 LDDDFVKKFLKPLLIGLAPBEBSLDNGKSOITEDPRALKTAEDNMLFKTNHLFFFL 136
 QY 119 LASVAVMFLVLYGVLRCTSVMAHLGSG-----MLGLLMQSAVYVGHSDGHVYVMT 170
 D 137 LSHIIVESIAMF-----ILSYFGMGWIPVTITAFVLTSGAQOAGMLQHDYGHLSVYK 189
 QY 171 TNGCNKVAQILSGNCLTGISIAMKWTNNAHIAACNSLDHDPDLOHMPVAVSSRFNSI 230
 D 190 KSLWNHIVHKFVYTGHLGASAMNWHRHPOHAKPNFHKQPDKSLHVFVLAEE--NQPL 247
 QY 231 TSHFYGRK---LEDFIARFLICYOHFTFVYVWCVARNVLYL--QTILLFSRRKQOD 284

```

Db      248 E-----YGRKKLKLYLPYN-----HHEHEFFLLIGPRLIPMYFOYQIIMTIRRRWVDL 296
QY      285 A-----LIMIGILVFWTWPPLVSLCPNMPERMPFLASFAVCSIOHI- 327
Db      297 AMALISTARFFYYIIPYIGLALVFLNFIREFLES---HW-----VTQNMHIW 344
QY      328 -QFCLNHPAANYVVGPPSGNDWFEEKOTSGTLDISCSASMDWFFGQLQFQLEHHLFPRLP 386
Db      345 MEIDLDDHY-----RDMFSSQLAATCNVEQSPFNDFMSGHLNFOJLEHHLFPTMPR 393
QY      387 CQARKISPLVSDLCCKKNLNPYR 408
Db      394 HNLHKLAPLVKSLCAKHGIEYQ 415

RESULT 7
110lecyl-CoA desaturase (EC 1.14.19.3) [validated] - human
N/Alternate names: Delta6 fatty acid desaturase; protein DKFZps86C201.1
C/Species: Homo sapiens (man)
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C/Accession: T13155; T08765
R/Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A/Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desatu
R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, March 1999
A/Reference number: Z16471
A/Accession: T08765
A/Molecule type: mRNA
A/Residues: 1-444 <CHO>
A/Cross-references: EMBL:AF126799; NID:G4406527; PID:G4406528; PIDN:AMD20018.1
R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, March 1999
A/Reference number: Z16471
A/Accession: T08765
A/Molecule type: mRNA
A/Residues: 'RTRG', 138-428, 'D', 430, 'W', 432-444 <WAM>
A/Cross-references: EMBL:AL050118
A/Experimental source: adult uterus; clone DKFZps86C201
C/Genetics:
A/Gene: GDB:FADS6
A/Cross-references: GDB:9956652
A/Note: DKFZps86C201.1
C/Superfamily: cytochrome b5 core homology
C/Keywords: cytochrome b5 core homology; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty
F/18-94/Domains: cytochrome b5 core homology <CBS>
F/53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match      18.0%; Score 441.5; DB 2; Length 444;
Best Local Similarity 28.1%; Pred. No. 2,2e-30;
Matches 128; Conservative 65; Mismatches 171; Indels 91; Gaps 16;

QY      14 EEIKGNKEDLMISIGKYYNVDWYKEHFGDVPISNAGDVTDAFIATHPGTAMSH 73
Db      24 EEIQKHLRTDRMLVLDKRYNITKMSIOHPGGORVGHVAGBDADAFAPFDLEF-- 81
QY      74 LEKFGYHNSDF-----KVSEVSKDYRKLADEFKGLFPTKGHVTSGTLASVA 123
Db      82 VGRFLKPLLIGELAPESPDSODHGNSKITDPRALRTAEDMNFKN-----H 130
QY      124 VMFLIVLYGVLRCTSV-W-----AHLSG-----MLGLIMQSAVYGHDSGHVYMTT 171
Db      131 VFLLLLLAHIALESIMFVYFGNGWITPLTIAFLATSOAGLQCHDYGLSLYRK 190
QY      172 NGFNVAQILSGNCTGISIAMWKMTNAHIACNLSDHDPDLOHMEVAVSSRFNSIT 231
Db      191 PKNNHLVHKREVIIGHLKASAMWNRHAFQHAKENIFHKDPDVMLTHVFLGE--WQPIE 248
QY      232 SHFYGRK-----LEPDFIARFLICYHFTFYVWKVAVANLYL--QTLLLSFRKQDRA 285
Db      249 ---YGRKKLKLYLPYN-----HHEHEFFLLIGPRLIPMYFOYQIIMTIRRRWVDL 297
QY      286 -----LIMIGILVFWTWPPLVSLCPNMPERMPFLASFAVCSIOHIQF 329

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Db      298 MAVSYIRFFITYIPYIGLIGALLFLNFIREFLES---HW-----VTQNMHIW 345
QY      330 CLNHFAANYVVGPPSGNDWFEEKOTSGTLDISCSASMDWFFGQLQFQLEHHLFPRLP 389
Db      346 EIDQEAAY-----RDMFSSQLAATCNVEQSPFNDFMSGHLNFOJLEHHLFPTMPR 396
QY      390 RKISPLVSDLCCKKNLNPYRSLSFWEANQWITRRLR 424
Db      397 HKIAPLVKSLCAKHGIEYQEKPLRLALDITRSK 431

RESULT 8
110lecyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - Caenorhabditis elegans
N/Alternate names: Delta6 fatty acid desaturase
C/Species: Caenorhabditis elegans
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 03-Jun-2002
C/Accession: T26280; T37238
R/Swinburne, J.; Alnecough, R.
Submitted to the EMBL Data Library, March 1996
A/Reference number: Z20188
A/Accession: T26280
A/Molecule type: DNA
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-473 <WIL>
A/Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2.4
A/Experimental source: clone W08D2
R/Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A/Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by heter
A/Reference number: Z21637; WUID:98149727; PMID:9480865
A/Accession: T37238
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-38,69-430, 'V', 432-473 <NAP>
A/Cross-references: EMBL:AF031477; NID:G3088519; PIDN:AACT15586.1; PID:G3088520
C/Genetics:
A/Gene: CESP:W08D2.4
A/Map position: 4
A/Intons: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C/Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

Query Match      16.4%; Score 401; DB 1; Length 473;
Best Local Similarity 25.3%; Pred. No. 7,6e-27;
Matches 124; Conservative 77; Mismatches 187; Indels 102; Gaps 18;

QY      20 NKEGDLIMISIGK-VYNVSDWYKEHFGDVPISNAGDVTDAFIATHPGTAMSH----- 52
Db      6 NAG-LRMVVDGKMLISELVYKHPGAVIQYSIPLNKNIETRGILTRGSSNALDI 64
QY      53 ---LAQDVTDAFIATHPGTAMSH-----LEKFF-----TGYHL 83
Db      65 LYFRRSDATHIFHAHBSGSAVYKQDLLKKGHEDEFLKQLEKRLDKVDINVAUYDV 124
QY      84 SDPKVSEVSKDYRKLADEFKGLFPTKGHVT-----SCTLASVVMFLIVLYGVLRCT 137
Db      125 SVAQEKVSEVSEFKLQKLDHDDLM--KANETVFLFKAIISTISIMFAFYLYLG----- 177
QY      138 SVVAHLGSGMLGLLMOGSAVYGHDSGHVYVMTTNGFNVAQILSGNCTGISIAMWKMT 197
Db      178 -W-YITSACLALANQOGKMLTHERCHQOPTKNRPLNTITSLFENFLQGSFSDWKK 234
QY      198 HNAHITACNSLDHDPDLOHMEVAVSSRFNSITSHFYGRKLEPDFIARFLICYHFTTY 257
Db      235 HNTHTAATVVIDHDGIDIDALPLFAF-----IPGDLCKYKASFEXALIKIVYQHLVPT 287
QY      258 PWCVCARVNLVYOTILLFSRRKYQDRA-----LIMIGILVFWTWPPLVSLCPNMP 308
Db      288 AMPLPMRFSWTSQVGVFENQMEYKYVQRNAFWEOATIVG--HWAVVFQFLPLPTW 344
QY      309 PERVMEVLAS--FAVCSIOHIQFCLNHPAANYVVGPPSG--NDWFEEKOTSGTLDISCAS 363

```

Db 345 PLRAVAFPISSQMGGLTAHV-VTFNNSVDKY--PANSRLINNFALQIITTRMTSP 401
Qy 364 SMDVFEGLQOLEHLLPRLPRCOLRKISPLVSDLCCKHNLPRSLSFMEANQMTITRL 423
Db 402 FIDMLGGGLNQLIEHLLPRLPRCOLRKISPLVSDLCCKHNLPRSLSFMEANQMTITRL 461
Qy 424 RTAA--LQAR 431
Db 462 KNMAEHIOAK 471

RESULT 9
T43319
Deltas5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 (validated) - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C/Accession: T43319, T24875
R/Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
FEBS Lett. 439, 215-218, 1998
A/Title: Functional identification of a fatty acid deltas desaturase gene from Caenorhabditis elegans
A/Reference number: Z22422; MUID:99059458; PMID:9845325
A/Accession: T43319
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-447 <MIC>
A/Cross-references: EMBL:AF078796; NID:g4003522; PIDN:AAC95143.1; PID:g4003523
R/Swinburne, J.
Submitted to the EMBL Data Library, October 1996
A/Reference number: Z19947
A/Accession: T24875
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-197, 'VSHIFNN', 198-447 <WIL>
A/Cross-references: EMBL:Z81122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
A/Experimental source: clone T13F2
C/Genetics:
A/Gene: CESP:T13F2.1; des-5
A/Map position: 4
A/Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 15.3%; Score 373.5; DB 1; Length 447;
Best Local Similarity 24.7%; Pred. No. 1.7e-24;
Matches 112; Conservative 78; Mismatches 198; Indels 65; Gaps 14;

Qy 26 WISIQGVNVSDWV-KEHGGDVPIISNLAGQVTDFAIYHPT---AW-SHLEK--- 76
Db 12 FIKIDGKMCQIDDAVLRSHPGGSA-ITTYKMDATTVFHTGSKAYQWLTLEKCEP 70
Qy 77 -----FTGYHLSDFKVSSEVSKDYKRLASEFSLGLFDTKGHYTS 116
Db 71 TOBEIPIDIDDPKIGIDVNMGTFFNISSEKSAQINSLFTDLRMRVRAEGLMD--GSPLEF 128
Qy 117 CTLASVAMFPLIVLYGVLRCTSVANHLGSGMLGLLMMQSAVYVGDGHVYVMTTNGRNK 176
Db 129 YIRKILFTITFLPAFLQYHTY--YLPASALMGVAMQGLMLHEPRAHQDLFKRRYYND 186
Qy 177 VAQLISGNCITGISIAWKWTNNAHIAICNSLDHDPDLQAMPVFAVSSRFNSITSHFYG 236
Db 187 LASYFVGNFLQFGSGGCKEQHNVHNAATVNGRGDLDLVPFAVAEHLNNSQ----- 242
Qy 237 RKLKEDFLARFLICYQHTFYRVMCVARVNLVLOTILL-----FSRRVQDRAL 286
Db 243 -----DSWVMTLFRWQHVTMFLPRLSLWLSQIIFVSQMPHYDYVNTAIEQ-- 295
Qy 287 NIMGLVFWTPPLVSCLPMPBERVWFVLAFAVCS--IOHIOFCNLHFAANYVGPSP 344
Db 296 --VGLSLHMAWSLGOYLFLPDKSTRIMFPLVSHLVGGGLSHV-VTFNHYSEKFA--LS 350
Qy 345 GN---DWFEKQTSGLTIDISCASSMDWFFGLQFQLEHLLPRLPRCOLRKISPLVSDLC 401

Db 351 SNINSNVACIQIMTRMRPGRPIDWMLGGLNQLIEHLLPPTMRHNLNTVPLVKEEPA 410
Qy 402 KENLPYRSLSPWEANQMTITRLTPRALQARDLT 434
Db 411 ANGLPYNVDITFTGFWLEIEQFRNIANVAAKLT 443

RESULT 10
H88791
protein T13F2.1 (imported) - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C/Accession: H88791
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: H88791
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-454 <STO>
A/Cross-references: GB:chr_IV; PIDN:CAB03352.1; PID:g3879828; GSPDB:GN00022; CESP:T13F2.1
A/Map position: 4
C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match 14.7%; Score 361; DB 2; Length 454;
Best Local Similarity 24.3%; Pred. No. 2.1e-23;
Matches 112; Conservative 78; Mismatches 198; Indels 72; Gaps 15;

Qy 26 WISIQGVNVSDWV-KEHGGDVPIISNLAGQVTDFAIYHPT---AW-SHLEK--- 76
Db 12 FIKIDGKMCQIDDAVLRSHPGGSA-ITTYKMDATTVFHTGSKAYQWLTLEKCEP 70
Qy 77 -----FTGYHLSDFKVSSEVSKDYKRLASEFSLGLFDTKGHYTS 116
Db 71 TOBEIPIDIDDPKIGIDVNMGTFFNISSEKSAQINSLFTDLRMRVRAEGLMD--GSPLEF 128
Qy 117 CTLASVAMFPLIVLYGVLRCTSVANHLGSGMLGLLMMQSAVYVGDGHVYVMTTNGRNK 176
Db 129 YIRKILFTITFLPAFLQYHTY--YLPASALMGVAMQGLMLHEPRAHQDLFKRRYYND 186
Qy 177 VAQLISGNCI-----TGISIAWKWTNNAHIAICNSLDHDPDLQAMPVFAVSSRFNS 229
Db 187 LASYFVGNFLQVSHIFNNGFSGCKEQHNVHNAATVNGRGDLDLVPFAVAEHLNNSQ----- 246
Qy 230 ITHSFYRKLEFPIARFLICYQHTFYRVMCVARVNLVLOTILL-----FSRR 279
Db 247 YSQ-----DSWVMTLFRWQHVTMFLPRLSLWLSQIIFVSQMPHYDYVNT 297
Qy 280 KVQDRALNIMGLVFWTPPLVSCLPMPBERVWFVLAFAVCS--IOHIOFCNLHFAANY 337
Db 298 AIYVQ-----VGLSLHMAWSLGOYLFLPDKSTRIMFPLVSHLVGGGLSHV-VTFNHYSE 352
Qy 338 VYVGPBSGN--DWFEKQTSGLTIDISCASSMDWFFGLQFQLEHLLPRLPRCOLRKISP 394
Db 353 KFA--LSSNINSNVACIQIMTRMRPGRPIDWMLGGLNQLIEHLLPPTMRHNLNTVMP 410
Qy 395 LVSDLCCKHNLPRSLSFMEANQMTITRLTALQARDLT 434
Db 411 LVKEFAANGLPYVVDYFTGFWLEIEQFRNIANVAAKLT 450

RESULT 11
T36617
Probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C/Accession: T36617
R/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A/Reference number: Z21610

A/Accession: T36617

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-345 <OL1>

A/Cross-references: EMBL:AL078610; PIDN: CAB44385.1; GSPDB: GNO0070; SCOEDB: SCH35.42C

A/Experimental source: strain A3(2)

C/Genetics:

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 9.0%; Score 221.5; DB 2; Length 345;

Best Local Similarity 24.7%; Pred. No. 2e-11;

Matches 89; Conservative 58; Mismatches 158; Indels 55; Gaps 14;

QY 94 DYKLAASEFKLGFDTKG----HTSCPLASVAVMFLVLYGVLRCTVMAHLSGML 148

DB 16 DFARLSKRVADAGILGRPGYTLRTAVTGLVAAAGAAFLVG----ASMTLAIAP 70

QY 149 LGLLMQSAVYGHDSGHVYVMTTNGFNKVAQILSGNCLTGISIAMWKTNNAHIIACNSL 208

DB 71 LAWYGVAVVAADHMAKQVFRRRASSELGRIAGASI-QMSYGWODKTRHIANPTE 129

QY 209 DHDPDLQHMVFAY-SSRFNSITSHFYGRKLEDFIARFLICYHFTFYVNCVAVNL 267

DB 130 DLDPDIG--PDLVWSPDQARAATG-----LPRLLGRQAFLFFPLTLBSGNL 176

QY 268 YLQTLILFRRKXQDRAIMIGILVFWTFPLLVSCLPMPEKVMFLASFAVCISIQH 327

DB 177 HVASGRAMARR-LKRRALD--GAL-----LHACAV-YLTALFWLPPGMAIARLAV 225

QY 328 QFCI-----NHPAANYVVP-----SGNDWFEKQSGTLTSCASSMDPFGGLQFOL 376

DB 226 HQCLFGYVLSAIPN-HKGMPLITADDPDLRQVLTNRNNGGLFTDLALGGLNHQI 284

QY 377 EHHLPRLPRCQRLKISPLVSDLCCKNLPYRSLSFWEANQWITRTIALQARDLTPN 436

DB 285 EHHLPSPMPSPNIRKARATIRRYCRDLGVY-----AETGLVASRLALTSLHDACTP 337

RESULT 12

Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synecocystis sp.

S35157

C/Species: Synecocystis sp.

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000

C/Accession: S35157; S76243

R/Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

Plant Mol. Biol. 22, 293-300, 1993

A/Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synecocystis S

A/Reference number: S35157; MUID: 9328363; PMID: 8389613

A/Accession: S35157

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-359 <RSD>

A/Cross-references: GB:J11421; NID:G349562; PIDN:AAA27286.1; PID:G349563

R/Kanejo, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamiizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-116, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

S.

A/Reference number: S74322; MUID: 97061201; PMID: 8905231

A/Accession: S76243

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-359 <KAN>

A/Cross-references: EMBL:D90914; GB:AB001339; NID:G1653477; PIDN:BA18502.1; PID:d101923

A/Experimental source: PCC 6803

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.3%; Score 202.5; DB 2; Length 359;

Best Local Similarity 23.6%; Pred. No. 9.2e-10;

Matches 79; Conservative 47; Mismatches 120; Indels 89; Gaps 15;

QY 125 MFLIVLYGVLRCTSVAAH-----LGSMLLGLLMMQSAVYGHDSGHVYVMTTN 172

DB 40 MYLKTIIIVMLFSAMAFULFAPVIRPVVLLGCMVLAIALAASFVNGDANNAVSSNP 99

QY 173 GFNKVAQILSGNCLTGISIAMWKTNH-AHIIACNSLDH-----PDLQHMPV 219

DB 100 HINRVLGMYTD--FVGLSFLWRRYRNHYLHHTYTNLIGHDVEIHGDGAVRMSPEQCHVG 157

QY 220 FAVSSRFNSITSHFYGRKLEDFIARFLICYHFTFYVNCVAVNLVLQTLILFSRR 279

DB 158 Y--RF-----QQFYIWL-----YLFIFPY-----WFLYDVYLVING 188

QY 280 KYQDRAL-----NIMGILVFWTFPLLVSCLP-----NWPE-----RVMFLASPA 320

DB 189 KIHDKIIPPOPLELASLIGIKMLIGY--VFGPLAIGFSLPEVLIGASVTYMTYGV 245

QY 321 VCSIQHIOFCLNHPAANYVGPSPG-----NDWFEKQSGTLTSCASSM-DWFEGLQ 373

DB 246 VCTI-----FMLAVLESTELFPDGSGLIDEMALICQRTTANFATNNPFWNMFPGGLN 301

QY 374 FQLEHLPRLPRCQRLKISPLVSDLCCKNLPYR 408

DB 302 HQVTHLPFNIQHINHYPOLENIKDYCOBGEVEYK 336

RESULT 13

S54809

linoleoyl-CoA desaturase (EC 1.14.19.3) - Spirulina platensis

N/Alternate names: Delta6-desaturase

C/Species: Spirulina platensis

C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 03-Jun-2002

C/Accession: S54809

R/Tanaka, Y.

submitted to the EMBL Data Library, May 1995

A/Reference number: S54809

A/Accession: S54809

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-368 <TAS>

A/Cross-references: EMBL:X87094; NID:G809109; PIDN:CAA60573.1; PID:G809110

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 7.7%; Score 189.5; DB 2; Length 368;

Best Local Similarity 24.2%; Pred. No. 1.3e-08;

Matches 80; Conservative 56; Mismatches 116; Indels 79; Gaps 19;

QY 115 TSCTLASVAVMFLVLYGVLRCTSVAAHLSGMLLGLLMMQSAV-VGHDSGHVYVMTTN 173

DB 45 TAILLAWVSAMTFVFGP--DVLMMKLLGCTVLFSGVSAVGFINSHDGNH-----CG 95

QY 174 FNVVAQI--LSGNCLT---GISIAWKKTTHA--HIIACNSLDHDPDLQHMPVAVSSRF 226

DB 96 YSKYQWVNYLSG--LTHDAIGVSSYLKMRHNVLTHTYTNLIGHDVEIHGDDELVRMS-- 151

QY 227 FNSITSHFGRKLEDFIARFLICYHFTF--YPMW---CYARVNLVLQTLILFSRR 279

DB 152 --SMERYWYR-----YQHWFTWFPYPIPIYWSJADV---QTLF--KR 189

QY 280 KYQDR-----ALNIMGILVFWTFPLLVSCLPMPEKVMFLASFAVCISIQ 325

DB 190 QYHDEIIPSTWTDINTLAFKAGAVFLI-IPVAVGSP-----LEAVIGASIYMTM 243

QY 326 HIOFCLNHPAANY-----YVGPSP---GNDWFEKQSGTLTSCASS--MDWFEGLQFOL 376

DB 244 GLVACVFMIAHVEBAEFLDPDNLHIDEMALAQKTVTFAPANNPIINWYVGLNYQT 303

QY 377 EHHLPRLPRCQRLKISPLVSDLCCKNLPY 407

DB 304 VHHLFPHICHIHYPKIAPILAEVCEBFGVNY 334

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 9.90156 Seconds
(without alignments)
2137.240 Million cell updates/sec

Title: US-09-857-524B-8

Perfect score: 2449
Sequence: 1 MEVVEKEXKYITSEELKGNH.....RDLTPAPKMLMEAVNTHG 450

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	439.5	17.9	444	1	PADS_BRARE
2	202.5	8.3	359	1	LCSD_SYN3
3	159	6.5	982	1	NIA_NEUCR
4	156.5	6.4	137	1	CYB5_ORYSA
5	154.5	6.3	134	1	CYB5_BRAOL
6	152.5	6.2	134	1	CYB5_TARAH
7	151.5	6.2	573	1	CYB2_HANAN
8	149.5	6.1	134	1	CYB2_ARATH
9	146.5	6.0	147	1	YDAA_SCHPO
10	146	6.0	905	1	NIA_FUSOX
11	144	5.9	133	1	CYB5_RABIT
12	143	5.8	120	1	CYB5_YEAST
13	142.5	5.8	135	1	CYB5_TOBAC
14	142.5	5.8	136	1	CYB5_TOBAC
15	141.5	5.8	146	1	CYB5_HUMAN
16	140	5.7	133	1	CYB5_HORSE
17	139.5	5.7	132	1	CYB5_BOROF
18	137	5.6	926	1	NIA_SBIOL
19	136.5	5.6	129	1	CYB5_SCHPO
20	136	5.6	384	1	SCS7_YEAST
21	136	5.6	894	1	NIA_BEABA
22	134	5.5	864	1	NIA_VOLCA
23	133.5	5.5	133	1	CYB5_BOVIN
24	133	5.4	133	1	CYB5_PIG
25	132.5	5.4	146	1	CYB5_RAT
26	131	5.3	131	1	CYB5_RHIST
27	131	5.3	133	1	CYB5_MOUSE
28	129.5	5.3	443	1	PD6C_RAT
29	129.5	5.3	902	1	PD6C_BRANA
30	129.5	5.3	443	1	PD6C_PHYTH
31	129	5.3	902	1	PD6C_ARATH
32	129	5.3	859	1	NIA_PICAN
33	129	5.3	900	1	NIA_LOTVA

34	129	5.3	920	1	NIA_CICIN	P43101 cichorium i
35	128.5	5.2	124	1	CYB1_SCHPO	O43391 echinosacch
36	128.5	5.2	375	1	D12_CREAL	O81931 crepis alpi
37	128.5	5.2	881	1	NIAI_PHAVU	P39865 phaseolus v
38	128	5.2	133	1	CYB5_HUMAN	P00167 homo sapien
39	127.5	5.2	911	1	NIA_LYCER	P17570 lycopersico
40	127	5.2	134	1	CYB5_DROME	Q9V4N3 drosophila
41	127	5.2	911	1	NIAI_BRANA	P39867 brassica na
42	127	5.2	918	1	NIA_CUCMA	P17569 cucurbita m
43	126.5	5.2	918	1	CYB5_NEUCR	O9P510 neurospora
44	126.5	5.2	890	1	NIA2_SOYBN	P39870 glycine max
45	126.5	5.2	909	1	NIA_PETRY	P36859 petunia hyb

ALIGNMENTS

RESULT 1	PADS_BRARE	STANDARD;	PRT;	444 AA.
AC	Q9DEX7;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-)			
GN	PADS2 OR PADS6.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver.			
RX	MEDLINE=21592990; Pubmed=11724940;			
RA	Haetings N., Agaba M., Tocher D.R., Leaever M.J., Dick J.R.,			
RA	Sargent J.R., Teale A.J.;			
RT	"A vertebrate fatty acid desaturase with delta5 and delta6			
RT	activities."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).			
CC	-1- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6			
CC	activities. May represent a component of the polyunsaturated fatty			
CC	acid biosynthesis pathway.			
CC	-1- PATHWAY: Polyunsaturated fatty acid biosynthesis.			
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			
CC	-1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.			
CC	-----			
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CC	-----			
DR	EMBL; AP309556; AAC25710.1; -			
DR	HSSP; P00173; 1EX			
DR	ZFIN; ZDB-GENE-011212-1; faad2.			
DR	InterPro; IPR001199; Cyt B5.			
DR	InterPro; IPR005804; FA desat fam.			
DR	Pfam; PF00487; FA desaturase; 1.			
DR	Pfam; PF00173; heme 1; 1.			
DR	ProDom; PD000612; Cyt B5; 1.			
DR	ProDom; PD001081; FA desat fam; 2.			
DR	PROSITE; PS00191; CYTOCHROME B5_1; FALSE_NEG.			
DR	PROSITE; PS02025; CYTOCHROME B5_2; 1.			
FW	Fatty acid biosynthesis; Oxidoreductase; Heme-			
FT	DOMAIN			
FT	18			
FT	53			
FT	76			
FT	52032 MW;			
SO	SEQUENCE			

Query Match 444 AA; 17.9%; Score 439.5; DB 1; Length 444;

Best Local Similarity 25.6%; Pred. No. 2.8e-29; Matches 123; Conservative 64; Mismatches 154; Indels 139; Gaps 15;

```
QY      12 TSEELKGNHNEGDLWISIOGKVYVSDVMYKHPGADVVISLNAQDVTDAFIAYHPGTAW 71
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      22 TWEEVGKHTKGDGDDVMYVERKVYVNSQWVKHPGLNLIHGVAEDATEAFATYHPNL-- 79
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      72 SHLEKFTGTHLSDFKXSEVSKDYK--LASESKL-----GLPDK-----GH 113
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      80 QLVARKYKLPRLIGLELASESPQDRQKNAALVEDPRALRELRLEAGCKRTOPLFPALHGH 139
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      114 VTSCCTLASVAVMFLIVYGYLRCSTSWAHLGSG-----MLGLMOSAAVYGHDSGH 165
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      140 I---LLELAIAFMWY-----FETGINTLIYAVALATQSQSGMQLQHPGH 184
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      166 YVWVTINGFNKVAOILSGNCLTGISIAMWKTWNAHHIACNSLDHPDLOHMPFAVSS- 224
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      185 LSVKPTSGMNLVHKVFYIHLKGASAGCMNRRHQHAKPPIPKKDDVNNLNAFVGVNV 244
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      225 -----RFSNITSHTYGRKLE---PDF 243
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      245 QPVEYGVKIKHLRYNHOHKYFPIGPBLIPYVFOFOIFNMISH--GMWVDLLMCISY 302
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      244 IARELCYGHFTFPPWVCVARVNLXLTPTLLFPRKRVQDALIMGILVFWTFPLLV 303
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      303 YVRFELCTQF-----YGVFMAILLNFVR-----PMSHFV--- 335
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      304 CLPMPRPVMEFVLSPAVCSIQHIOFCINLFPAAVYVGPSPGNDMFEKOTSGTLDISCAS 363
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      336 -----W-----VTQMSHI PNINDY-----ENQDMLMQVATCNIGSA 370
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      364 SMDWFEGLOFQLEHHLFPRLPQCRQKISPLVSDLCQHNLPYRSLSPWEANQWTRTL 423
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      371 FNDWFSHLNFQIENHHLFPTVPRHNYRAAPRALCEKYQGVKQEXTLYGAFADIIRSL 430
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
LLCD_SYNY3 STANDARD; PRT; 359 AA.
AC Q08871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Llnoleoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
DE D86 OR SL00262.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystia.
OC NCBI_TaxID=1148;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93283633; PubMed=8389613;
RA Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RT "Isolation of a delta 6-desaturase gene from the cyanobacterium
RT Synecocystis sp. strain PCC 6803 by gain-of-function expression in
RT Anabaena sp. strain PCC 7120."
RL Plant Mol. Biol. 22:293-300(1993).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugura M., Sasamoto S., Kilmura T.,
RA Hosouchi T., Matsuno A., Muraiki A., Nakazaki N., Naito K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions";
RL DNA Res. 3:109-136(1996).
CC -I- CATALYTIC ACTIVITY: Llnoleoyl-CoA + AH(2) + O(2) = gamma-
CC llnoleoyl-CoA + A + 2 H(2)O.
CC -I- COPACTOR: IRON.
CC
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CC -----
DR EMBL, L11421, AAA27286.1; -.
DR EMBL, D90914, BAA18502.1; -.
DR InterPro, IPR005804, FA_desat_1; FA desat fam.
DR Pfam, PF00487, FA_desaturase; 1.
DR ProDom, PD001081, FA_desat_fam; 1.
KW Oxidoreductase, Iron, Complete proteome.
SQ
Sequence 359 AA; 41425 MW; 33FBI65AFB96C05F CRC64;

Query Match      8.3%; Score 202.5; DB 1; Length 359;
Beat Local Similarity 23.6%; Pred. No. 1.4e-09;
Matches 79; Conservative 47; Mismatches 120; Indels 89; Gaps 15;

QY 125 MFLIVLGVLEFCISVMAH-----LGSMLGLGLMOSAYVYGHDSGHVVMWTN 172
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 40 MYLTLIIVLMFSAFVFLPAPVIFPVRLGCGVLAIALAASFVNGHDANHVAYSNP 99
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 173 GFNVVAOILSGNCLTGSIAMWKTHN-AHHIACNSLDHD-----PDLOAMPV 219
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 100 HINNVLGTTVD--FVGLSSFLMKIRRHVYLNHTTYNIIIGHDVEIHGDGAVKMSPEQEHVGI 157
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 FAVSFRFENSTISHPYGRKLEFDIAFLICYQHTFYPVWCARVNLVYLTILLFSRR 279
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 158 Y-----RF-----QQFYIMGL-----YLFIPY-----WPLYDVVLVANKG 188
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 280 KVQDPAI-----NIMGLVMTWTFPLVSLP-----NMPE-----RWPFVLASFA 320
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 189 KYHHKIKIPFQPLFLASLIGIKLIMLGY--VFGLPLALGSIPEVLIGASVTYMTYGI 245
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 321 VCSIQHIOQCLMHNAAVYVGPSPG-----NDMFEKQTSGLDISCASSW-DMFPFGLQ 373
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 246 VCTI---FMIAHVLVESTIEPLTPGESGALDDWAICQIRTTANFATNPPMWFVCGSLN 301
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 374 FOLEHHLPFRLPRLCQLRKISPLVSDLCCKHNL.PYR 408
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 302 HQVTHHLPFNICHIVPOLENIIDVQGEPEVEVK 336
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
NIA_NEUCR STANDARD; PRT; 982 AA.
ID AC P08619;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).
GN Nit-3.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OC NCBI_TaxID=5141;
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=91287699; PubMed=1829499;
RA Okamoto P.M., Fu Y.-H., Marzluff G.A.;
RT "Nit-3, the structural gene of nitrate reductase in Neurospora
RT crassa; nucleotide sequence and regulation of mRNA synthesis and
RT turnover.";
RL Mol. Genet. 227:213-223(1991).
RN [2]
RP PRELIMINARY PARTIAL SEQUENCE AROUND HIS-652.
RA Le K.H.D., Lederer F.;
RT "On the presence of a heme-binding domain homologous to cytochrome b5
RT in Neurospora crassa assimilatory nitrate reductase.";
RL Embo J. 2:1909-1914(1983).
RN [3]

```

RP MUTANTS.
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=93241176; PubMed=8479443;
RA Okamoto P.M., Garrett R.H., Marzluff G.A.;
RT "Molecular characterization of conventional and new repeat-induced
RT mutants of nit-3, the structural gene that encodes nitrate reductase
RT in Neurospora crassa.";
RL Mol. Gen. Genet. 238:81-90(1993).
RN (4)
RP MUTAGENESIS.
RX MEDLINE=93360901; PubMed=8355655;
RA Okamoto P.M., Marzluff G.A.;
RT "Nitrate reductase of Neurospora crassa: the functional role of
RT individual amino acids in the heme domain as examined by
RT site-directed mutagenesis.";
RL Mol. Gen. Genet. 240:221-230(1993).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NADPH(+) + H(2)O = nitrate + NADPH.
CC -1- COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEME IRON,
CC AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS
CC CALLED CYTOCHROME B-557.
CC -1- PATHWAY: Nitrate assimilation (denitrification).
CC -1- SUBUNIT: Homodimer.
CC -1- INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AND RESPONDS RAPIDLY
CC TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL; X61303; CAA43600.1; -.
DR HSP, P00171; 1R03.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR000572; Euk_Mb_oxred.
DR InterPro; IPR005066; Mo-Co_dimer.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; oxidored_molyb; 1.
DR PRINTS; PR00406; CYB5RDPTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; EDWOPTERIN.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KM Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
KM Nitrate assimilation.
FT METAL 240 240 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 295 295 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 499 499 INTERCHAIN (POTENTIAL).
FT DOMAIN 621 691 HEME-BINDING (BY SIMILARITY).
FT METAL 652 652 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 675 675 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT DOMAIN 718 982 FLAVIN-BINDING DOMAIN (BY SIMILARITY).
FT NP_BIND 952 961 NADP (BY SIMILARITY).
FT MUTAGEN 652 652 H->A: LITTLE LOSS OF ENZYME ACTIVITY.
FT MUTAGEN 675 675 H->A: LOSS OF ENZYME ACTIVITY.
SQ SEQUENCE 982 AA; 108432 MW; 87838C031B19687F CRC64;

Query Match 6.5%; Score 159; DB 1; Length 982;
Best Local Similarity 41.0%; Pred. No. 2e-05;
Matches 32; Conservative 15; Mismatches 31; Indels 0; Gaps 0;
QY 3 VVEKEKTIYSEELKHNKGGDLMSIQKYVNSDWKHEPGDVPISNLAGQVDTAF 62
DB 612 VDEKVTLLTLEELRHGDEEPWFVNGVYNGTPFLEHGGAASITGAAGQVDTDF 671
QY 63 IAYHGTAMSHLEKFTFG 80
DB 672 LAHSNNKAMPYTHIG 689
RESULT 4
CB5_ORYSA STANDARD; PRT; 137 AA.
AC P49100.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Callus;
RX MEDLINE=94325476; PubMed=8049375;
RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
RT vitro protein targeting".
RL Plant Mol. Biol. 25:527-537(1994).
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; X75670; CAA53366.1; -.
DR PIR; S46307; S46307.
DR HSP, P00171; 1EHB.
DR Glemene; P49100; -.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KM Electron transport; Transmembrane; Heme; Iron; Microsome.
FT TRANSMEM 108 128 POTENTIAL.
FT METAL 41 41 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 137 AA; 15296 MW; 4260C9D33B60FPA CRC64;
Query Match 6.4%; Score 156.5; DB 1; Length 137;
Best Local Similarity 41.9%; Pred. No. 3.3e-06;
Matches 31; Conservative 16; Mismatches 26; Indels 1; Gaps 1;
QY 8 KKYITSEELKHNKGGDLMSIQKYVNSDWKHEPGDVPISNLAGQVDTAF 66
DB 6 KKYITTEEVAKHNSKDCWLIGIKYVNSKFLDHPGDDVLISGKQATDDFEDVGH 65
QY 67 PGTAMSHLEKFTFG 80
|| : : : : : ||

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Db          66  TTARAMMDEYYVG  79

RESULT 5
ID  CYB5_BRAOL  STANDARD;  PRT;  134 AA.
AC  P40934;
DT  01-FEB-1995 (Rel. 31, Created)
DT  01-FEB-1995 (Rel. 31, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Cytochrome b5.
GN  CYB5.
OS  Brassica oleracea (Cauliflower).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eustosids II; Brassicales; Brassicaceae; Brassica.
OX  NCBI_TaxID=3712;
RN  [1]
RP  SEQUENCE FROM N.A., AND SEQUENCE OF 6-47 AND 75-89.
RC  STRAIN=cv. Cauliflora;
RC  Kearns E.V., Keck P., Somerville C.R.;
RT  "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
RT  (Brassica oleracea L.).";
RL  Plant Physiol. 99:1254-1257(1992).
CC  -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC  carrier for several membrane bound oxygenases.
CC  -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
CC  CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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-----
DR  EMBL; M87514; AAA32990.1; -.
DR  PIR; T14454; T14454.
DR  HSSP; P00171; 1EHB.
DR  InterPro; IPR001199; Cyt_B5.
DR  Pfam; PF00173; heme_1.1; B5.
DR  PRINTS; PR00363; CYTOCHROMEBS.
DR  ProDom; PD000612; Cyt_B5; 1.
DR  PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR  PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW  Electron transport; Transmembrane; Heme; Iron; Mitosome.
FT  TRANSMEM 107 127
FT  METAL 40 40 POTENTIAL.
FT  METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT  VARIANT 5 5 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT  VARIANT 5 5 K -> N.
SQ  SEQUENCE 134 AA; 15062 MW; 764DC24A4CDD591 CRC64;

Query Match: 6.3%; Score 154.5; DB 1; Length 134;
Best Local Similarity 41.3%; Pred. No. 4.8e-06;
Matches 31; Conservative 15; Mismatches 28; Indels 1; Gaps 14.

Oy 7 EKKYITSEELGHNNEGDLMTISIOQKYVNSDWMYKEHGQVPIENLAGQVTDPAF-IAY 65
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 4 EKKVVGFEVSGHNTKDCWMLISGKYVDVPPFMDHGGGDEVLLSSTGKATNDFEDVG 63
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 66 HPGTAMSHLEKFTG 80
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 64 HSDTARDWMEKYIG 78
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
ID  CY51_ARATH  STANDARD;  PRT;  134 AA.
AC  Q42342; Q9SB05;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Cytochrome b5 isoform 1.
GN ATG53560 OR MNC6.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosoids II; Brassicales; Brassicaceae; Arabidops.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99097071; PubMed=9890378;
RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohra D.;
RT "Mitochondrial electron transfer in higher plants: cloning and
RL heterologous expression of NADH-cytochrome b5as reductase from
 Arabidopsis";
 Plant Physiol. 119:353-361(1999).
 [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneo T., Kotani H., Miyajima N.,
RT Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen
RL physically assigned P1 and PAC clones.";
RN DNA Res. 5:297-308(1998).
 [3]
RP SEQUENCE OF 1-113 FROM N.A.
RC STRAIN=cv. Columbia;
RA Cooke R., Landie M., Raynal M., Delany M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 carrier for several membrane bound oxygenases (by similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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CC -----

DR EMBL; AB007801; BAU74839.1; -.
DR EMBL; AB015476; BAB09732.1; -.
DR EMBL; F200001.CAA23377.1; -.
DR PIR; TS2469; TS2469.
DR HSP; P00171; IEHB.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEB5.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
KW PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Iron; Mitosome;
KM Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 1 3 MSS -> ARA (IN REF. 3).
SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60F7C873FD CRC64;

Query Match 6.2%; Score 152.5; DB 1; Length 134;
Best Local Similarity 37.2%; Pred.No. 7e-06;
Matches 29; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

OY 4 VEKEKKITTEELKHNKGEDLMWISIGKYVNVSDWKHEHGVDPIPSNLAGQDVTDAF- 62
 : ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
db 1 MSRRKVLSFEERYSKAKTKDCMLLGSKYYDVTPFPDDHPGDDEVLLSSGTGDATNDFE 60

QY 63 IAHPTAMSHLEKFTG 80
DB 61 DVGHSDTARDMDXFTG 78

RESULT 7
ID CYB2 HANAN STANDARD; PRT; 573 AA.
AC P09437;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b2, mitochondrial precursor (EC 1.1.2.3) (L-lactate dehydrogenase [Cytochrome]) (L-lactate ferricytochrome c oxidoreductase) (L-LCR).
GN CYB2.
OS Hansenula anomala (Yeast) (Candida pelliculosa).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4927;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90045973; PubMed=2813072;
RA Kistler Y., Tegen M., Gervais M.,
RT "Nucleotide sequence of the Hansenula anomala gene encoding flavocytochrome b2 (L-lactate:cytochrome c oxidoreductase).",
RL Nucleic Acids Res. 17:8381-8381(1989).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=90088451; PubMed=2688640;
RA Black M.T., Gunn F.J., Chapman S.K., Reid G.A.,
RT "Structural basis for the kinetic differences between flavocytochromes b2 from the yeasts Hansenula anomala and Saccharomyces cerevisiae.",
RL Biochem. J. 263:973-976(1989).
[3]
RN SEQUENCE OF 80-163.
RX Hamont P.-Y., Thomas M.-A., Labeyrie F., Lederer F.,
RA "Amino-acid sequence of the cytochrome-b5-like heme-binding domain from Hansenula anomala flavocytochrome b2.",
RL Eur. J. Biochem. 169:539-546(1987).
CC -1- CATALYTIC ACTIVITY: (S)-lactate + 2 ferricytochrome c = pyruvate + 2 ferrocyclochrome c.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial intermembrane space.
CC -1- MISCELLANEOUS: THIS ENZYME BINDS FMN AND PROTOHEME IX PROSTHETIC GROUPS.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -1- SIMILARITY: TO SPINACH GLYOXALATE OXIDASE (33% IDENTITY), TO P. PUTIDA S-MANDELATE DEHYDROGENASE, AND TO M. SMEGMATIS LACTATE 2-MONOOXYGENASE.
CC -----
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CC -----
CC EMBL: X16051; CAA34183.1; -.
CC PIR: S06600; S06600.
CC HSSP: P00175; ILCO.
CC InterPro: IPR001199; Cyt B5.
CC InterPro: IPR003009; FMN enzyme.
CC InterPro: IPR000262; FMN_hydroxycac_dh.
CC Pfam: PF01070; FMN_dh; 1.
CC Pfam: PF00173; heme_1; 1.
CC PRINTS: PR00363; CYTOCHROMEBS.
CC PRODOM: PD000612; Cyt_B5; 1.
CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00557; FMN HYDROXY ACID DH; 1.
KW Electron transport; Respiratory chain; Oxidoreductase; Flavoprotein;
KW FMN; Heme; Mitochondrion; Transit peptide.
FT TRANSIT 1 73
FT CHAIN 74 573
FT DOMAIN 80 163
FT METAL 115 115
FT METAL 138 138
FT ACT_SITE 432 432
FT ACT_SITE 432 432
FT ACT_SITE 435 435
FT SEQUENCE 573 AA; 64202 MW; 83E6F45C580BC8 CRC64;
SQ
Query Match 6.2%; Score 151.5; DB 1; Length 573;
Best Local Similarity 35.9%; Pred. No. 4.5e-05;
Matches 33; Conservative 16; Mismatches 36; Indels 5; Gaps 3;
QY 11 ITSEELGNHKEGDLWISIQKVVNSDVKWEHPGDPVPSNLGQDVFIAVHPTA 70
DB 83 LTPETVSGHKKDDLVVVLNGQVYDLPVPHNGGKIIIRVAGKATKFIHHPDT 142
QY 71 WSHLEKFP-TGYHLSDFKVSBSKDYKRLASE 101
DB 143 ---IEKFIPEKHLGFL-VGFEEQEELSLDE 170
RESULT 8
ID CY52 ARATH STANDARD; PRT; 134 AA.
AC O48845;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cytochrome b5 isoform 2.
GN ATG32720 OR F24L7.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buel C.R., Ketchum K.A., Lee J.J., Romling C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.,
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.",
RT Nature 402:761-768(1999).
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases (By similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
CC EMBL: AC003974; AAC04491.1; -.
CC PIR: T00796; T00796.
CC HSSP: P04166; 1B5M.


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DR InterPro:IPR001199; Cyt_B5.
DR Pfam: PF00173; heme_1; 1
DR PRINTS: PR00363; CYTOCHROMB5.
DR ProDom: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS02055; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family;
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
SQ SEQUENCE 134 AA; 15016 MM; B405F5430F5716C1 CRC64;
Query March 6.1%; Score 149.5; DB 1; Length 134;
Best Local Similarity 40.0%; Pred. No. 1.2e-05;
Matches 30; Conservative 15; Mismatches 29; Indels 1; Gaps 1;
QY 7 EKKYITSEELKGNHKEGDLMTISIOGKYNVSDWMEKHEGVPISNLAGDPVTAFL-TAY 65
D 4 EAKFTLSEVSEHNQADHCWLVINGKYNNVTKFLEHDHGSDVLSSITGKATDDFEDVG 63
Db 66 HPGTAWSHLKEKFTG 80
64 HSESAREWMEQYVG 78
RESULT 9
YDAA SCHPO STANDARD; PRT; 147 AA.
AC 010352;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ClF12.10c in chromosome I.
GN SPAC1F12.10C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RX NCB1
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21849401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks J., Peat N., Hayles U., Baker S., Basham D., Bowman S.,
RA Scourie K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.U., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voigtkeert G., Aert R., Robben J., Grymoultz B.,
RA Weltsch J., Vastreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabell C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Weller H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu S., Dreano S., Gloux S., Lelaune V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hout C., Moore K., Huret S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cernutti L., Lowe T., McCombie W.R., Paulsen I., Fotschkin J.,
RA Shpakovski G.V., Useery D., Bartell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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CC -----
DR EMBL; Z69944; CAA93814.1; -.
DR PIR; S67453; S67453.
DR HSSP; P00175; ILTD.
DR GenedB_Spomb; SPAC1P12.10c; -.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
FT METAL 106 106 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 129 129 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 147 AA; 16667 MW; B874B59F52B1AF1D CRC64;

Query Match 6.0%; Score 146.5; DB 1; Length 147;
Best Local Similarity 41.3%; Pred. No. 2,5e-05;
Matches 31; Conservative 13; Mismatches 24; Indels 7; Gaps 2;

QY 11 ITSEELKGNHKEGDLWISIGKRYNVSWMYKEHGGDVPISNLAGQDVTAFIAYHGT 70
DB 74 VTKEELAKHKTKEKWCWIAIRKQVNSAVLPYHPAGCKRILDVAGRDATVIFMKFH--A 130
QY 71 WSH---LEKPFQGY 81
DB 131 WYNEEALLKTSFVG 145

RESULT 10
NIA_FUSOX STANDARD; PRT; 905 AA.
AC P39863;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase (NADPH) (EC 1.7.1.3) (NR).
GN NIA.
OS Fusarium oxysporum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypococreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5507;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=FOM24;
RX MEDLINE=93380674; PubMed=8370541;
RA Dielez A., Langin T., Gerlinger C., Brygoo Y., Debussci M.-J.;
RT "The nia gene of Fusarium oxysporum: isolation, sequence and
RT development of a homologous transformation system.";
RL Gene 131:61-67(1993).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.
CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC AND ONE MOLYBDENUM ATOM.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPYRIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----

DR EMBL; Z22549; CAAB0270.1; .

DR PIR; JN0803; JN0803.

DR HSBP; P04166; 1E0E.

DR InterPro; IPR001199; Cyt_B5.

DR InterPro; IPR001834; Cyt_B5_reductase.

DR InterPro; IPR000572; Elk_Mb_oxred.

DR InterPro; IPR001709; FPN_Cyt_reductase.

DR InterPro; IPR005066; Mo-co_dimer.

DR InterPro; IPR001433; Oxred_FAD/NAD(P).

DR Pfam; PF00970; FAD_binding_6; 1.

DR Pfam; PF00173; heme_1; 1.

DR Pfam; PF03404; Mo-co_dimer; 1.

DR Pfam; PF00175; NAD_binding_1; 1.

DR Pfam; PF00174; oxidored_mol_yb; 1.

DR PRINTS; PR00406; CYTB5BDTASB.

DR PRINTS; PR00363; CYTOCHROME_B5.

DR PRINTS; PR00407; EMOPTERIN.

DR PRINTS; PR00371; FPNCR.

DR PRODOM; PD000612; Cyt_B5; 1.

DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.

DR PROSITE; PS00559; MOLYBDOPROTEIN_EUK; 1.

DR Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum; Nitrate assimilation.

KM DOMAIN 3

FT METAL 179 179 POLY-THR.

FT METAL 230 230 MOLYBDENUM-PTERIN (POTENTIAL).

FT DISULFID 428 428 MOLYBDENUM-PTERIN (POTENTIAL).

FT DOMAIN 550 620 INTERCHAIN (POTENTIAL).

FT METAL 581 581 HEME-BINDING (BY SIMILARITY).

FT METAL 604 604 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

FT DOMAIN 645 905 FLAVIN-BINDING DOMAIN (BY SIMILARITY).

FT NP_BIND 875 884 NADP (BY SIMILARITY).

SQ SEQUENCE 905 AA; 101898 MW; D5D8E23F971ACDA CRC64;

Query Match 6.0%; Score 146; DB 1; Length 905;

Best Local Similarity 36.3%; Pred. No. 0.00022;

Matches 33; Conservative 14; Mismatches 32; Indels 12; Gaps 1;

QY 2 EVEKE-----KRYITSEELKGNKEGDLWISIOGKYVNSDWYKEHGGDVP 49

DB 528 EVVVKPEKQICMTNPQINRKITTEELKAKHSGEERPVVVGAYVDGPIYLSGHPGGA 587

QY 50 ISNLAGQDVDTAFIAYHPGTAWSHLEKFTTG 80

DB 588 IFGAAGQDATEEFMAHSENAKAMLPYHIG 618

RESULT 11

CYB5_RABIT STANDARD; PRT; 133 AA.

ID CYB5_RABIT

AC P00169; Q28726; Rel. 01, Created

DT 21-JUN-1986 (Rel. 01, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cytochrome b5.

GN CYB5.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxId=9986;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=8912816; PubMed=322252;

RA Darluah N., Fisher C.W., Steggle A.W.;

RT "The nucleotide sequence of rabbit liver cytochrome b5 mRNA.";

RL Protein Seq. Data Anal. 1:351-353(1988).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX STRAIN=New Zealand white;

RX MEDLINE=92328788; PubMed=1627141;

RA Takamatsu H., Kozusum Y., Suzuki A., Kawasaki T.;

RT "Molecular cloning of rabbit cytochrome b5 genes: evidence for the occurrence of two separate genes encoding the soluble and microsomal forms.";

RL Biochem. Biophys. Res. Commun. 185:845-851(1992).

RN (3)

RP SEQUENCE OF 8-45 AND 49-90.

RX MEDLINE=69108767; PubMed=5709273;

RA Tawgita A., Kobayashi M., Kajihara T., Hagihara B.;

RT "Primary structure of rabbit liver cytochrome b5.";

RL J. Biochem. 64:727-730(1968).

RN (4)

RP SEQUENCE OF 6-7 AND 46-48.

RX MEDLINE=70289989; PubMed=5272324;

RA Tawgita A., Kobayashi M., Tani S., Kyo S., Rashid M.A., Yoshida Y., Kajihara T., Hagihara B.;

RT "Comparative study of the primary structures of cytochrome b5 from four species.";

RL Proc. Natl. Acad. Sci. U.S.A. 67:442-447(1970).

RN (5)

RP SEQUENCE OF 4-97.

RX MEDLINE=71001482; PubMed=5506260;

RA Ozols J.;

RT "Amino acid sequence of rabbit liver microsomal cytochrome b5.";

RL J. Biol. Chem. 245:4863-4874(1970).

RN (6)

RP SEQUENCE OF 91-133.

RX MEDLINE=80049603; PubMed=500581;

RA Kondo K., Tajima S., Sato R., Narita K.;

RT "Primary structure of the membrane-binding segment of rabbit cytochrome b5.";

RL J. Biochem. 86:1119-1128(1979).

RN (7)

RP SEQUENCE OF 98-133.

RX MEDLINE=80115672; PubMed=7354043;

RA Takagaki Y., Geher G.B., Nihel K., Khorana H.G.;

RT "Amino acid sequence of the membranous segment of rabbit liver cytochrome b5. Methodology for separation of hydrophobic peptides.";

RL J. Biol. Chem. 255:1536-1541(1980).

RN (8)

RP SEQUENCE OF 1-10.

RX MEDLINE=89323209; PubMed=2752049;

RA Ozols J.;

RT "Structure of cytochrome b5 and its topology in the microsomal membrane.";

RL Biochim. Biophys. Acta 997:121-130(1989).

RN (9)

RP STRUCTURE BY NMR OF 6-99.

RX MEDLINE=20117684; PubMed=10651812;

RA Banci L., Bertini I., Rosato A., Scacchiari S.;

RT "Solution structure of oxidized microsomal rabbit cytochrome b5 factors determining the heterogeneous binding of the heme.";

RL Eur. J. Biochem. 267:755-766(2000).

CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES.

CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=liver, Membrane-bound;

CC IsoId=P00169-1; Sequence=Displayed;

CC Name=2; Synonyms=Erythrocyte, Cytoplasmic;

CC IsoId=P00169-2; Sequence=VSP_001244, VSP_001245;

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

CC -----

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CC EMBL; M24844; AAB03878.1; -
 CC EMBL; D10901; BAA01712.1; -
 DR PIR; J0316; JN0316.
 DR PIR; S03373; CERB5.
 DR PDB; 1D09; 20-MAR-00.
 DR InterPro; IPR001199; Cyt B5.
 DR Pfam; PF00173; heme 1; 1.
 DR Prodom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;
 KM Alternative splicing; 3D-structure.
 FT INIT MET 0 0
 FT MOD RES 1 1 ACETYLATION.
 FT DOMAIN 1 90 HEME-BINDING.
 FT METAL 43 43 MEMBRANE-BINDING.
 FT METAL 67 67 IRON (HEME AXIAL LIGAND).
 FT VARSPLIC 97 97 IRON (HEME AXIAL LIGAND).
 FT VARSPLIC 97 97 T -> P (in isoform 2).
 FT VARSPLIC 97 97 /FTID=VSP_001244.
 FT VARSPLIC 98 133 Missing (in isoform 2).
 FT CONFLICT 61 61 /FTID=VSP_001245.
 FT CONFLICT 103 103 N -> D (IN REF. 3 AND 5).
 FT CONFLICT 103 103 D -> N (IN REF. 6).
 SQ SEQUENCE 133 AA; 15218 MW; 284BAEC20BC39720 CRC64;

Query Match 5.9%; Score 144; DB 1; Length 133;
 Best Local Similarity 28.6%; Pred. No. 3.6e-05;
 Matches 36; Conservative 25; Mismatches 65; Indels 0; Gaps 0;

QY 5 EKEKYYTSELKGNKEGDLWISIOGKVVNSDPMVHEHGGVPIISNLGQVTDPIAFIA 64
 DB 5 DKVQKYYTLEIKKHNKSKTWMILHKVVDLTFLEHGGSEVLRBOAGGDATEFED 64
 QY 65 YHGTAWSHLEKFFTYGHLSDPKVSEVSKDYRKLAESFSLGLFTDKGHVTSCTLASVAV 124
 DB 65 VGHSTDAEELSKFTIIGELHPDDRSLKSLKPMETLITVDNSNMTWTVIPIALSALVAL 124
 QY 125 MFLIVL 130
 DB 125 MYRLYM 130

RESULT 12
 CYB5_YEAST STANDARD; PRT; 120 AA.
 AC P40312;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 GN CYB5 OR YNL111C OR N1949.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NC NCB1_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FL100;
 RX MEDLINE=94237477; PubMed=8181746;
 RA Tsiang G., Eshner J.-C., Rouguille C., Cullin C., Pompon D.;
 RT "Cloning and characterization of a yeast cytochrome b5-encoding gene
 which suppresses ketoconazole hypersensitivity in a NADPH-P-450
 reductase-deficient strain.";
 RL Gene 142:123-127 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97245296; PubMed=9090055;
 RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
 RA Pallavicini A., Lanfranchi G., Valle G.;
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of

RT Saccharomyces cerevisiae reveals an unusually high number of
 RT overlapping open reading frames.";
 RL Yeast 13:261-266 (1997).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases. It plays a role in
 CC fatty-acid desaturation and is also involved in several steps of
 CC the steroid biosynthesis pathway, particularly in the 4-
 CC demethylation of the 4,4'-dimethyl zymosterol.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC or send an email to license@lsb-sib.ch).

DR EMBL; L22494; AAA67468.1; -
 DR EMBL; Z69382; CAA93396.1; -
 DR EMBL; Z71387; CAA95990.1; -
 DR PIR; S63052; S63052.
 DR HSSP; P04166; IEUE.
 DR SGD; S0005055; CYB5.
 DR GO; GO:0005792; Cytochrome b5.
 DR GO; GO:0016126; Steroid biosynthesis; IDA.
 DR InterPro; IPR001199; Cyt B5.
 DR Pfam; PF00173; heme 1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR Prodom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 KM Electron transport; Transmembrane; Heme; Iron; Microsome.
 FT TRANSHEM 96 118 POTENTIAL.
 FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 17 17 E -> Q (IN REF. 1).
 SQ SEQUENCE 120 AA; 13297 MW; 598BEF2A6730CAD19 CRC64;

Query Match 5.8%; Score 143; DB 1; Length 120;
 Best Local Similarity 29.9%; Pred. No. 3.8e-05;
 Matches 38; Conservative 25; Mismatches 52; Indels 12; Gaps 3;

QY 9 KYITSELKGNKEGDLWISIOGKVVNSDPMVHEHGGVPIISNLGQVTDPIAFIY-HP 67
 DB 3 KVTSGEVAEHNPENFWIILDDKVTDSQFKDEHFGDEIIMDLGGQDATESFVDIGHS 62
 QY 68 GTAWSHLEKFFTYGHLSDPKVSEVSKDYRKLAESFSLGLFTDKGHVTSCTLASVAVMFL 127
 DB 63 DEALRLRLKGLYI-----DVDKTSERVSV--KVTSEKSGSGGLVILALIML 111
 QY 128 IYLYGVL 134
 DB 112 GVAVYVL 118

RESULT 13
 CYB5_TOBAC STANDARD; PRT; 135 AA.
 AC P49089;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5, seed isoform.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoties;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 NC NCB1_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Samsun; TISSUE=seed;
 RA MEDLINE=96009039; PubMed=7580860;
 RA Napier J.A., Smith M.A., Stobart A.K., Shewry P.R.;
 RT "isolation of a cDNA encoding a cytochrome b5 specifically expressed
 in developing tobacco seeds.";
 RL Planta 197;200-202(1995).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
 CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS.
 CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING SEEDS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 DR EMBL; X80008; CAA56318.1; -.
 DR PIR; S49200; S49200.
 DR HSSP; P00171; ICTO.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 KM Electron transport; Transmembrane; Heme; Iron; Microsome;
 KM Multigene family.
 FT TRANSSEM 107 127
 FT METAL 40 40
 FT METAL 64 64
 FT METAL 64 64
 FT SEQUENCE 135 AA; 14669 MW; A36CCN081A72EBC8 CRC64;
 SQ
 Query Match 5.8%; Score 142.5; DB 1; Length 135;
 Best Local Similarity 36.0%; Pred. No. 4.8e-05;
 Matches 27; Conservative 17; Mismatches 30; Indels 1; Gaps 1;
 QY 7 EKKYITSEELKGNKEDLWISIQKVVYNSDWKHEHGGVPIISNLAGOVDTAFIAY-65
 DB 4 QSKVFTLAEVSQHNNADCVLISGKYVNTKFLDHPGGDEVLLSATGKDATDFFDVG 63
 QY 66 HPGTAMSHLEKFTFG 80
 DB 64 HSSSARAMLDEYYVG 78

RESULT 14
 CYB5_TOBAC
 ID CYB5_TOBAC STANDARD; PRT; 136 AA.
 AC P49096;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 CC NCBI_TaxID=4097;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Leaf;
 RC MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in

RT vitro protein targeting.";
 RL Plant Mol. Biol. 25;527-537(1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
 CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
 CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
 CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS.
 CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
 CC LEVELS IN THE LEAF.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 DR EMBL; X71441; CAA50575.1; ALT_INIT.
 DR EMBL; X68140; CAA48240.1; -.
 DR HSSP; P04166; IB5M.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 KM Electron transport; Transmembrane; Heme; Iron; Microsome;
 KM Multigene family.
 FT TRANSSEM 107 127
 FT METAL 40 40
 FT METAL 64 64
 FT CONFLICT 10 11
 FT CONFLICT 105 105
 FT SEQUENCE 136 AA; 14979 MW; DACE9E695B2835F CRC64;
 SQ
 Query Match 5.8%; Score 142.5; DB 1; Length 136;
 Best Local Similarity 37.3%; Pred. No. 4.9e-05;
 Matches 28; Conservative 16; Mismatches 30; Indels 1; Gaps 1;
 QY 7 EKKYITSEELKGNKEDLWISIQKVVYNSDWKHEHGGVPIISNLAGOVDTAFIAY-65
 DB 4 ETKVFTLAEVSQHNNADCVLISGKYVNTKFLDHPGGDEVLLSATGKDATDFFDVG 63
 QY 66 HPGTAMSHLEKFTFG 80
 DB 64 HSSSARAMLDEYYVG 78

RESULT 15
 CYB5_HUMAN
 ID CYB5_HUMAN STANDARD; PRT; 146 AA.
 AC O43169;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5 outer mitochondrial membrane isoform precursor.
 GN CYB5M OR OMB5.
 OS Homo sapiens (Human).
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RA Ishibashi K.;
 RT "Cytochrome b5 and aquaporins share the last transmembrane amino acids

```

RT sequence."
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial outer membrane (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; AB009282; BAA23735.1; -
DR HSSP; P04166; 1B5M.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Mitochondrion; Outer membrane; Transmembrane;
KW Heme; Iron.
FT PROPEP 1 11 BY SIMILARITY.
FT CHAIN 12 146 CYTOCHROME B5 OUTER MITOCHONDRIAL
FT DOMAIN 12 103 MEMBRANE ISOFORM.
FT TRANSMEM 119 136 HEME-BINDING.
FT METAL 55 55 POTENTIAL.
FT METAL 79 79 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 146 AA; 16332 MW; 2FF7DBA297124E19 CRC64;

Query Match 5.8%; Score 141.5; DB 1; Length 146;
Best Local Similarity 27.6%; Pred. No. 6,4e-05;
Matches 43; Conservative 22; Mismatches 50; Indels 41; Gaps 5;

QY 4 VEKEKTYITSEELKGNKEDLMISIQKYYNVDWYKEHGGDVPISNLAGQDVTDAF-62
DB 16 VETSVYYRLEAEVAKRNSLKEVLVIHGRVYDVTPLNEHGGGEVLLBOAGVDASESFE-75
QY 63 IAYHPGTAMSHLKEKFTG-YHLSDEKVSVDYRKXLAESFSLGLPDTKGHTSCTLAS-121
DB 76 DVGHSSDAREMLKQYIIGDIHPSDLKPESSGSDPSQ-----NDT-----114
QY 122 VAVMFLIVLYGVLRCTSVMAH---LGGSMILGLMW-153
DB 115 -----CKSCWAYWILPIIGAVLGLFLY-136

```

Search completed: January 1, 2004, 06:30:56
 Job time : 9.90156 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 / Search time 40.388 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-8
Perfect score: 2449
Sequence: 1 MEVVEKEKKYITSEELKGN.....RDLTPAPKMLMEAVNTWG 450

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_rodent:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_unclassified:*
- 14: sp_virus:*
- 15: sp_bacteriap:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	77.7	449	09ZRP7	Q9ZRP7 arabidopsis
2	1899	77.5	449	08LB96	Q8LB96 arabidopsis
3	1887	77.1	449	09ZRP8	Q9ZRP8 brassica na
4	1801.5	73.6	446	09FR82	Q9FR82 borago offi
5	1801	73.5	458	043469	Q43469 helianthus
6	1749.5	71.4	446	09ZRP9	Q9ZRP9 ricinus com
7	1692.5	69.1	446	08LBD7	Q8LBD7 aquilegia v
8	1670	68.2	448	08VZ22	Q8VZ22 echium gent
9	1656	67.6	448	09SAU5	Q9SAU5 borago offi
10	1655	67.6	448	004353	Q04353 borago offi
11	1653	67.5	448	08VZ21	Q8VZ21 echium pita
12	1597	65.2	449	08L717	Q8L717 argania spi
13	1463	59.7	469	09ZT18	Q9ZT18 triticum ae
14	688.5	28.1	523	09HDC8	Q9HDC8 mucor rouxi
15	562.5	23.0	568	08NKG9	Q8NKG9 saccharomyc
16	557.5	22.8	520	09LEW9	Q9LEW9 ceratodon p

17	548.5	22.4	573	3	Q8NKG8	Q8NKG8 kluyveromyc
18	544	22.2	483	10	Q9LEW0	Q9LEW0 ceratodon p
19	518.5	21.2	459	10	Q944W4	Q944W4 pythium irr
20	512.5	20.9	525	10	Q9ZNM2	Q9ZNM2 physcomitrite
21	502.5	20.5	457	3	Q9UVV3	Q9UVV3 mortierella
22	500.5	20.4	467	3	Q9HEV4	Q9HEV4 mortierella
23	500.5	20.4	467	3	Q96VC3	Q96VC3 mucor circi
24	498.5	20.4	457	3	Q8X173	Q8X173 mortierella
25	492.5	20.1	457	3	Q9UVV3	Q9UVV3 mortierella
26	492.5	20.1	457	3	Q9HEV1	Q9HEV1 mortierella
27	492.5	20.1	457	3	Q8X174	Q8X174 mortierella
28	492	20.1	477	10	Q8RXB0	Q8RXB0 phaeodactyl
29	456	18.6	454	13	Q8BSW7	Q8BSW7 oncorhynch
30	455.5	18.6	444	11	Q9ZOR9	Q9ZOR9 mus musculu
31	453	18.5	452	13	Q8UMM5	Q8UMM5 oncorhynch
32	451.5	18.4	444	11	Q9Z122	Q9Z122 ratius norv
33	450.5	18.4	454	13	Q8QGE2	Q8QGE2 salmo salar
34	447	18.3	419	10	Q9SMQ9	Q9SMQ9 euglena gra
35	445.5	18.2	447	11	Q9ZOR3	Q9ZOR3 ratius norv
36	444.5	18.2	445	13	Q8AY64	Q8AY64 sparus aura
37	441.5	18.0	444	4	Q95864	Q95864 homo sapien
38	441.5	18.0	447	11	Q9EPV4	Q9EPV4 ratius norv
39	439.5	17.9	454	13	Q90ZEB	Q90ZEB oncorhynch
40	439	17.9	501	4	Q8NCG0	Q8NCG0 homo sapien
41	436	17.8	445	4	Q9Y5Q0	Q9Y5Q0 homo sapien
42	435	17.8	444	4	Q96139	Q96139 homo sapien
43	435	17.8	444	4	Q96T10	Q96T10 homo sapien
44	435	17.8	444	4	Q60427	Q60427 homo sapien
45	433	17.7	444	4	Q9NRP8	Q9NRP8 homo sapien

ALIGNMENTS

RESULT 1
Q9ZRP7 PRELIMINARY; PRT; 449 AA.

AC 01-MAY-1999 (TREMURel. 10, Created)
DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
DT 01-MAR-2003 (TREMURel. 23, Last annotation update)
DE Delta-8 sphingolipid desaturase (ATG61580/F2A19_180).
GN SLD1 OR F2A19.180 OR ATG61580.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=flower, MAINLY GREEN PARTS, and Root;
RX MEDLINE=99003197; PubMed=9786850;
RA Sperling P., Zaehring U., Heinz E.;
RT "A sphingolipid desaturase from higher plants. Identification of a new
RT cytochrome b5 fusion protein.";
RL J Biol. Chem. 273:28590-28596(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA De Haan M., Maarse A.C., Grievell L.A., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Queller F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bousset L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ikeda J., Jiang P.X., Jones T., Kamuya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narisaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Becker J.R.;
 RT "Arabidopsis cDNA clones";
 RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RP
 [5]
 SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashizaki Y., Huan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Seki M., Kim C.J., Narusaka M., Quach H.T., Sakurai T., Satou M.,
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Becker J.,
 RA Theologis A., Davis R.W.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL, AJ224161; CA11858.1; -;
 DR EMBL, AL132962; CAB71088.1; -;
 DR EMBL, AF28420; AAL16189.1; -;
 DR EMBL, BT000442; AAN17419.1; -;
 DR HSSP, P00171; 115U.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE, PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 KM
 SQ SEQUENCE 449 AA; 51675 MW; 145048F9FD1D35964 CRC64;
 Query Match 77.7%; Score 1902; DB 10; Length 449;
 Best Local Similarity 74.7%; Pred. No. 1.6e-167;
 Matches 334; Conservative 54; Mismatches 58; Indels 0; Gaps 0;
 QY 5 EKEKKYITSEELKGNKEDLWISIQKYYNVDWVKEHFGDVPISNLAGDVTDAFIA 64
 DB 4 ETEKKYITNEDLKKHNSGDLMTAIOGKYVNSDWIKTHPGDVTILNVGQDVTDAFIA 63
 QY 65 YHGTAMSHLEKFFTGTHLSDPKVSEVSKDYRKLAESFKLGLFDTKGHTVTSCTLASVAV 124
 DB 64 FHGTAMHHDHLLFTGYHIRDFOVSEVSRDYRMAAEFRKGLGFENKGHVTLTYTLAFVAA 123
 QY 125 MFLIVYGVLCSTSVANHLGSGMLGLLMOQSAVYVGHDSGHVYVMTNGFNKVAQILSGN 184
 DB 124 MFLGVLYGVLCSTSVFAHQIAAALLGLWLTQSAVYIGHDSGHVYVMSKSYNRFQILSGN 183
 QY 185 CLTGSIAMWKTHNAHNLACNSLDHDPDLOHMPVFAVSRRFNSITSHFYGRKLEFDP 244
 DB 184 CLTGSIAMWKTHNAHNLACNSLDYDPDLOHMPVFAVSTKFFSSITSRFYDRKLTFFDPV 243
 QY 245 ARFLICYOHFTFYPVWCVARVNLVLOTILLFSRRKVDORALNIMGILVFWTFWFPPLVSC 304
 DB 244 ARFLVYOHFTFYPVWCVRINLFIOTFLLFSRRKVPDRALNFAGLVFWTFWFPPLVSC 303
 QY 305 LPMWPERVFWVLASFVCSIOHIOFCLNHFANVYVGPSPGNDMFEKOTSGTLDISCAS 364
 DB 304 LPMWPERFFVFWLSTFVTLAQHIOFTLNHFAADVVPRTGSDWFEKQAAAGTIDISCRSY 363
 QY 365 MDWFFGGLQFOLEHNLFRPLPRCOLRKISPLVSDLCCKGNLPRYSLSFWEANQWTRTLR 424
 DB 364 MDWFFGGLQFOLEHNLFRPLPRCHLRKVSPPVQELCKGNLPRYSMSWFEANVLTINTLK 423
 QY 425 TAAIQARDLTNPAPKXLLMEAVNTHG 450
 DB 424 TAAIQARDVANPVKXLLVWEALNTHG 449

DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Delta-8 sphingolipid desaturase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volovicky N., Town C.D., Troughan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.A.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL, AY087345; AAM64895.1; -;
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE, PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 KM
 SQ SEQUENCE 449 AA; 51744 MW; A1EB57B8CE03E18 CRC64;
 Query Match 77.5%; Score 1899; DB 10; Length 449;
 Best Local Similarity 74.7%; Pred. No. 3e-167;
 Matches 333; Conservative 54; Mismatches 59; Indels 0; Gaps 0;
 QY 5 EKEKKYITSEELKGNKEDLWISIQKYYNVDWVKEHFGDVPISNLAGDVTDAFIA 64
 DB 4 ETEKKYITNEDLKKHNSGDLMTAIOGKYVNSDWIKTHPGDVTILNVGQDVTDAFIA 63
 QY 65 YHGTAMSHLEKFFTGTHLSDPKVSEVSKDYRKLAESFKLGLFDTKGHTVTSCTLASVAV 124
 DB 64 FHGTAMHHDHLLFTGYHIRDFOVSEVSRDYRMAAEFRKGLGFENKGHVTLTYTLAFVAA 123
 QY 125 MFLIVYGVLCSTSVANHLGSGMLGLLMOQSAVYVGHDSGHVYVMTNGFNKVAQILSGN 184
 DB 124 MFLRVLYGVLCSTSVFAHQIAAALLGLWLTQSAVYIGHDSGHVYVMSKSYNRFQILSGN 183
 QY 185 CLTGSIAMWKTHNAHNLACNSLDHDPDLOHMPVFAVSRRFNSITSHFYGRKLEFDP 244
 DB 184 CLTGSIAMWKTHNAHNLACNSLDYDPDLOHMPVFAVSTKFFSSITSRFYDRKLTFFDPV 243
 QY 245 ARFLICYOHFTFYPVWCVARVNLVLOTILLFSRRKVDORALNIMGILVFWTFWFPPLVSC 304
 DB 244 ARFLVYOHFTFYPVWCVRINLFIOTFLLFSRRKVPDRALNFAGLVFWTFWFPPLVSC 303
 QY 305 LPMWPERVFWVLASFVCSIOHIOFCLNHFANVYVGPSPGNDMFEKOTSGTLDISCAS 364
 DB 304 LPMWPERFFVFWLSTFVTLAQHIOFTLNHFAADVVPRTGSDWFEKQAAAGTIDISCRSY 363
 QY 365 MDWFFGGLQFOLEHNLFRPLPRCOLRKISPLVSDLCCKGNLPRYSLSFWEANQWTRTLR 424
 DB 364 MDWFFGGLQFOLEHNLFRPLPRCHLRKVSPPVQELCKGNLPRYSMSWFEANVLTINTLK 423
 QY 425 TAAIQARDLTNPAPKXLLMEAVNTHG 450
 DB 424 TAAIQARDVANPVKXLLVWEALNTHG 449

RESULT 2
 OBLB96
 ID OBLB96 PRELIMINARY; PRT; 449 AA.
 AC OBLB96;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, last sequence update)

RESULT 3
 Q9ZRP8
 ID Q9ZRP8 PRELIMINARY; PRT; 449 AA.
 AC Q9ZRP8;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
GN Delta-8 sphingolipid desaturase.
GN SIDL1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Drakkar; TISSUE=ripening embryos;
RA MEDLINE=99003197; PubMed=9786850;
RX Sperling P.; Zaehring U.; Heinz E.;
RT "A sphingolipid desaturase from Higher Plants Identification of a New
RT Cytochrome b5 Fusion Protein";
RL J. Biol. Chem. 273:28590-28596(1998).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ224160; CA11857.1; -.
DR HSSP; P82291; ICXY.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 449 AA; 51490 MW; FEFEE37AF9D390C1 CRC64;
Query Match 77.1%; Score 1887; DB 10; Length 449;
Best Local Similarity 74.7%; Pred. No. 3.9e-166;
Matches 333; Conservative 52; Mismatches 61; Indels 0; Gaps 0;
QY 5 EKEKKYITSEELKHNKEDLMISIQGKYNNVSDWYKHPGQDVPISNLAGQDVTDAFI 64
DB 4 QTKRKFITSDDLKKNQGDLMISIQGKYVDVSHWVSKHPGGAAILNLAGQDVTDAFI 63
DB 64 YHPTARHLENLHNGYHVDKDHVSVDYRRLAEPSSKRGLEPKGHVTLVTLTCAAA 123
QY 65 YHPTARHLEKFTGYHLSDFKSEVSKDYRKLAEPSSKRGLEPKGHVTSCTLASVA 124
DB 64 YHPTARHLENLHNGYHVDKDHVSVDYRRLAEPSSKRGLEPKGHVTLVTLTCAAA 123
QY 125 MFELIVLVGLVLRCTSVVAHLSGMLGLLMMQSAVYVGHDSGHVYVMTTNGFNKVAQILSG 184
DB 124 MAAVYVGVAVCTIMAHILSAVLGLIMISAVYVGHDSGHVYVMTTNGFNKVAQILSG 183
QY 185 CLTGISIAWKMKTNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 244
DB 184 CITGISIAWKMKTNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 243
QY 245 ARFLICYOHFTFYVVCVAVNLVLTLLFSRRKQORALNMGILVFTWFPPLVSC 304
DB 244 ARFLISYOHMSFYVIMCVGRINLEIOTLLFSRRVYDPRALNMGILVFTWFPPLVSC 303
QY 305 LPMNREVMFLAFAVCSIOHIOFCINHPANVYVPGSGNDMPFEKOTSGTLDISCAS 364
DB 304 LPMNREVMFLAFAVCSIOHIOFCINHPANVYVPGSGNDMPFEKOTSGTLDISCAS 363
QY 365 MDWFFGGLOFOLBNHLPRLPRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 424
DB 364 MDWFFGGLOFOLBNHLPRLPRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 423
QY 425 TAAAOARDLTNPAPKULMEAVNTG 450
DB 424 KAAVQARDVTPVLENLMEALNTG 449

RESULT 4
ID Q9FR82 PRELIMINARY; PRT; 446 AA.
AC Q9FR82;
DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DT Delta 8-sphingolipid desaturase.
GN SIDL1.
OS Borago officinalis (Borraghe) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Boraginaceae; Borago.
OX NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21092516; PubMed=11368168;
RA Libisch B.; Michaelson L.V.; Lewis M.J.; Shewry P.R.; Napier J.A.;
RT "Chimeras of Delta8-fatty acid and Delta8-sphingolipid desaturases";
RL Biochem. Biophys. Res. Commun. 279:779-785(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=21260464; PubMed=11368168;
RA Sperling P.; Libisch B.; Zaehring U.; Napier J.A.; Heinz E.;
RT "Functional identification of a delta 8-sphingolipid desaturase from
RT Arch. Biochem. Biophys. 388:293-298(2001).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF133728; AAG43277.1; -.
DR HSSP; P00171; 115U.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 446 AA; 50926 MW; EBD579F035A3AF0C CRC64;
Query Match 73.6%; Score 1801.5; DB 10; Length 446;
Best Local Similarity 71.8%; Pred. No. 3.2e-158;
Matches 321; Conservative 58; Mismatches 67; Indels 1; Gaps 1;
QY 4 VEKPKYITSEELKHNKEDLMISIQGKYNNVSDWYKHPGQDVPISNLAGQDVTDAFI 63
DB 1 MEGTKKYSISGEBLEKHNQGLDVMISIQGKYVNTDWMKKHPGQDVPISNLAGQDVTDAFI 60
DB 64 AYHPTARHLEKFTGYHLSDFKSEVSKDYRKLAEPSSKRGLEPKGHVTSCTLASVA 123
DB 61 AYHPTARHLEKFTGYHLSDFKSEVSKDYRKLAEPSSKRGLEPKGHVTSCTLASVA 120
QY 124 VMEFLIVLVGLVLRCTSVVAHLSGMLGLLMMQSAVYVGHDSGHVYVMTTNGFNKVAQILSG 183
DB 121 LILCGCYVGLVLRCTSVVAHLSGMLGLLMMQSAVYVGHDSGHVYVMTTNGFNKVAQILSG 180
QY 184 NCLTGISIAWKMKTNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 243
DB 181 NCLTGISIAWKMKTNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 240
QY 244 IAAFLICYOHFTFYVVCVAVNLVLTLLFSRRKQORALNMGILVFTWFPPLVSC 303
DB 241 IAAFLICYOHFTFYVVCVAVNLVLTLLFSRRKQORALNMGILVFTWFPPLVSC 300
QY 304 CLPMPERVMFLAFAVCSIOHIOFCINHPANVYVPGSGNDMPFEKOTSGTLDISCAS 363
DB 301 CLPMPERVMFLAFAVCSIOHIOFCINHPANVYVPGSGNDMPFEKOTSGTLDISCAS 360
QY 364 SMWFFGGLOFOLBNHLPRLPRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 423
DB 361 SMWFFGGLOFOLBNHLPRLPRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 420
QY 424 RTAALQARDLTNPAPKULMEAVNTG 450
DB 421 RTAALQARDLTNPAPKULMEAVNTG 446

RESULT 5

Q43469
ID Q43469 PRELIMINARY; PRT; 458 AA.
AC Q43469;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Delta-8 sphingolipid desaturase.
GN SLDI.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OC NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Indred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=96028121; PubMed=7586718;
RA Sperling P., Schmidt H., Heinz E.;
RT "A cytochrome b5-containing fusion protein similar to plant acyl lipid
desaturases";
RT Eur. J. Biochem. 232:798-805(1995).
RL [2]
RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Indred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=2116801; PubMed=1171153;
RA Sperling P., Blume A., Zaehneringer U., Heinz E.;
RT "Further characterization of delta 8-sphingolipid desaturases from
higher plants";
RT Biochem. Soc. Trans. 28:638-641(2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: X87143; CAA60621.1; -.
DR HSSP: P00171; 1F03.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR DR PROSITE: P550255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 458 AA; 52231 MW; D182287AB0E9245 CRC64;

Query Match 73.5%; Score 1801; DB 10; Length 458;
Best Local Similarity 71.6%; Pred. No. 3.7e-158;
Matches 317; Conservative 55; Mismatches 71; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNHKEGDLWISIQKVVNVSDWVKEHFGDVPISNLAGQDVTDAFIAYHP 67
DB 16 KKITSEELKGNHNPNDLWISILGKVVNVSEMAKHEHGGAPLNLNLAGQDVTDAFIAYHP 75
QY 68 GTAMSHLEKFFTGTHLSDFKVSEVSKDYRKLASFSKLGFDTKGHVTSCTLASVAWML 127
DB 76 GTAMKHLDFGTGTHLSDFKVSEVSKDYRKLASFSKLGFDTKGHVTSCTLASVAWML 135
QY 128 IYLVYGLRCSWAHAGSGMLGLMMQSAVYGHDSGHYVMTNGNKNKAQILSGNCLT 187
DB 136 ACYVGLVYSGSFIMHLSGAILGLAMWQIAYLGLDASHYQMMARGNKKAAGLFTGCIT 195
QY 188 GISIAMKWTNNAHNLHACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 247
DB 196 GISIAMKWTNNAHNLHACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 255
QY 248 LICQGHFTFYVWCVARVNLVYLTILLFSRRKVQDRAINIMGILVFWTWFPPLVSCLPN 307
DB 256 FVSGYHLYFPYVWCVARVNLVYLTILLFSRRKVQDRAINIMGILVFWTWFPPLVSCLPN 315
QY 308 WPERVWVFLASFAVCSIOHIOFCLNHFANVYVGPSSGNDWFEKQSGTLDISCASSMDW 367
DB 316 WPERVWVFLASFAVCSIOHIOFCLNHFANVYVGPSSGNDWFEKQSGTLDISCASSMDW 375

QY 368 FFGGLQFOLEHHLPRLPRCOLRKISPLVSDLCCKGNLPLYSLSFWEANQWTRITRLTA 427
DB 376 FFGGLQFOLEHHLPRLPRCHLRISIPICRCLCKKNLPLYSLSFYDANVTTLKTLRTA 435
QY 428 LOARDLTNPAPKNLMEANTNG 450
DB 436 LOARDLTNPAPKNLMEANTNG 458

RESULT 6
ID Q92TY9 PRELIMINARY; PRT; 446 AA.
AC Q92TY9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Desaturase/cytochrome b5 protein.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoside I; Malpighiales; Euphorbiaceae; Ricinus.
OC NCBI_TaxID=3988;
RN [1]
RN RP
RP SEQUENCE FROM N.A.
RC TISSUE=Seed endosperm;
RX MEDLINE=97268723; PubMed=9108131;
RA Savanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
cytochrome b5 domain results in the accumulation of high levels of
delta6-desaturated fatty acids in transgenic tobacco";
RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF005096; AAD01240.1; -.
DR HSSP: P00171; 115U.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR DR PROSITE: P550255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 446 AA; 51418 MW; A1954FDB2DDB600F CRC64;

Query Match 71.4%; Score 1749.5; DB 10; Length 446;
Best Local Similarity 69.1%; Pred. No. 2.1e-153;
Matches 306; Conservative 58; Mismatches 78; Indels 1; Gaps 1;

QY 8 KKYITSEELKGNHKEGDLWISIQKVVNVSDWVKEHFGDVPISNLAGQDVTDAFIAYHP 67
DB 5 KKITSEELKGNHNPNDLWISILGKVVNVSEMAKHEHGGAPLNLNLAGQDVTDAFIAYHP 64
QY 68 GTAMSHLEKFFTGTHLSDFKVSEVSKDYRKLASFSKLGFDTKGHVTSCTLASVAWML 127
DB 65 GTAMKHLDFGTGTHLSDFKVSEVSKDYRKLASFSKLGFDTKGHVTSCTLASVAWML 123
QY 128 IYLVYGLRCSWAHAGSGMLGLMMQSAVYGHDSGHYVMTNGNKNKAQILSGNCLT 187
DB 124 LSYVGLVYSGSFIMHLSGAILGLAMWQIAYLGLDASHYQMMARGNKKAAGLFTGCIT 193
QY 188 GISIAMKWTNNAHNLHACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 247
DB 184 GISIAMKWTNNAHNLHACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 243
QY 248 LICQGHFTFYVWCVARVNLVYLTILLFSRRKVQDRAINIMGILVFWTWFPPLVSCLPN 307
DB 244 LVSQYHLYFPYVWCVARVNLVYLTILLFSRRKVQDRAINIMGILVFWTWFPPLVSCLPN 303
QY 308 WPERVWVFLASFAVCSIOHIOFCLNHFANVYVGPSSGNDWFEKQSGTLDISCASSMDW 367
DB 304 WPERVWVFLASFAVCSIOHIOFCLNHFANVYVGPSSGNDWFEKQSGTLDISCASSMDW 363

QY 368 FFGGLQFQLEHHLPRPLRCQRLKISPLVSDLCCKHNLPRYSFWEANQMTITRTAA 427
 DB 364 FHGGLQFQMEHHLPRPLRVLRLKRSFVRELCKKHNLPRYSASFMANELFTLRAAA 423

QY 428 LQARDLNPAPKXNLMEAVNTHG 450
 DB 424 LQARDLNPAPKXNLMEAVNTHG 446

RESULT 7

Q8BLD7 PRELIMINARY; PRT; 446 AA.
 AC Q8BLD7;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Spinnolipid long chain base delta 8 desaturase.
 OS Aquilegia vulgaris.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Ranunculaceae; Aquilegia.
 OX NCBI_TaxID=3451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Longman A.J., Michaelson L.V., Napier J.A.;
 RT "Isolation and characterization of a cDNA encoding a delta 8
 spinnolipid desaturase from Aquilegia vulgaris."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF406816; AA03619.1; -.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA desat fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR PRINTS; PR00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD01081; FA desat fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;

Query Match 69.1%; Score 1692.5; DB 10; Length 446;
 Best Local Similarity 66.7%; Pred. No. 4e-148;
 Matches 297; Conservative 63; Mismatches 84; Indels 1; Gaps 1;

QY 6 KEKVTISEELKGNKEGDLWISIOGKYVNSDVWKEHFGDVPISNLAGODVDAFIAY 65
 DB 3 EKREITISEELKGNKEGDLWISIOGKYVNSDVWKEHFGDVPISNLAGODVDAFIAY 62
 QY 66 HPGTAMSHLEKFTGYHLSDFPKVSEVSKDYRKLASFEKGLFPTKGHTSCTLASVAVM 125
 DB 63 HPGTAMSHLEKFTGYHLSDFPKVSEVSKDYRKLASFEKGLFPTKGHTSCTLASVAVM 121
 QY 126 FLIVGLVRLCTSVMAHLGSGMLGLLWMOGAYVGHDSGHVYVMTNGFNKVAQILSGNC 185
 DB 122 MAISVGLVGLSDGTMAHLGSGMLGLLWMOGAYVGHDSGHVYVMTNGFNKVAQILSGNC 181
 QY 186 LTGISIAMKWTNNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIA 245
 DB 182 LTGISIAMKWTNNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIA 241
 QY 246 RELCYOHFTFYVWCVAVNVLQYITILLFSRRKVDORAININGILVMTMPLVSC 305
 DB 242 RELCYOHFTFYVWCVAVNVLQYITILLFSRRKVDORAININGILVMTMPLVSC 301
 QY 306 PNWERVWVFLASFAVCSIOHIOFCLNHPAANVYVPPSGNDWPEKOTSGTLDISCASSM 365
 DB 302 PNWERVWVFLASFAVCSIOHIOFCLNHPAANVYVPPSGNDWPEKOTSGTLDISCASSM 361
 QY 366 DMFEGLOFQLEHHLPRPLRCQRLKISPLVSDLCCKHNLPRYSFWEANQMTITRTAA 425
 DB 362 DMFEGLOFQLEHHLPRPLRCQRLKISPLVSDLCCKHNLPRYSFWEANQMTITRTAA 421

QY 426 AALQARDLNPAPKXNLMEAVNTHG 450
 DB 422 AALQARDLNPAPKXNLMEAVNTHG 446

RESULT 8
 Q8VZ22 PRELIMINARY; PRT; 448 AA.

AC Q8VZ22;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 OS Echinum gentianoides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Boraginaceae; Echinum.
 OX NCBI_TaxID=173991;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 Echinum: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055117; AAL23580.1; -.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA desat fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD01081; FA desat fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51428 MW; C2A937951B87C183 CRC64;

Query Match 68.2%; Score 1670; DB 10; Length 448;
 Best Local Similarity 64.8%; Pred. No. 4.8e-146;
 Matches 287; Conservative 75; Mismatches 81; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNKEGDLWISIOGKYVNSDVWKEHFGDVPISNLAGODVDAFIAY 67
 DB 6 KKYITSEELKGNKEGDLWISIOGKYVNSDVWKEHFGDVPISNLAGODVDAFIAY 65
 QY 66 GTAMSHLEKFTGYHLSDFPKVSEVSKDYRKLASFEKGLFPTKGHTSCTLASVAVM 127
 DB 66 GTAMSHLEKFTGYHLSDFPKVSEVSKDYRKLASFEKGLFPTKGHTSCTLASVAVM 125
 QY 128 FLVGLVRLCTSVMAHLGSGMLGLLWMOGAYVGHDSGHVYVMTNGFNKVAQILSGNCLT 187
 DB 126 FLVGLVRLCTSVMAHLGSGMLGLLWMOGAYVGHDSGHVYVMTNGFNKVAQILSGNCLT 185
 QY 188 GISISIAMKWTNNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIA 247
 DB 186 GISISIAMKWTNNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIA 245
 QY 248 LICQOHTFYVWCVAVNVLQYITILLFSRRKVDORAININGILVMTMPLVSC 307
 DB 246 LICQOHTFYVWCVAVNVLQYITILLFSRRKVDORAININGILVMTMPLVSC 305
 QY 308 WPEVWVFLASFAVCSIOHIOFCLNHPAANVYVPPSGNDWPEKOTSGTLDISCASSMDW 367
 DB 306 WPEVWVFLASFAVCSIOHIOFCLNHPAANVYVPPSGNDWPEKOTSGTLDISCASSMDW 365
 QY 368 FFGGLQFQLEHHLPRPLRCQRLKISPLVSDLCCKHNLPRYSFWEANQMTITRTAA 427
 DB 366 FFGGLQFQLEHHLPRPLRCQRLKISPLVSDLCCKHNLPRYSFWEANQMTITRTAA 425
 QY 428 LQARDLNPAPKXNLMEAVNTHG 450
 DB 426 LQARDLNPAPKXNLMEAVNTHG 446

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-deaturase.
 GN D6DS.
 OS Ectium pitaridi var. pitaridi.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Ectium.
 OX NCB1_TaxID=174255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Marto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 RT Ectium: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055118; AAL23581.1; -.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_deatc_fam.
 DR Pfam; PF00487; FA_deaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD00612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_deatc_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51394 MW; 486D6EA905DE263 CRC64;

Query Match 67.5%; Score 1653; DB 10; Length 448;
 Best Local Similarity 64.3%; Pred. No. 1.8e-144;
 Matches 285; Conservative 75; Mismatches 83; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNHKGDMISIOGKVVNSDVKKEHPCGADVPIISLAGODVDAFIAYHP 67
 DB 6 KKYITAEELKGNHKGDMISIOGKVVNSDVKKEHPCGADVPIISLAGODVDAFIAYHP 65
 QY 68 GTAWSHLEKFTGYHLSDFKVSSEVSKDYRKLASSEFSKGLFPTKGHTVSTLASVAVMFL 127
 DB 66 GSTWMLDSFPTGYHLSDFKVSSEVSKDYRKLASSEFSKGLFPTKGHTVSTLASVAVMFL 125
 QY 128 IYLVGVLRCTSWMAHLSGMLGLIMQSAVYGHDSGHVYVNTTNGFNKVAQILSGNCLT 187
 DB 126 MSVGVLRCEGVYHLSGMLGLIMQSAVYGHDSGHVYVNTTNGFNKVAQILSGNCLT 185
 QY 188 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFNSITSHFYGRKLEPFIFARF 247
 DB 186 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFNSITSHFYGRKLEPFIFARF 245
 QY 248 LICVGHFTFYPMCVARVNLVLTILLFSRRKVDORALNIMGLVFTWPELVASCLEN 307
 DB 246 FVSHQHTFYPMCVARVNLVLTILLFSRRKVDORALNIMGLVFTWPELVASCLEN 305
 QY 308 WPERVMTFLASPAVCSIOHICLNHPAANYVGPSPGNDMEKQTSCTLDISCPMMDM 367
 DB 306 WGERIMFVIALSVYGMQVQFSLNHFPSSVYGVKPNNGNMFETQDCTLDISCPMMDM 365
 QY 368 FFGGLQFQLEHNLPRRLPCOLRKISPLVSDCKKHNLPYRSLSPWENOMTIRTLRTAA 427
 DB 366 FHGGLQFQLEHNLPRRLPCOLRKISPLVSDCKKHNLPYRSLSPWENOMTIRTLRTAA 425
 QY 428 LQARDLTNPAPKNLMEAVNTHG 450
 DB 426 LQARDLTNPAPKNLMEAVNTHG 448

RESULT 12
 Q8L717 PRELIMINARY; PRT; 448 AA.
 AC 08L717;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-6-deaturase.
 OS Argania spinosa.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Sapotaceae; Argania.
 OX NCB1_TaxID=85884;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA El Filali A., Anderson M., Abbas K.;
 RT "Characterization and cloning of delta-6-desaturase in Argania spinosa
 RT fruit."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY131238; AAM94345.1; -.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_deatc_fam.
 DR Pfam; PF00487; FA_deaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD00612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_deatc_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;

Query Match 65.2%; Score 1597; DB 10; Length 448;
 Best Local Similarity 61.6%; Pred. No. 2.8e-139;
 Matches 273; Conservative 78; Mismatches 92; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNHKGDMISIOGKVVNSDVKKEHPCGADVPIISLAGODVDAFIAYHP 67
 DB 6 KKYITSEELKGNHKGDMISIOGKVVNSDVKKEHPCGADVPIISLAGODVDAFIAYHP 65
 QY 68 GTAWSHLEKFTGYHLSDFKVSSEVSKDYRKLASSEFSKGLFPTKGHTVSTLASVAVMFL 127
 DB 66 ASTWKNLDFPTGYHLSDFKVSSEVSKDYRKLASSEFSKGLFPTKGHTVSTLASVAVMFL 125
 QY 128 IYLVGVLRCTSWMAHLSGMLGLIMQSAVYGHDSGHVYVNTTNGFNKVAQILSGNCLT 187
 DB 126 MSVGVLRCEGVYHLSGMLGLIMQSAVYGHDSGHVYVNTTNGFNKVAQILSGNCLT 185
 QY 188 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFNSITSHFYGRKLEPFIFARF 247
 DB 186 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFNSITSHFYGRKLEPFIFARF 245
 QY 248 LICVGHFTFYPMCVARVNLVLTILLFSRRKVDORALNIMGLVFTWPELVASCLEN 307
 DB 246 FVSHQHTFYPMCVARVNLVLTILLFSRRKVDORALNIMGLVFTWPELVASCLEN 305
 QY 308 WPERVMTFLASPAVCSIOHICLNHPAANYVGPSPGNDMEKQTSCTLDISCPMMDM 367
 DB 306 WGERIMFVIALSVYGMQVQFSLNHFPSSVYGVKPNNGNMFETQDCTLDISCPMMDM 365
 QY 368 FFGGLQFQLEHNLPRRLPCOLRKISPLVSDCKKHNLPYRSLSPWENOMTIRTLRTAA 427
 DB 366 FHGGLQFQLEHNLPRRLPCOLRKISPLVSDCKKHNLPYRSLSPWENOMTIRTLRTAA 425
 QY 428 LQARDLTNPAPKNLMEAVNTHG 450
 DB 426 LQARDLTNPAPKNLMEAVNTHG 448

RESULT 13
 Q9ZTU8 PRELIMINARY; PRT; 469 AA.
 AC 09ZTU8;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE S276.
 GN S276.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OX NCB1_TaxID=4565;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 24905;
 RX MEDLINE=20563795; PubMed=1112411;
 RA Laoteng K., Mammontarat R., Tanticharoen M., Cheevadhanarak S.;
 RT "Delta(6)-desaturase of *Mucor rouxii* with high similarity to plant
 RT delta(6)-desaturase and its heterologous expression in *Saccharomyces
 cerevisiae*.";
 RL Biochem. Biophys. Res. Commun. 279:17-22(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF296076; AAG36960.1; -.
 DR EMBL: AF296076; AAG36960.1; -.
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROMEBS.
 DR ProDom: PD000612; Cyt B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 DR PROSITE: PS00038; HLH_1; 1.
 KW Heme.
 SQ SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;
 Query Match 59.7%; Score 1463; DB 10; Length 469;
 Best Local Similarity 57.6%; Pred. No. 7.6e-127;
 Matches 255; Conservative 79; Mismatches 107; Indels 2; Gaps 2;
 QY 9 KYTSELKHNKNGEGLMISIGKRVNVSDVKEHPRGQDVPIINLAGQDVTDAFIAYHG 68
 DB 28 RMISTELQHAADADLMSISGDVYDVTWLNHHPGEVPLITLGAQDADTFMAYHNP 87
 QY 69 TAWSHLEKFTGYHLSDFKVEVKDYKRLASEFSKGLPDTKGHYVTSCTLASVAWFLI 128
 DB 88 SVAPLRLRFVVG-RITDYTYPPASADPRRLAQLSSGLTERVGHPTKFLVMSVLCI 146
 QY 129 VLYGVRLCTSVMAHLSGMLGLIMQSAVYGHDSGHVYVMTTNGFNKAQIISGNCITG 188
 DB 147 ALCYVLACSGSTGAMFAGGLIGFTWIGSGWIGHDSGHQITRRPALNRLIQVVSNCITG 206
 QY 189 ISIAWKKMTNAHHIHCNSLDHDPDLOHMPVAVSSSFNSITSHPRGLRDFIARFL 248
 DB 207 LGIAWKKFNNTNHHISCSLDHDPDLOHLPFANVTGLFNNLMSVCERLTAADALSKEF 266
 QY 249 ICYQHFTEYVVCVARNLVLTILLFSRRKYODRALNIMGILVETWPEPLVSCLEPN 308
 DB 267 VSYQHHTFYVWGFARINLVOSIVLITQKVRQRRLLEAGVAFFWVPLVSCLEPN 326
 QY 309 PERVMEVLASFAVCSIQHIOFCLNHPANVYVGPSPGNDWPEKQTSGLTIDISCASSMDW 368
 DB 327 WERVAVFLASFVITGIQHVQFCINHFSSAVYVGPKNQDWFPERQTAGTIDIKCSPMWDMF 386
 QY 369 FGGLOLEHNLPRRLPRCQARKISPIVSDLCCKHNLPRSLSPFWENOMTITRLTAAL 428
 DB 387 HGGLOQOVERHNLPRRLPRCHYRWAPLVRDLCKKHGLSYGAATFWANVTWTLRAAL 446
 QY 429 QARD-LTNPAKMLLWEAVNTHG 450
 DB 447 QAREATTGAAPKLVWEALNTHG 469
 RESULT 14
 Q9HDS8 PRELIMINARY; PRT; 523 AA.
 AC Q9HDS8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE Delta-6 desaturase.
 OS Mucor rouxii.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 NCBI_TaxID=29923;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 24905;
 RX MEDLINE=20563795; PubMed=1112411;
 RA Laoteng K., Mammontarat R., Tanticharoen M., Cheevadhanarak S.;
 RT "Delta(6)-desaturase of *Mucor rouxii* with high similarity to plant
 RT delta(6)-desaturase and its heterologous expression in *Saccharomyces
 cerevisiae*.";
 RL Biochem. Biophys. Res. Commun. 279:17-22(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF296076; AAG36960.1; -.
 DR EMBL: AF296076; AAG36960.1; -.
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 DR PROSITE: PS00038; HLH_1; 1.
 KW Heme.
 SQ SEQUENCE 523 AA; 60622 MW; A03727AF39EB7857 CRC64;
 Query Match 28.1%; Score 688.5; DB 3; Length 523;
 Best Local Similarity 28.5%; Pred. No. 4.7e-55;
 Matches 147; Conservative 87; Mismatches 199; Indels 83; Gaps 7;
 QY 6 KEKYYTSELKHNKNGEGLMISIGKRVNVSDVKEHPRGQDVPIINLAGQDVTDAFIAY 65
 DB 17 RSSNIYTEBEFQRLIKQSGVPIFEQKYRVNFMFAKHGGEAALRSALGRDVTDEIRTW 76
 QY 66 HPTAASHLEKFTGYHLSDF----- 86
 DB 77 HRPQVY---EKMINLYCIDWPDVIRPASKQOHTFTPKEDKPYLTATWBSGFTVQAV 133
 QY 87 -----KVESESKD-----YRKLASEFSKGLPDTKGHYVTSCTLAS 121
 DB 134 DDAIQDLHKHSHSLDKADVLOKDLNGDDIRNAYRGLAEVLAKGF-----KCNWYK 186
 QY 122 VA-----VMEIIVLYGVRLCTSVMAHLSGMLGLIMQSAVYGHDSGHVYVMTTNGF 174
 DB 187 YAREGCRYTLIFLSIMFTLKTGETNHYMAGAFFAMFHNQLVFTAHDAHGHEITKSEI 246
 QY 175 NKVAQLISGNCCLGISIAWKKMTNAHHIHCNSLDHDPDLOHMPVAVSSSFNSITSHPR 234
 DB 247 DHVIGVLIANFTGSLGMLKDNHNVHHIVTNHPEDPDIOHVPFMAITTKFPNNIYSTV 306
 QY 235 YGRKLEFDFIARFLCYQHFTEYVVCVARNLVLTILLFSRRKYODRALNIMGILV 294
 DB 307 YKRVLPFDDAASRFVNHQHYLYLILSPFRNLHRSFAYLLTCKNVRRTLELVGITTF 366
 QY 295 WTWPEPLVSCLEPNRPRVMEVLASFAVCSIQHIOFCLNHPANVYVGPSPGNDWPEKQTS 354
 DB 367 FVWFGLSLSTLPTNIRIAYIVMSYMLTFRPLVQILSHFGSTEDRGPD-BEPFAKMR 425
 QY 355 GTLIDISCASSMDWFFGGLOLEHNLPRRLPRCQARKISPIVSDLCCKHNLPRSLSPFW 414
 DB 426 TTMDVDCPEWLDWFFGGLOLYQAVNHLFPRLPRLNINLCQVPLVKKFCDEGLHYMYNFT 485
 QY 415 ANQWTRTLRTALQARDLTNPAPKML-LWEAVNTH 449
 DB 486 GNGVVLGTLKSYADQVGFNNEVAKSAEITANDKEH 521
 RESULT 15
 Q8NKG9 PRELIMINARY; PRT; 568 AA.
 AC Q8NKG9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)

	DB	Purative delta 8-sphingolipid desaturase.
	OS	Saccharomyces kluyveri (yeast).
	OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
	CC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.
	OX	NCBI_TaxID:4934;
	RN	[1]
	RP	SEQUENCE FROM N.A.
	RC	STRAIN=IPO 1685;
	RA	Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
	RT	"Isolation and characterization of the genes encoding delta 8-
	RT	sphingolipid desaturase from Saccharomyces kluyveri and Kluyveromyces
	RL	lactis";
	CC	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
	DR	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
	DR	EMBL; AB085669; BAB93117.1; --
	DR	InterPro; IPR001199; Cyt_B5.
	DR	InterPro; IPR005804; FA_desat_fam.
	DR	Pfam; PF00487; FA_desaturase; 1.
	DR	Pfam; PF00173; heme_1; 1.
	DR	Prodont; PD001081; FA_desat_fam; 1.
	DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.
	KW	Heme.
	SQ	SEQUENCE 568 AA; 66465 MW; 1158BE7B876D6E8C CRC64;
Qy	Query March	23.0%; Score 562.5; DB: 3; Length 568;
Dd	Best Local Similarity	26.1%; Pred. No. 2.4e+33;
	Matches 141;	Conservative 83; Mismatches 193; Indels 123; Gaps 11.
Qy	11 ITSEELKGNKEGDLMISIOCKVYVSVSWVEHPGADVPISLAGQVDAFIAYH----	66
Dd	5 ISRSEIEDRIARGQAIVIEGLVNLLEKMIKFHPGGDKAIIHHMIGRDATDEMKAHCBET	64
Qy	67 -----	66
Dd	65 VEIERKWRIGRIDOWENFLPPIOGVFPLNQHDSTDLSNKMIAPTSDQPKFIKN	124
Qy	67 -----	84
Dd	125 EKHNCGEDVKIYIPKIQGYIPLSLNKEAYEKCVTDPAVDNDNELVRQDETLPDL	184
Qy	85 DFKVSE-VSKDYRKLAESFKLGFDTRKGHTVSCITLAVAWFLVLVGVL-RCTSVAAH	142
Dd	185 DPKTQEWMLSKYNNKMHNEIIAAGLQCNPPRYVELTIRIGLLFALSYLVLIHRDDKFM--	242
Qy	143 LGSGLMLGLLMQSAVYGDSGHVVMVTNGFNKYAQILSGNCLTGISIAMKWTHNAH	202
Dd	243 --SAFSMGCAAOQLVFIFIAHDAGHSISTHYOLDNFIMGIIMSWSGLSLGWKKRHNVNH	300
Qy	203 IACNSLDHDPLOHMFPVAVSRFPNSTITSFHFGKLKLFDFIARLCYQHFTFYPVVCV	262
Dd	301 LITNDPHDPDIQHLFFFAVSTRLEDNTYSTYEKEFLWFDAFAKKVVPWMNYLYPMIAF	360
Qy	263 ARVNLY-----LOTILLFLFSRRKVOD--RALNIIGILVFWTW-FPLLVSCL-PNNPERVME	314
Dd	361 GRFLYLRLSMWHVLLGLGRPRKGAKMFYFELCGILFFNNYMFYLLVGCCKIQOTGMDRFOY	420
Qy	315 VLASFVACSIOHIQFCNLHFPAANY-VGPESGNDVFEKQTSGTLDISCASSMDWEFGGLQ	373
Dd	421 IMVSHITMTLVNOITLISHFAMSTSDLGVGEGFRPQRLTSS--MDVDCPRMLDFILGGLQ	478
Qy	374 FOLSHHLFPRRLPROCRLKISPLVSLDCKKHNLPRYSLSFWENQWTITLTALTALOARDL	433
Dd	479 FOVVHHLFPRRLPRNLRAAOPLYVEECSEKVIKSIYGFSGKNGVALLPKOLEIAVOACTMM	538

Search completed: January 1, 2004, 06:33:56
Job time : 41.588 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 15.634 Seconds
(without alignments)
1217.848 Million cell updates/sec

Title: US-09-857-524B-8
Perfect score: 2449
Sequence: 1 MEVKEKKYITSEELKGN.....RDLTPAPKLLMEAVNTG 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues
Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1712	69.9	452	4	US-08-934-254-27 Sequence 27, Appl
2	1650	67.4	448	1	US-08-366-779-5 Sequence 5, Appl
3	1650	67.4	448	1	US-08-789-936-5 Sequence 5, Appl
4	1650	67.4	448	4	US-08-934-254-5 Sequence 5, Appl
5	1633	66.7	446	2	US-08-833-610-5 Sequence 5, Appl
6	1633	66.7	446	3	US-08-834-033A-15 Sequence 15, Appl
7	1091	44.5	252	2	US-08-834-655-7 Sequence 7, Appl
8	1091	44.5	252	3	US-08-834-033A-8 Sequence 8, Appl
9	1091	44.5	252	3	US-09-363-574-7 Sequence 7, Appl
10	1091	44.5	252	4	US-09-363-526-7 Sequence 7, Appl
11	502.5	20.5	457	2	US-08-834-655-2 Sequence 2, Appl
12	502.5	20.5	457	3	US-08-834-033A-2 Sequence 2, Appl
13	502.5	20.5	457	3	US-09-363-574-2 Sequence 2, Appl
14	502.5	20.5	457	4	US-09-363-526-2 Sequence 2, Appl
15	502.5	20.5	457	4	US-09-330-235-18 Sequence 18, Appl
16	502.5	20.5	458	4	US-09-439-261-10 Sequence 10, Appl
17	502.5	20.5	458	4	US-09-439-261-44 Sequence 44, Appl
18	502.5	20.5	458	4	US-09-227-613-11 Sequence 11, Appl
19	502.5	20.5	458	4	US-09-227-613-41 Sequence 41, Appl
20	500.5	20.4	457	2	US-08-833-610-4 Sequence 4, Appl
21	500.5	20.4	457	3	US-08-834-033A-14 Sequence 14, Appl
22	496	20.3	125	2	US-08-834-655-8 Sequence 8, Appl
23	496	20.3	125	3	US-08-834-033A-9 Sequence 9, Appl
24	496	20.3	125	3	US-09-363-574-8 Sequence 8, Appl
25	496	20.3	125	4	US-09-363-526-8 Sequence 8, Appl
26	436	17.8	445	4	US-09-048-888-1 Sequence 1, Appl
27	429	17.5	444	4	US-09-048-888-3 Sequence 3, Appl

28	425	17.4	444	4	US-09-439-261-11 Sequence 11, Appl
29	425	17.4	444	4	US-09-227-613-12 Sequence 12, Appl
30	425	17.4	445	4	US-09-439-261-39 Sequence 39, Appl
31	425	17.4	445	4	US-09-439-261-45 Sequence 45, Appl
32	422.5	17.3	432	4	US-09-439-261-9 Sequence 9, Appl
33	422.5	17.3	432	4	US-09-227-613-9 Sequence 9, Appl
34	422.5	17.3	465	4	US-09-439-261-40 Sequence 40, Appl
35	422.5	17.3	465	4	US-09-227-613-38 Sequence 38, Appl
36	418.5	17.1	444	4	US-09-439-261-43 Sequence 43, Appl
37	418.5	17.1	444	4	US-09-227-613-42 Sequence 42, Appl
38	385.5	15.7	355	2	US-08-834-655-5 Sequence 5, Appl
39	385.5	15.7	355	3	US-08-834-033A-6 Sequence 6, Appl
40	385.5	15.7	355	3	US-09-363-574-5 Sequence 5, Appl
41	385.5	15.7	355	4	US-09-363-526-5 Sequence 5, Appl
42	370.5	15.1	104	2	US-08-834-655-6 Sequence 6, Appl
43	370.5	15.1	104	3	US-08-834-033A-7 Sequence 7, Appl
44	370.5	15.1	104	3	US-09-363-574-6 Sequence 6, Appl
45	370.5	15.1	104	4	US-09-363-526-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-934-254-27
; Sequence 27, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-934-254-27
Query Match 69.9%; Score 1712; DB 4; Length 452;
Best local Similarity 69.6%; Pred. No. 7,1e-180;
Matches 311; Conservative 54; Mismatches 78; Indels 4; Gaps 4;
QY 8 KYITSEELKGNKGDLWISIQKAYNVSDVWKEHGGDVPISNLAGDVTDAFYAHP 67
DB 6 KYITAEEDRRHNKSGDLMISIQKAYVDCSMAAEHFGGEVPLSLIAGDVTDAFYAHP 65
QY 68 GRAWSHLEKFFPG-VHLSDFKXSVSKDYRKLASERSKGLPDTKQHTVSTLASVAWVF 126

Db	66	GIAMRHLDPLFTYIYLLKDFEVSSEISKDPRRLINEMSSGILEKKGHHIMTFYGVAVMM	1250
Qy	127	LILYGLVLRCTSVMAHIGSGMLLGLIMMOASAYVGDSCGHVYMTTNGCFNKTAQOILSNCUL	1860
Db	126	AAIYGVGLASESGVAMLCGALLGLIMTOAAVYGDSCGHVQYMPFRGNGNRITQOIAENIL	1850
Qy	187	TGISIAMWKTNAAHHIACNSLDHDPDLOHMEVFVAVSSRFNSITSHFGRKLEFEIAR	2460
Db	186	TGISIAMWKTNAAHHIACNSLDYDDPDLOHIEVFVAVSTRLFNSITSYVGRVLFDFEAR	2450
Qy	247	FLICYOHTFFYPWMCVAVNLYLQTTLLLFSSRKVQDRALNIMGILVFTWTFPLVSLCP	3060
Db	246	FLVSYQHMTYYPWMI FGRVNLFIQTFLLLTRRDVDBALNIMGIAVFWMTFPLVSCLP	3050
Qy	307	NMEBERVMTLASAVCSIOHIOFCNLHFPAAANYVGPBGNDMEFKQISGTLDISCASSMD	3660
Db	306	NMEBERFEFVLISPAVAIAOHVOFTLNHFSGDYVGPBKDWMFEKQTKGTLIDITCPRPMD	3650
Qy	367	WFGGGLQFOLEHNLFRRLPRCQLRKISPLVSLDCKKHNLPRYSLSFW-EAQMWTIRLRT	4250
Db	366	WFGGGLQFOLEHNLFRRLPRGQLRKIAFLARDLCKKGKMPYRSFGFQMDAVYTRIRLTD	4240
Qy	426	AALOARDLTN-PAPKULM-EAVNTHG 450	
Db	426	AAVQARDLNSAPCPKULGYGEAANTHG 452	

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1      RESULT 2
2      US-08-366-779-5
3      Sequence 5, Application US/08366779
4      Patent No. 5614393
5      GENERAL INFORMATION:
6      APPLICANT: Thomas, Terry L.
7      APPLICANT: Reddy, Avutu S.
8      APPLICANT: Nuccio, Michael
9      APPLICANT: Freysinet, Georges L.
10     APPLICANT: Numbers, Andrew N.
11     TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
12     TITLE OF INVENTION: DELTA 6-DESATURASE
13     NUMBER OF SEQUENCES: 25
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Scully, Scott, Murphy & Presser
16     STREET: 400 Garden City Plaza
17     CITY: Garden City
18     STATE: New York
19     COUNTRY: United States
20     ZIP: 11530
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: Patentm Release #1.0, Version #1.25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/08/366,779
28     FILING DATE: 30-DEC-1994
29     CLASSIFICATION: 800
30     ATTORNEY/AGENT INFORMATION:
31     NAME: Presser, Leopold
32     REGISTRATION NUMBER: 19,827
33     REFERENCE/DOCKET NUMBER: 8383GYXW
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: (516) 742-4343
36     TELEFAX: (516) 742-4366
37     TELEX: 230 901 SANS UR
38     INFORMATION FOR SEQ ID NO: 5:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 448 amino acids
41     TYPE: amino acid
42     TOPOLOGY: linear
43     MOLECULE TYPE: DNA (genomic)
44     US-08-366-779-5

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Query Match	67.4%	Score 1650	DB 1	Length 448
Best Local Similarity	63.2%	Pred. No. 4.8e-173		
Matches 280	Conservative 78	Mismatches 85	Indels 0	Gaps 0

Qy	8	KKTIITEELKGNKSGDLMISIOGKVVYVSDMYKBNPGGVDVPIISNLGADVTDAFIYAP	67
Dp	6	KKTIITSDLNKNDHKDGLDLMISIOGKAVYVSDMYVDNHPGGSPLKSLAGQEVTDFAVAFHP	65
Qy	68	GTAMSHLEKFFPGYHLSDFPKYSBVSUKYRKLAASEPKLGLPDTGHTVSTCLASVAMFL	127
Dp	66	ASTMKMLDKFFPGYLYLKYVSVSEVSKDVRKLVFEFSKMGLDKKGHIMFAELTFCIALFLFA	125
Qy	128	IYLVGLVRCSTSWAHNGSGMLLGLTMMOMOSAVYVGDHSGYVMTTNGENFKYAOILSGCLT	187
Dp	126	MSYVGLVFCBGVLVHLFSGCLMGFLMTIOGSHIGHDAGHYVAVSVSRILNKFMGFIPAANCIS	185
Qy	188	GISIAWKKWTHNAHHIACNSLDHDELDHMEVFVAVSSRFENSISSHFYGRKLEDFIARF	247
Dp	186	GISIGWKKNNHNAHHIACNSLEBEDLDYIIFPLVAVSSRFGLSTSHFYBKRLTFDLSLRF	245
Qy	248	LITCYQFTPTPYMCVARNVLQYITLLIFSSRKQYODRNLINMGLVYVMTWTPRLLVGLPLN	307
Dp	246	FVSYQMTPTPYIMCARLMMVQVSLITMLTITKRNVSYRQELGLCVLSIYPLLVSLPLN	305
Qy	308	WPSRVWFVLAFAVCSIOHIOFCNLHFAFANYVGPSPSGNDWFEKOTSGTLDISCASSMDW	367
Dp	306	WGRIMFVLAISLVYGMQVQVPSLHNFSSYYVGGPKNNMFEEKQTGTDLDISCPMMDW	365
Qy	368	FFGGLOFOLLEHHLFPRLLPRCOLRKISPLVSDLCCKKNLPIYRSLSPFWEAQMTIRTLRTAA	427
Dp	366	FHGSGFOFIEHHLPFMPRCNLKRKISPIVIELCKKGNLPYVAVSFRKANEMWTIRTLRTNTA	425
Qy	428	LOARDLITNPARKNLLMEAVNTHG	450
Dp	426	LOARDITKPLPKVLWEALHTHG	448

RESULT 3
 US-08-789-936-5
 Sequence 5, Application US/08789936
 Patent No. 5789220
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freysinet, Georges L.
 APPLICANT: Numberg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,936
 FILING DATE: 28-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/366,779
 FILING DATE: 30-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 83832YXW

TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
US-08-789-936-5

Query Match 67.4%; Score 1650; DB 1; Length 448;
Best Local Similarity 63.2%; Pred. No. 4.8e-173;
Matches 280; Conservative 78; Mismatches 85; Indels 0; Gaps 0;

QY 8 KKITSEELKGNKEDLMISTQKYYNVDWYKHEPGGVPIISNLAGDVTDAFTAYHP 67
DB 6 KKITSEELKGNKEDLMISTQKYYNVDWYKHEPGGVPIISNLAGDVTDAFTAYHP 65
QY 68 GTAMSHLEKFTGYHLSDFKVSVDYKRLASEPSKLGFDTKGHVTSCTLASVAVMFL 127
DB 66 ASGWKNDKFFFTGYHLSDFKVSVDYKRLASEPSKLGFDTKGHVTSCTLASVAVMFL 125
QY 128 IYLYGLRCTSVVAHLSGSMGLGLMWQSAVYGHDSGHVYVMTTNGFNKVAQILSGNCLT 187
DB 126 MSYVGLVFCBGVLVHLSFGCLMGFLMIQSGMIGHDAGHYVVDSDRLNKMGIFANCLIS 185
QY 188 GISIAMKKTTHNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAH 247
DB 186 GISIAMKKTTHNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAH 245
QY 248 LICYOHFTFPYVAVCVAVNYLYQTILLPSRRKVDORALINIMGLVFWMTFPLVSCLPN 307
DB 246 FVSYOHFTFPYVAVCVAVNYLYQTILLPSRRKVDORALINIMGLVFWMTFPLVSCLPN 305
QY 308 WPERVWFVLAFAVCSIOHIOFCLNFAANVYVGPSPGNDWFEKQTSGLTIDISCASSMDW 367
DB 306 WGERIMFVLAISLVYGMQVQFSLNHFSSVYVYKRGKNNWFEKQDGTIDISCPPMDW 365
QY 368 FPGGLQFQLEHHLFPRLPFCQLRKISPLVSDCKKNLPYRSISFWANQWTRTLRTAA 427
DB 366 FPGSQFQLEHHLFPRMPRCNLKISPYVIELCKKNLPYVYASFANEMTLRTLRNTA 425
QY 428 LQARDLTNPAPKRLMEAVNTHG 450
DB 426 LQARDITKPLPKNLWEALHTHG 448

RESULT 4
US-08-934-254-5
Sequence 5, Application US/08934254
Patent No. 6355861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-934-254-5

Query Match 67.4%; Score 1650; DB 4; Length 448;
Best Local Similarity 63.2%; Pred. No. 4.8e-173;
Matches 280; Conservative 78; Mismatches 85; Indels 0; Gaps 0;

QY 8 KKITSEELKGNKEDLMISTQKYYNVDWYKHEPGGVPIISNLAGDVTDAFTAYHP 67
DB 6 KKITSEELKGNKEDLMISTQKYYNVDWYKHEPGGVPIISNLAGDVTDAFTAYHP 65
QY 68 GTAMSHLEKFTGYHLSDFKVSVDYKRLASEPSKLGFDTKGHVTSCTLASVAVMFL 127
DB 66 ASGWKNDKFFFTGYHLSDFKVSVDYKRLASEPSKLGFDTKGHVTSCTLASVAVMFL 125
QY 128 IYLYGLRCTSVVAHLSGSMGLGLMWQSAVYGHDSGHVYVMTTNGFNKVAQILSGNCLT 187
DB 126 MSYVGLVFCBGVLVHLSFGCLMGFLMIQSGMIGHDAGHYVVDSDRLNKMGIFANCLIS 185
QY 188 GISIAMKKTTHNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAH 247
DB 186 GISIAMKKTTHNAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAHIAH 245
QY 248 LICYOHFTFPYVAVCVAVNYLYQTILLPSRRKVDORALINIMGLVFWMTFPLVSCLPN 307
DB 246 FVSYOHFTFPYVAVCVAVNYLYQTILLPSRRKVDORALINIMGLVFWMTFPLVSCLPN 305
QY 308 WPERVWFVLAFAVCSIOHIOFCLNFAANVYVGPSPGNDWFEKQTSGLTIDISCASSMDW 367
DB 306 WGERIMFVLAISLVYGMQVQFSLNHFSSVYVYKRGKNNWFEKQDGTIDISCPPMDW 365
QY 368 FPGGLQFQLEHHLFPRLPFCQLRKISPLVSDCKKNLPYRSISFWANQWTRTLRTAA 427
DB 366 FPGSQFQLEHHLFPRMPRCNLKISPYVIELCKKNLPYVYASFANEMTLRTLRNTA 425
QY 428 LQARDLTNPAPKRLMEAVNTHG 450
DB 426 LQARDITKPLPKNLWEALHTHG 448

RESULT 5
US-08-833-610-5
Sequence 5, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KUNTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THORNDY, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/833,610
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAB-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.123.000US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-833-610-5

Query Match 66.7%; Score 1633; DB 2; Length 446;
 Best Local Similarity 63.0%; Pred. No. 3.5e-171;
 Matches 278; Conservative 78; Mismatches 85; Indels 0; Gaps 0;

QY 8 KKYITSEELGHNKGGDLWISIOGKYVNSDWVKEHGGDVPISNLAGDVTDAFIAYHP 67
 DB 6 KKYITSEELGHNKGGDLWISIOGKAYDSDWVADHGGSPFLKSLAGQVTDAPFAVHP 65
 QY 68 GTAWSHLEKFFTGTHLSDFKVSEVSKDYRKLAESFKLGFTDKGHTVSTCLASVAVMFL 127
 DB 66 ASTWKMLDKFETGYLKDYSVSESVKYRKLVFEFSKGLYDKKGHIMFATLCFIAMLFA 125
 QY 128 IVLYGRLCTSVNAHLGSGMLGLLMMQSAVGHDSGHVYVMTNGNKAQIISGNCIT 187
 DB 126 MSYGVLFCEGVVHLFPGCLMGFLMTQSGWIGHDGHVWVSDSLNKFMGIFAANCIS 185
 QY 188 GISIAWKKWTHNAHITACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 247
 DB 186 GISIAWKKWTHNAHITACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 245
 QY 248 LICVGHFTFYVNCVAVNLVYQITILLFSRRKVQDRAINIGILVFWTFFPLVSCLPN 307
 DB 246 FVSGQWHTFPIPCARLNNVYVSLIMLTRKNSYRAQELGCLVFSIWPPLVSCLPN 305
 QY 308 WPERVWFVLASFAVCSIQHIOFCLNHPAANYVGPSPGNDWFEKQISGTLDISCASMDW 367
 DB 306 WGERIMFVLASLSTVGMOQVQFSLNHFSSVYVGKPGKNWFEKQTDGTLDISCPMMDW 365
 QY 368 FFGGLQFQLEHHLFPRPLRCQRLKISPLVSDLCCKNLPYRSLSPFANQMTIRTLRTAA 427
 DB 366 FFGGLQFQLEHHLFPRKPRCNLRKISPLVYELCKKNLPYNYASFANEMTLRTLRNTA 425
 QY 428 LQARDLTNPAPKULMEAVNT 448
 DB 426 LQARDITKPLPKULVMEALHT 446

RESULT 6
 US-08-834-033A-15
 ; Sequence 15, Application US/08834033A
 ; Patent No. 6075183
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; APPLICANT: MUKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
 STREET: 2001 FERRY BUILDING
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,033A
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: WARD, MICHAEL R.
 REGISTRATION NUMBER: 38,651
 REFERENCE/DOCKET NUMBER: CGAB-300.USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-033A-15

Query Match 66.7%; Score 1633; DB 3; Length 446;
 Best Local Similarity 63.0%; Pred. No. 3.5e-171;
 Matches 278; Conservative 78; Mismatches 85; Indels 0; Gaps 0;

QY 8 KKYITSEELGHNKGGDLWISIOGKYVNSDWVKEHGGDVPISNLAGDVTDAFIAYHP 67
 DB 6 KKYITSEELGHNKGGDLWISIOGKAYDSDWVADHGGSPFLKSLAGQVTDAPFAVHP 65
 QY 68 GTAWSHLEKFFTGTHLSDFKVSEVSKDYRKLAESFKLGFTDKGHTVSTCLASVAVMFL 127
 DB 66 ASTWKMLDKFETGYLKDYSVSESVKYRKLVFEFSKGLYDKKGHIMFATLCFIAMLFA 125
 QY 128 IVLYGRLCTSVNAHLGSGMLGLLMMQSAVGHDSGHVYVMTNGNKAQIISGNCIT 187
 DB 126 MSYGVLFCEGVVHLFPGCLMGFLMTQSGWIGHDGHVWVSDSLNKFMGIFAANCIS 185
 QY 188 GISIAWKKWTHNAHITACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 247
 DB 186 GISIAWKKWTHNAHITACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDIARF 245
 QY 248 LICVGHFTFYVNCVAVNLVYQITILLFSRRKVQDRAINIGILVFWTFFPLVSCLPN 307
 DB 246 FVSGQWHTFPIPCARLNNVYVSLIMLTRKNSYRAQELGCLVFSIWPPLVSCLPN 305
 QY 308 WPERVWFVLASFAVCSIQHIOFCLNHPAANYVGPSPGNDWFEKQISGTLDISCASMDW 367
 DB 306 WGERIMFVLASLSTVGMOQVQFSLNHFSSVYVGKPGKNWFEKQTDGTLDISCPMMDW 365
 QY 368 FFGGLQFQLEHHLFPRPLRCQRLKISPLVSDLCCKNLPYRSLSPFANQMTIRTLRTAA 427
 DB 366 FFGGLQFQLEHHLFPRKPRCNLRKISPLVYELCKKNLPYNYASFANEMTLRTLRNTA 425
 QY 428 LQARDLTNPAPKULMEAVNT 448
 DB 426 LQARDITKPLPKULVMEALHT 446

RESULT 7

US-08-834-655-7

; Sequence 7, Application US/08834655

; Patent No. 5968809

; GENERAL INFORMATION:

; APPLICANT: KNOTZON, DEBORAH

; APPLICANT: MURKERT, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,655

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: RAE-VENTER, BARBARA

; REGISTRATION NUMBER: 32,750

; REFERENCE/DOCKET NUMBER: CGNE.124.000S

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 328-4400

; TELEFAX: (650) 328-4477

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-834-655-7

; Query Match 44.5%; Score 1091; DB 2; Length 252;

; Best Local Similarity 74.9%; Pred. No. 8e-112;

; Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVRCTSVMAHLGSGMLGLIMWQSAVYGHDSGHVYVMTTNGFNKVAQILSGNCLTG 188
DB 2 VLVGVLACTSVFHAQIAALLGLIMQSAVYIGHDSGHVYVMTTNGFNKVAQILSGNCLTG 61
QY 189 ISIAAMKMTNNAHIAACNSLDHPDLOHMPVFAVSSRFNSISHPYGRLEDFIARFL 248
DB 62 ISIAAMKMTNNAHIAACNSLDHPDLOHMPVFAVSTKFFSSLSRKYDRKLTGCPVARFL 121
QY 249 ICYQHTFFYPVNCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWPPLVSCLPNW 308
DB 122 VSYQHFTYYPVNCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWPPLVSCLPNW 181
QY 309 PERVMVVLASFAVCSIQHIOFCINHPAANYVGPBGNDWFEEKQSGTLDISCASSMDWF 368
DB 182 PERFFVFTSFTYALQHIQFTLNHPADVYVGPBGNDWFEEKQAGTIDISCRSYMDWF 241
QY 369 FGGLOPQLEHH 379
DB 242 FGGLOPQLEHH 252

RESULT 8

US-08-834-033A-8

; Sequence 8, Application US/08834033A

; Patent No. 6075183

; GENERAL INFORMATION:

; APPLICANT: KNOTZON, DEBORAH

; APPLICANT: MURKERT, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,033A

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-300.USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-834-033A-8

; Query Match 44.5%; Score 1091; DB 3; Length 252;

; Best Local Similarity 74.9%; Pred. No. 8e-112;

; Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVRCTSVMAHLGSGMLGLIMWQSAVYGHDSGHVYVMTTNGFNKVAQILSGNCLTG 188
DB 2 VLVGVLACTSVFHAQIAALLGLIMQSAVYIGHDSGHVYVMTTNGFNKVAQILSGNCLTG 61
QY 189 ISIAAMKMTNNAHIAACNSLDHPDLOHMPVFAVSSRFNSISHPYGRLEDFIARFL 248
DB 62 ISIAAMKMTNNAHIAACNSLDHPDLOHMPVFAVSTKFFSSLSRKYDRKLTGCPVARFL 121
QY 249 ICYQHTFFYPVNCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWPPLVSCLPNW 308
DB 122 VSYQHFTYYPVNCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWPPLVSCLPNW 181
QY 309 PERVMVVLASFAVCSIQHIOFCINHPAANYVGPBGNDWFEEKQSGTLDISCASSMDWF 368
DB 182 PERFFVFTSFTYALQHIQFTLNHPADVYVGPBGNDWFEEKQAGTIDISCRSYMDWF 241
QY 369 FGGLOPQLEHH 379
DB 242 FGGLOPQLEHH 252

RESULT 9

US-09-363-574-7

; Sequence 7, Application US/09363574

Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-7

Query Match 44.5%; Score 1091; DB 3; Length 252;
Best Local Similarity 74.9%; Pred. No. 8e-112;
Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVLRCTSVMAHLGSGMLLGLIMQSAVYVGHDSGHVYVMTTNGPKVAQILSGNCLTG 188
DB 2 VLVGVLACTSVFAHQIAALLGLIMIQSAVYIGHDSGHVYVMTSNGSYNRFAGQLLSGNCLTG 61
QY 189 ISIAMKMTNNAHHAICNSLDHDPDLOHMPVFAVSSRFNSITSHFGKLEFDFIARFL 248
DB 62 ISIAMKMTNNAHHAICNSLDYDPDLOHMPVFAVSTKFFSLSRPFDRKLTGCPVARFL 121
QY 249 ICYQHFTEYVPMCVARVNLVLOTLLFSRRKQODRALNIMGILVFWTWPEPLVSCLPNW 308
DB 122 VSYQHFTEYVPMCVARVNLVLOTLLFSRRKQODRALNIMGILVFWTWPEPLVSCLPNW 181
QY 309 PERVMFLASFAVCSIOHIOFCLNHPAANYVGPSPGNDMEFEKOTSGTLDISCASSNDWF 368
DB 182 PERFFVFTSFTYALOHIOFTLNHPADVYVGPPTGSDMEFEKQAGTIDISCRSYNDWF 241
QY 369 FGGILOFQLEHH 379
DB 242 FGGILOFQLEHH 252

RESULT 10
US-09-363-526-7
Sequence 7, Application US/09363526
Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-7

Query Match 44.5%; Score 1091; DB 4; Length 252;
Best Local Similarity 74.9%; Pred. No. 8e-112;
Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVLRCTSVMAHLGSGMLLGLIMQSAVYVGHDSGHVYVMTTNGPKVAQILSGNCLTG 188
DB 2 VLVGVLACTSVFAHQIAALLGLIMIQSAVYIGHDSGHVYVMTSNGSYNRFAGQLLSGNCLTG 61
QY 189 ISIAMKMTNNAHHAICNSLDHDPDLOHMPVFAVSSRFNSITSHFGKLEFDFIARFL 248
DB 62 ISIAMKMTNNAHHAICNSLDYDPDLOHMPVFAVSTKFFSLSRPFDRKLTGCPVARFL 121
QY 249 ICYQHFTEYVPMCVARVNLVLOTLLFSRRKQODRALNIMGILVFWTWPEPLVSCLPNW 308
DB 122 VSYQHFTEYVPMCVARVNLVLOTLLFSRRKQODRALNIMGILVFWTWPEPLVSCLPNW 181
QY 309 PERVMFLASFAVCSIOHIOFCLNHPAANYVGPSPGNDMEFEKOTSGTLDISCASSNDWF 368
DB 182 PERFFVFTSFTYALOHIOFTLNHPADVYVGPPTGSDMEFEKQAGTIDISCRSYNDWF 241
QY 369 FGGILOFQLEHH 379
DB 242 FGGILOFQLEHH 252

RESULT 11
US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,655
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.124.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-2

Query Match 20.5%; Score 502.5; DB 2; Length 457;

Best Local Similarity 30.2%; Pred. No. 1.5e-46;
 Matches 130; Conservative 72; Mismatches 191; Indels 37; Gaps 11;

11 ITSEELKGNK--EGDLWISIGKYNVSDWKEHGGVPSINLGGVDTDAFIAYHPG 68
 16 LNAEALNEGKKAEPFLMIIDNKYDVAREFVDPHGGSVILTHV-GKSGTDFDTFHP 74
 69 TAWSHLEKFTG--YHLSDFKVSXKDYRKLASFSKGLFDTKGHTSCTLASAVAM 125
 75 AAMETLANFYVGDIIDSDRDIKNDDFAAEVRKRTLFQSLGYVD-----SSKAYVAFKVS 129
 126 FLIVLYGVLR-----TSVAHLGSGMLGLIMQSAVYVGHDSGHVYVMTTNGRNKA 178
 130 FNLCTWGLSTVIVAKKGOTSTLANVLSAALLGLFWQCCGMLADFLHGVFQDRFGDLF 189
 179 QILSGNCLGSIAMWKMTNNAHIAICNSLDHDPDLQHPVFAVSS---RFFNSITSHFY 235
 190 GAFLGVCVCGFSSSWMKDKNTNHAAPNVHGEDPDIOTHPLLTWSHALEMFSVDVDEEL 249
 236 GRKLEDFIARFLICYOHTFYVPMCVARNLYLTITLLF-----SRKRVDRALN 287
 250 TR-----MMSRFVNLQGTWTFYFPLISFARLSWCLQSLFLVLPNGQAHKSGARVPISLVE 304
 288 IMKILFTWTFPLVLSCLPNWP-ERVMFVLASFAVC-SIOHIOFCLNHPAANYVGPSPG 345
 305 QSLAHMTWYLTATMPLFIKDPVNMVLYPLVSAVCGNLATIVFSINHGMPVISEEAV 364
 346 N-DWPKQTSGLDISGASSMDFPGSLQRLSHHLFPRLPBRCQAKISPLVSDLCRKN 404
 365 DMDFETKQIITGADVHGLFANMFTEGLNQTIEHHLFSPMPRNFSTKIQPAVETLCKKN 424
 405 LPYRSLSFWE 414

DB 425 VRYHTTGME 434

RESULT 12

US-08-834-033A-2
 Sequence 2, Application US/08834033A

Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNUTZON, DEBORAH

APPLICANT: MIKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,033A

FILING DATE: 11-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-300.USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 20.5%; Score 502.5; DB 3; Length 457;

Best Local Similarity 30.2%; Pred. No. 1.5e-46;
 Matches 130; Conservative 72; Mismatches 191; Indels 37; Gaps 11;

11 ITSEELKGNK--EGDLWISIGKYNVSDWKEHGGVPSINLGGVDTDAFIAYHPG 68
 16 LNAEALNEGKKAEPFLMIIDNKYDVAREFVDPHGGSVILTHV-GKSGTDFDTFHP 74
 69 TAWSHLEKFTG--YHLSDFKVSXKDYRKLASFSKGLFDTKGHTSCTLASAVAM 125
 75 AAMETLANFYVGDIIDSDRDIKNDDFAAEVRKRTLFQSLGYVD-----SSKAYVAFKVS 129
 126 FLIVLYGVLR-----TSVAHLGSGMLGLIMQSAVYVGHDSGHVYVMTTNGRNKA 178
 130 FNLCTWGLSTVIVAKKGOTSTLANVLSAALLGLFWQCCGMLADFLHGVFQDRFGDLF 189
 179 QILSGNCLGSIAMWKMTNNAHIAICNSLDHDPDLQHPVFAVSS---RFFNSITSHFY 235
 190 GAFLGVCVCGFSSSWMKDKNTNHAAPNVHGEDPDIOTHPLLTWSHALEMFSVDVDEEL 249
 236 GRKLEDFIARFLICYOHTFYVPMCVARNLYLTITLLF-----SRKRVDRALN 287
 250 TR-----MMSRFVNLQGTWTFYFPLISFARLSWCLQSLFLVLPNGQAHKSGARVPISLVE 304

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:37:05 ; Search time 85.7267 Seconds
(without alignments)
1053.214 Million cell updates/sec

Title: US-09-857-524B-8

Perfect score: 2449
Sequence: 1 MEVVEKEKKYITSEELKGNH.....RDLTPAPKLLMEAVNTHG 450

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US09C_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1801	73.5	458	US-10-340-779A-11	Sequence 11, Appl1
2	1712	69.9	452	US-10-029-756-27	Sequence 27, Appl1
3	1655	67.6	448	US-10-340-779A-13	Sequence 13, Appl1
4	1650	67.4	448	US-10-029-756-5	Sequence 5, Appl1
5	560.5	22.9	366	US-10-369-493-4137	Sequence 4137, Ap
6	518.5	21.2	459	US-09-967-477B-8	Sequence 8, Appl1
7	516	21.1	453	US-09-769-863-14	Sequence 14, Appl1
8	516	21.1	453	US-10-054-534B-14	Sequence 14, Appl1
9	516	21.1	453	US-10-431-952-14	Sequence 14, Appl1
10	502.5	20.5	457	US-10-278-391-4	Sequence 4, Appl1
11	502.5	20.5	458	US-10-191-513A-11	Sequence 11, Appl1
12	502.5	20.5	458	US-10-191-513A-41	Sequence 41, Appl1
13	436	17.8	445	US-10-262-617-1	Sequence 1, Appl1
14	429	17.5	444	US-10-262-617-3	Sequence 3, Appl1
15	425	17.4	444	US-10-191-513A-12	Sequence 12, Appl1

16	422.5	17.3	432	US-10-191-513A-9	Sequence 9, Appl1
17	422.5	17.3	465	US-10-191-513A-38	Sequence 38, Appl1
18	419	17.1	443	US-10-340-779A-20	Sequence 20, Appl1
19	418.5	17.1	444	US-10-191-513A-42	Sequence 42, Appl1
20	401	16.4	473	US-10-369-493-6108	Sequence 6108, Ap
21	364	14.9	448	US-10-340-779A-4	Sequence 4, Appl1
22	363.5	14.8	323	US-10-191-513A-17	Sequence 17, Appl1
23	361	14.7	454	US-10-369-493-6107	Sequence 6107, Ap
24	345	14.1	439	US-09-967-477B-4	Sequence 4, Appl1
25	343.5	14.0	470	US-09-769-863-20	Sequence 20, Appl1
26	343.5	14.0	470	US-10-054-534B-20	Sequence 20, Appl1
27	343.5	14.0	470	US-10-431-952-20	Sequence 20, Appl1
28	312	12.7	456	US-09-967-477B-6	Sequence 6, Appl1
29	303.5	12.4	365	US-10-156-761-9835	Sequence 9835, Ap
30	297	12.1	456	US-10-054-534B-33	Sequence 33, Appl1
31	293.5	12.0	430	US-10-120-637A-69	Sequence 69, Appl1
32	293.5	12.0	443	US-10-120-637A-55	Sequence 55, Appl1
33	293	12.0	442	US-10-054-534B-35	Sequence 35, Appl1
34	287.5	11.7	439	US-10-054-534B-31	Sequence 31, Appl1
35	286.5	11.7	353	US-10-156-761-9130	Sequence 9130, Ap
36	285.5	11.7	439	US-09-769-863-29	Sequence 29, Appl1
37	285.5	11.7	439	US-10-054-534B-29	Sequence 29, Appl1
38	285.5	11.7	439	US-10-431-952-29	Sequence 29, Appl1
39	284.5	11.6	287	US-10-191-513A-14	Sequence 14, Appl1
40	284.5	11.6	288	US-10-191-513A-15	Sequence 15, Appl1
41	282.5	11.5	446	US-10-340-779A-3	Sequence 3, Appl1
42	282.5	11.5	446	US-10-340-779A-14	Sequence 14, Appl1
43	282	11.5	360	US-10-191-513A-39	Sequence 39, Appl1
44	273.5	11.2	446	US-09-903-456-30	Sequence 30, Appl1
45	273.5	11.2	446	US-10-278-391-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-340-779A-11
: Sequence 11, Application US/10340779A
: Publication No. US20030152983A1
: GENERAL INFORMATION:
: APPLICANT: Napier, Johnathan A.
: APPLICANT: Michaelson, Louise
: APPLICANT: Stobart, Keith
: TITLE OF INVENTION: Desaturase
: FILE REFERENCE: 005407.00004
: CURRENT APPLICATION NUMBER: US/10/340.779A
: CURRENT FILING DATE: 2003-03-24
: PRIOR APPLICATION NUMBER: US 09/582,034
: PRIOR FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: PCT/GB96/03895
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: UK 9814034.6
: PRIOR FILING DATE: 1998-06-29
: PRIOR APPLICATION NUMBER: UK 9727256.1
: PRIOR FILING DATE: 1997-12-23
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11
: LENGTH: 458
: TYPE: PRT
: ORGANISM: Helianthus annuus
: US-10-340-779A-11
Query Match 73.5%; Score 1801; DB 12; Length 458;
Best Local Similarity 71.6%; Pred. No. 1.5e-174;
Matches 317; Conservative 55; Mismatches 71; Indels 0; Gaps 0;

Query 8 KKYITSEELKGNHKEGDIWISIOGKYVNVSDWYKREHGGVPSNLAGOVDTAFIVHP 67
DB 16 KKYITSEELKGNHNPDLWISIGKYVNVEMAKHGGAPLNLNLAGOVDTAFIVHP 75
Query 68 GTAWSHLEKFTGYHLSDFKVSSEVSKDYRLKASEFSLGLPDTKGHTSCTLASAVAVFL 127

Db 76 GTAMKHLDKLFTGYHLKDYOVSDISRDYKRLASEFAKAGFEKKHGVYSLCFVSLLS 135
 QY 128 ILYGVLRCTSVMAHLGSGMLLGLLWMSAYVGHDSGHVYVMTTNGFNKVAQILSGNCLT 187
 Db 136 ACYGVGLVSSGFYIMHLSGAILGLAMQALYLGHDGCHYQMMATRGKNGAGIFIGNCIT 195
 QY 188 GISIAWMTNNAHIAACNSLDHDPDLQHPMPVAVSSRFNSITSHFYGRKLEPFIARF 247
 Db 196 GISIAWMTNNAHIAACNSLDYDPLQHLPMALVSSKLFNSITSVFYGRQLFDFPLARF 255
 QY 248 LICYGFTFPPVNCVAVNLYLQTLILLFSSRKVODRALNMGILVFWTFPLVSCLPN 307
 Db 256 FVSYQHYLYPIPCVAVNLYLQTLILLSKRXIPRGILNLTLLFTWTFPLVSRLPN 315
 QY 308 WPERVWFLVASFVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 367
 Db 316 WPERVWFLVASFVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 375
 QY 368 FFGGLQFQLEHHLFPRLPRLCQRLKISPLVSDLCCKHNLPRYSLSFWEANQMTIRTLRTA 427
 Db 376 FFGGLQFQLEHHLFPRLPRLCQRLKISPLVSDLCCKHNLPRYSLSFWEANQMTIRTLRTA 435
 QY 428 LQARDLTNPAPKULWEAVNTHG 450
 Db 436 LQARDLTNPAPKULWEAVNTHG 458

RESULT 2

US-10-029-756-27
 ; Sequence 27, Application US/10029756
 ; Publication No. US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/029,756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 452 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-10-029-756-27

Query Match 69.9%; Score 1712; DB 14; Length 452;

Best Local Similarity 69.6%; Pred. No. 1.7e-165;
 Matches 311; Conservative 54; Mismatches 78; Indels 4; Gaps 4;

QY 8 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHPPGSDVPSINAGODVDAFIAYHP 67
 Db 6 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHPPGSDVPSINAGODVDAFIAYHP 65
 QY 68 GTAMSHLEKFTG-YHLSDPKVSEVSKDYRKLASEFSKGLPDTKGHTVSCITLASVAVNF 126
 Db 66 GTAMSHLEKFTG-YHLSDPKVSEVSKDYRKLASEFSKGLPDTKGHTVSCITLASVAVNF 125
 QY 127 LILYGVLRCTSVMAHLGSGMLLGLLWMSAYVGHDSGHVYVMTTNGFNKVAQILSGNCL 186
 Db 126 LILYGVLRCTSVMAHLGSGMLLGLLWMSAYVGHDSGHVYVMTTNGFNKVAQILSGNCL 185
 QY 187 TGSIAMWKTNNAHIAACNSLDHDPDLQHPMPVAVSSRFNSITSHFYGRKLEPFIARF 246
 Db 186 TGSIAMWKTNNAHIAACNSLDYDPLQHLPMALVSSKLFNSITSVFYGRQLFDFPLARF 245
 QY 247 FLICYGFTFPPVNCVAVNLYLQTLILLFSSRKVODRALNMGILVFWTFPLVSCLPN 306
 Db 246 FLICYGFTFPPVNCVAVNLYLQTLILLFSSRKVODRALNMGILVFWTFPLVSCLPN 305
 QY 307 WPERVWFLVASFVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 366
 Db 306 WPERVWFLVASFVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 365
 QY 367 WFGGLQFQLEHHLFPRLPRLCQRLKISPLVSDLCCKHNLPRYSLSFWEANQMTIRTLRT 425
 Db 366 WFGGLQFQLEHHLFPRLPRLCQRLKISPLVSDLCCKHNLPRYSLSFWEANQMTIRTLRT 425
 QY 426 AALQARDLTNPAPKULWEAVNTHG 450
 Db 426 AALQARDLTNPAPKULWEAVNTHG 452

RESULT 3

US-10-340-779A-13
 ; Sequence 13, Application US/10340779A
 ; Publication No. US20030152963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Napier, Johnathan A.
 ; APPLICANT: Michaelson, Louise
 ; APPLICANT: Stobart, Keith
 ; TITLE OF INVENTION: Desaturase
 ; FILE REFERENCE: 005407, 00004
 ; CURRENT APPLICATION NUMBER: US/10/340,779A
 ; CURRENT FILING DATE: 2003-03-24
 ; PRIOR APPLICATION NUMBER: US 09/582,034
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: PCT/GS98/03895
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: UK 9814034.6
 ; PRIOR FILING DATE: 1998-06-29
 ; PRIOR APPLICATION NUMBER: UK 9727256.1
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PaasSEQ for windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Borego officinalis
 US-10-340-779A-13

Query Match 67.6%; Score 1655; DB 12; Length 448;
 Best Local Similarity 63.4%; Pred. No. 1.1e-159;
 Matches 281; Conservative 78; Mismatches 84; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHPPGSDVPSINAGODVDAFIAYHP 67
 Db 6 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHPPGSDVPSINAGODVDAFIAYHP 65
 QY 68 GTAMSHLEKFTG-YHLSDPKVSEVSKDYRKLASEFSKGLPDTKGHTVSCITLASVAVNF 127

APPLICANT: Dae, Tapas
 APPLICANT: Thurmond, Jennifer M.
 APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 FILE REFERENCE: 6763 US.P1
 CURRENT APPLICATION NUMBER: US/10/054,534B
 CURRENT FILING DATE: 2002-01-22
 PRIOR APPLICATION NUMBER: US 09/769,863
 PRIOR FILING DATE: 2001-01-25
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 453
 TYPE: PRT
 ORGANISM: Saprolegnia diclina
 US-10-054-534B-14

Query Match 21.1%; Score 516; DB 12; Length 453;
 Best Local Similarity 29.0%; Pred. No. 1.2e-43;
 Matches 128; Conservative 89; Mismatches 174; Indels 50; Gaps 13;

QY 5 EKEKYYTSELKGNKKGDMISIQKVVNSDVKVKEHFGDVPISNLAGQVTDAPFA 64
 DB 5 QKAEK-ISMATIRREHNRQDNAMIVIHKKVYDISAF-EDHPGVVMTQ-AGEDATDAFAV 61
 QY 65 YHPGTAMSHLEKFTG-----YHLSDFKVSSEVK-----DYRKLASSEFKLGL 107
 DB 62 FHPSSALKLEQYVGVGDOSTAIVDTISD---EVKQSQSDFIASRKLRLVKKLGL 117
 QY 108 FDTKGVHTSCTLASVAVMFLIVLVLRCTSVMAHLSGMLGLMMQSAVYVGHSGHYV 167
 DB 118 YDSKLYLVKCASTLSIALVSAIICLHFDSTAMVVAVILGLFYQCCGLMHLDFLHQ 177
 QY 168 VMTNGNKNVQAQLISGNCITGSIAMWKTNNAHIACN-----SLDHPDLOHMPVF 220
 DB 178 VFENHLFGDLVGVVGNLMQGSVQWKKNGNTHAIPNLATPELAFHGDPIDITWPI 237
 QY 221 AVSRFPNSITSHFYGRKLEPFIARFLICYQHTFYPVNCVARNVYLQITILLF---- 276
 DB 238 AMSLK-----MAQHAVDSP-----VGLFPMRYQVLYPILLFARISVWISAMAFYVNG 288
 QY 277 ---SRKVVQDRAINIMGILVFWTW-FPLVSCLPNMPERVMFVLASPAVCSI-OHIOFCL 331
 DB 289 PGCFDVKVQVPLERAGLLIYGNLGLVYAANMSLLQAAFLFVSQASGCLFLAMVFSV 348
 QY 332 NHFAANYVGPSPGNDWEKQTSGLDSCASSNDWFFGGLQFQLEHHLFRLPRCOLRK 391
 DB 349 GHNGMEVF-DKDSKPFQWKLQVLSRNVTSLSLWDFWGGIANYQIDHLLFPMVPRHNLPA 407
 QY 392 ISPLVSDLCCKKHLPYRSLSF 412
 DB 408 LNVLVKSLCKQYDIPYHETGF 428

RESULT 9
 US-10-431-952-14
 Sequence 14, Application US/10431952
 Publication No. US20030190733A1

GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pradip
 APPLICANT: Huang, Yung-sheng
 APPLICANT: Dae, Tapas
 APPLICANT: Thurmond, Jennifer
 APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 FILE REFERENCE: 6763 US.O1
 CURRENT APPLICATION NUMBER: US/10/431,952
 CURRENT FILING DATE: 2003-05-08
 PRIOR APPLICATION NUMBER: US/09/769,863
 PRIOR FILING DATE: 2001-01-25
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 14
 LENGTH: 453
 TYPE: PRT
 ORGANISM: Saprolegnia diclina
 US-10-431-952-14

Query Match 21.1%; Score 516; DB 12; Length 453;
 Best Local Similarity 29.0%; Pred. No. 1.2e-43;
 Matches 128; Conservative 89; Mismatches 174; Indels 50; Gaps 13;

QY 5 EKEKYYTSELKGNKKGDMISIQKVVNSDVKVKEHFGDVPISNLAGQVTDAPFA 64
 DB 5 QKAEK-ISMATIRREHNRQDNAMIVIHKKVYDISAF-EDHPGVVMTQ-AGEDATDAFAV 61
 QY 65 YHPGTAMSHLEKFTG-----YHLSDFKVSSEVK-----DYRKLASSEFKLGL 107
 DB 62 FHPSSALKLEQYVGVGDOSTAIVDTISD---EVKQSQSDFIASRKLRLVKKLGL 117
 QY 108 FDTKGVHTSCTLASVAVMFLIVLVLRCTSVMAHLSGMLGLMMQSAVYVGHSGHYV 167
 DB 118 YDSKLYLVKCASTLSIALVSAIICLHFDSTAMVVAVILGLFYQCCGLMHLDFLHQ 177
 QY 168 VMTNGNKNVQAQLISGNCITGSIAMWKTNNAHIACN-----SLDHPDLOHMPVF 220
 DB 178 VFENHLFGDLVGVVGNLMQGSVQWKKNGNTHAIPNLATPELAFHGDPIDITWPI 237
 QY 221 AVSRFPNSITSHFYGRKLEPFIARFLICYQHTFYPVNCVARNVYLQITILLF---- 276
 DB 238 AMSLK-----MAQHAVDSP-----VGLFPMRYQVLYPILLFARISVWISAMAFYVNG 288
 QY 277 ---SRKVVQDRAINIMGILVFWTW-FPLVSCLPNMPERVMFVLASPAVCSI-OHIOFCL 331
 DB 289 PGCFDVKVQVPLERAGLLIYGNLGLVYAANMSLLQAAFLFVSQASGCLFLAMVFSV 348
 QY 332 NHFAANYVGPSPGNDWEKQTSGLDSCASSNDWFFGGLQFQLEHHLFRLPRCOLRK 391
 DB 349 GHNGMEVF-DKDSKPFQWKLQVLSRNVTSLSLWDFWGGIANYQIDHLLFPMVPRHNLPA 407
 QY 392 ISPLVSDLCCKKHLPYRSLSF 412
 DB 408 LNVLVKSLCKQYDIPYHETGF 428

RESULT 10
 US-10-278-391-4

Sequence 4, Application US/10278391
 Publication No. US20030159164A1
 GENERAL INFORMATION:

APPLICANT: KOPCHIK, JOHN J.
 KELLER, BRUCE
 HUANG, YUNG-SHENG
 KIRCHNER, STEPHEN J.
 MUKERJI, PRADIP

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
 PRODUCTS

NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 MONTGOMERY STREET, SUITE 2200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/278,391
 FILING DATE: 23-Oct-2002
 CLASSIFICATION: 800

NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (458)...(458)
OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41

Query Match 20.5%; Score 502.5; DB 15; Length 458;
Best Local Similarity 30.2%; Pred. No. 2.9e-42;
Matches 130; Conservative 72; Mismatches 191; Indels 37; Gaps 11;

QY 11 ITSEELKHNK--BEDLMISIQKYYNSDWKKEHFGDVPISNLAGDVTDAFLAHYH 68
DB 16 LNAELNKGKDAEPFLMIIDNKYDREVPDPHGGSVILITHV-GDGDVDVDFTHPE 74
QY 69 TAWSHLEKFTG---YHLSDFKVSSEKDYRKLAESFSLGLPDTKHVTSCTLASVAVM 125
DB 75 AAMETLANFYGGDDIDSDRDIKNDDFAAEVRKRLTLFQSLGYD---SKAYYAFKVS 129
QY 126 FLIVLYGLRC-----TSVAHLGSGMLLGLMMOGAYVGHDSGHVYVVTNGFNKVA 178
DB 130 FNLCTWGLSTIVAKMGQSTLANVLSAALLGLFQCGGWLADHLHHQVQDRFWGDLF 189
QY 179 QILGNCITGISIMWKTHNAHHIACNSLDHDPDLOHMPVAVS---RFPNITSHFY 235
DB 190 GATLGVCQGGSSSMWKDKNTHAARVNHGEDPDIHPLLTSEHALEMFSVDPBEL 249
QY 236 GRKLEPFIARFL-ICYHFTFY--PVNVCARVNLVLOTILLF-----SRKYQDRALN 287
DB 250 TR-----MMSFMYLNTQTFYFPLISFARLSWCQSLFVLPNGOAHKPSGARPLISVE 304
QY 288 IMGILVFTWPEPLVLSCLPNP-ERVMFVLASFAVC-SIOHIOPLNHPAANVYVGPSPG 345
DB 305 QLSLHMWTYLTATMFLFIKDPVNNLVYELVSOAVCGMLAIVSLNNGMPVLSKEAV 364
QY 346 N-DWFEKOTSTLDISCASSMDWFFGGLQFQLEHHLFRLRCQRLKISPLVSLCKKN 404
DB 365 DMDFETKQIITGRDVHPLGFANWFQGLNLYQIEHLLFSPMRHNSFKIQPAVELTCKKN 424
QY 405 LPYRSLSEWE 414
DB 425 VRYHTGMIE 434

RESULT 13

US-10-262-617-1
Sequence 1, Application US/10262617
Publication No. US2003007747A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
FILE REFERENCE: PP-0494-1 DIV
CURRENT APPLICATION NUMBER: US/10/262.617
PRIORITY FILING DATE: 2002-09-30
PRIORITY FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CD1

US-10-262-617-1

Query Match 17.8%; Score 436; DB 15; Length 445;
Best Local Similarity 28.4%; Pred. No. 1.7e-35;
Matches 127; Conservative 65; Mismatches 179; Indels 76; Gaps 15;

QY 14 EELGNKREGDLMISIQKYYNSDWKKEHFGDVPISNLAGDVTDAFLAHYHGTAWSH 73
DB 26 EQLAHQDPGDKMLVIRRAYDISRWAOHGGSRLLGHGAEDATDAFRAHQDL--NF 83
QY 74 LEKFTGHLSDFFVSEVS-----KDYRKLAESFSLGLPDK-----GHVT 115
DB 84 VRKFLQPLLIGLAEPSQDGPINAOVLVEDFRALHOAEDMKLFDSPTFEFLGHIL 143
QY 116 SCLTASVAVMFLVLYGLVLAICTSVMAHLGSGMLLGLMMOGAYVGHDSGHVYVVTNGFN 175
DB 144 A--MEVAMLLIYLLPQGVPSALA---AFITAIQAOQSWCQHDHGHASIFKRSWN 196
QY 176 KVAQILGNCITGISIMWKTHNAHHIACNSLDHDPDLOHMPVAVSRRFNSITSHFY 235
DB 197 HVAQKFMGQKGFSAHMANFRHQHAKNIFPKDQDVTAAPVFLGE-----SSVEY 250
QY 236 GRKLEPFIARFL-ICYHFTFY--PVNVCARVNLVLOTILLFRRKXQDRALNMG 290
DB 251 GKRR-----RYLPYNOQHLYFFLIGPLTL--VNEVE-----MLAY 287
QY 291 ILVFWTWPEPL-----VSCLPNM--PERVMFVLASFAVCSIOHIOPLNHPAAN 337
DB 288 MLVCMQADLLMAASFAARFPLSLTPPYGVGVLFVAAVAVLSHFWITQNHLPKE 347
QY 338 VYVGPSPGNDWFEKOTSTLDISCASSMDWFFGGLQFQLEHHLFRLRCQRLKISPLV 397
DB 348 --IGHEHGRWVSSQLATCNVBSLFTNWFSGHLNQHIEHLLFRRPRHNSVAVPLV 405
QY 398 DLCKGNLPYRSLSEWEANQTTITLR 424
DB 406 SLCAKHGLSYEVKPFALTALVDIVASLK 432

RESULT 14

US-10-262-617-3
Sequence 3, Application US/10262617
Publication No. US2003007747A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
FILE REFERENCE: PP-0494-1 DIV
CURRENT APPLICATION NUMBER: US/10/262.617
PRIORITY FILING DATE: 2002-09-30
PRIORITY FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 444
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CD1
US-10-262-617-3

Query Match 17.5%; Score 429; DB 15; Length 444;
Best Local Similarity 28.3%; Pred. No. 8.7e-35;
Matches 128; Conservative 66; Mismatches 181; Indels 76; Gaps 15;

QY 9 KYITSEELKHNKREGDLMISIQKYYNSDWKKEHFGDVPISNLAGDVTDAFLAHYH-- 66
DB 18 RYFTWDEVAORSQGEERMLVIDRKVYNISFTRRHHPGSSVISHYACQDATDPVAFHIN 77


```

QY      67  PGLAMSHLEKPEFTGY-----HLSDPKYSEVSDRYKLASEPSKGLPFTKGHVTSCTLA 120
Db      78  KGLVKKYKNNSLILIGELSPBQSPSEFPETKKNELTDEFELNATYERKML-----MK 126
QY      121  SVAWVELLYLVGVLNC-----TSVAHLGSGMLLGLLWMOQSAVVGDSGHVYV 168
Db      127  ANHVFFLLYLHLIILLDDGAAMLTLMVFGTSPFLPFLCAVLVLSAVQAGMLQHDPFHLISV 186
QY      169  MTNGFNKVAQILSGNCLTGISIAWKKYTHNAHLICNSLDHDPDLOHNPV-FVSSRF 227
Db      187  FSTSKWNHLHHFVLIGHLKGABASWNNHNFQHNKPCFRKDPDINMHPFSPAL----- 241
QY      228  NSITSHFYGRKLEPDFIARFL-ICYOHFFFYPMCAVNNLYQTLILLF--SRKAVODR 284
Db      242  GKLSVEIGKQKK-----KMYEPYNOHKYFELIGRPALLPLFYQWYIFFYVIOKKWVDI 296
QY      285  ALNI-MGILVFWTWEPPL-----VSCI-PNMPSRVMEVLASPAVCSIOHTQFCI 331
Db      297  AMMIFYYRFFLITYPPLGLKAKAFLGLFYVRFLEBSW-----FVW-----VTQNNHLPNH 347
QY      332  NHFAANVYVGPSSGNDWEFEKQTSGLDIDISCASSMDWFEGLOFOLEHHLPRLLPRCOLRX 391
Db      348  DH-----DRNMDWVSTQLQATCNVYKSAFNDFSGHLNFQIEHHLFPTPRRNYHK 398
QY      392  ISPLVSDLCCKGHNLPRSLSFWEANQWTRTLR 424
Db      399  VAPLVQSLCAKRGIEYQSKPPLISAPADIIHSK 431

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Oy      169 MTNNGNKVAQILSGNCLTGISIAWMKMTYNAHHIACNSLDHDEDLQHMPEFAVSSRFN 228
      187 FTSISKNNHLHHFVIGHLKGAPASWMMNMHQHAKRCPFKDDIDMHPFFALGKILS 246
Oy      229 SITSHFYGRKLEFDFIARFLICYQHTEYPVWCVARVNLQTLILLF--SRKKVODRAL 286
      247 VELGROKKKXMYM-----HQKKYFELLGPALLPLYPQWYIFVFIQRKKWDLAW 298
Oy      287 NI-MGLIVWWTMPRL-----VSCU--PWMPERWMPVLASFVCSIQHIOFCLNH 333
      299 MIFFYRFLLYVPLPLGLKAPLGLFFIYRFLESNM-----FW-----VTQNNHLPWIDH 349
Oy      334 FAANVYVGPSPGNDNPEKOTSGTLDISCASSMDNPFGLQFOLEHNLFPRLPRCOLKIS 393
      350 -----DRNMDVSTQLLATCNVHKSAPNDNPFSGHLNFOIENHLFPTMPRNHYKVA 400
Oy      394 PLVSDLCCKKHNLPYRSLSPFEANQWITIRLR 424
      401 PLVQSLCARKGIEYQSKPLLSAFADIIHSLK 431
Db

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Search completed: January 1, 2004, 06:58:37
Job time : 86.7267 secs

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RESULT 15
US-10-191-513A-12
: Sequence 12, Application US/10191513A
: Publication No. US20030104596A1
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Mukerji, Pardeep
: APPLICANT: Leonard, Amanda E.
: APPLICANT: Huang, Yung-Sheng
: APPLICANT: Tapas, Dae
: TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
: FILE REFERENCE: 6295.US.D3
: CURRENT APPLICATION NUMBER: US/10/191,513A
: CURRENT FILING DATE: 2002-09-25
: PRIOR APPLICATION NUMBER: US 09/227,613
: PRIOR FILING DATE: 1999-01-08
: PRIOR APPLICATION NUMBER: PCT/US98/07422
: PRIOR FILING DATE: 1998-04-10
: PRIOR APPLICATION NUMBER: US 08/833,610
: PRIOR FILING DATE: 1997-04-11
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 444
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-191-513A-12

```

Query Match	17.48; Score 425; DB 15; Length 444;
-------------	--------------------------------------

Best Local Similarity 27.3%; Pred. No. 2.2e-34;
Matches 123; Conservative 67; Mismatches 189; Indels 72; Gaps 12;

```

Qy 9 KYIISBEELGHNKEDGDMWISIOGKYVYNVSDMKHEHGGVDPISNLAGODVTDAFIAYH-- 66
Db 18 RYFTWDEVAORSGCEERMLVIRDKYVNIISEFTRRHGSGRVSISHVAGODATPEVAFHIN 77
Qy 67 PGLAWSHLEKFTGY-----HLSDFKYSVEGDKYKCLASBPSKGLPDTKGHYVSTCLA 120
Db 78 KGLVKKYKYNSSLIGELSPQPSFEPPTKNKELTDFERELATYVERMGL-----WK 126
Qy 121 SVAAWELLVIVGVLC-----TSWAHLGSMULLGLIMWQSAVGHDSGHYV 168
Db 127 ANHVEFLLYLHLIILLDGAAMLTWVFGSPFLFLCAVLISAVQAQSMQLDHPHLSV 186

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:39:42 ; Search time 2065.16 seconds
(without alignments)
16303.117 Million cell updates/sec

Title: US-09-857-524B-16
Perfect score: 823
Sequence: 1 ccccccaaacaccctcgtt.....cgtnaagacttggttagcat 823

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank1:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
7: gb_ph:*
8: gb_pl:*
9: gb_pl:*
10: gb_ro:*
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38: gb_ro:*
39: gb_ro:*
40: gb_ro:*
41: gb_ro:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	531.6	64.6	1788	8	AF031194	AF031194 Triticum
2	272.4	33.1	96312	2	AP005554	AP005554 Oryza sat
3	120.4	14.6	1681	8	AY234124	AY234124 Primula f
4	113.8	13.8	1385	8	AY234126	AY234126 Primula f
5	107	13.0	1618	8	AY234127	AY234127 Primula v
6	106.8	13.0	1702	6	AR200409	AR200409 Sequence
7	98.8	12.0	1410	8	AY234125	AY234125 Primula f
8	95.4	11.6	11000	2	RN52A06_00	BN511200 Rattus no
9	94.8	11.5	1594	6	AX007239	AX007239 Sequence
10	94.8	11.5	1610	6	BN44160	AJ224160 Brassica
11	94.8	11.5	30391	2	AC084799	AC084799 Mus muscu
12	93.6	11.4	840	8	CNS01BNS	AL114464 Botrytis
13	93	11.3	144979	2	AC016280	AC016280 Homo sapi
14	92.6	11.3	108409	14	AF083424	AF083424 Acelline h
15	92.6	11.3	220469	2	AC074307	AC074307 Mus muscu
16	92.2	11.2	2000	8	OSNIA134	X15820 Oryza sativ
17	92.2	11.2	2817	6	AX660410	AX660410 Sequence
18	92.2	11.2	2877	6	AX654602	AX654602 Sequence
19	92.2	11.2	2877	6	AX660148	AX660148 Sequence
20	92.2	11.2	149879	2	AP005381	AP005381 Oryza sat
21	92.2	11.2	163285	2	AP004585	AP004585 Oryza sat
22	92.2	11.2	252689	2	AC079433	AC079433 Mus muscu
23	91.8	11.2	205691	2	AC087227	AC087227 Mus muscu
24	91.4	11.1	77884	2	AC139551	AC139551 Homo sapi
25	91.4	11.1	164751	2	BX293567	BX293567 Danio rer
26	90.6	11.0	300695	2	AC079431	AC079431 Mus muscu
27	90.4	11.0	265537	2	AC087228	AC087228 Mus muscu
28	90	10.9	150695	2	AC023576	AC023576 Homo sapi
29	89.8	10.9	8043	8	AF153448	AF153448 Zea mays
30	89.8	10.9	202083	2	AC023833	AC023833 Mus muscu
31	88.8	10.8	222707	2	AC079425	AC079425 Mus muscu
32	88.6	10.8	81417	2	AC023265	AC023265 Homo sapi
33	88.6	10.8	141892	2	AC023197	AC023197 Mus muscu
34	88.4	10.7	78320	2	AC023212	AC023212 Homo sapi
35	88.2	10.7	75628	2	AC021793	AC021793 Homo sapi
36	88	10.7	110000	2	BX119993_0	BX119993 Mus muscu
37	87.6	10.6	235310	2	AC094274	AC094274 Rattus no
38	87.2	10.6	266935	2	AC144767	AC144767 Mus muscu
39	87	10.6	1080	8	CNS019XP	AL112229 Botrytis
40	86.8	10.5	3163	6	AX647321	AX647321 Sequence
41	86.8	10.5	74138	2	AC021272	AC021272 Homo sapi
42	86.6	10.5	69515	2	AC099971	AC099971 Mus muscu
43	86.6	10.5	76052	2	AC023262	AC023262 Homo sapi
44	86.4	10.5	33058	2	AC100211	AC100211 Mus muscu
45	86.4	10.5	134940	2	AC018939	AC018939 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AF031194 1788 bp mRNA linear PLN 29-JAN-1999
DEFINITION Triticum aestivum S276 (S276) mRNA, complete cde.
ACCESSION AF031194
VERSION AF031194.1 GI:4104055
KEYWORDS
SOURCE
ORGANISM Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticaceae; Triticum.
REFERENCE
AUTHORS Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D.
TITLE Aluminum tolerance in yeast conferred by over-expression of wheat

Pred. No. is the number of results predicted by chance to have a

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
SUBMITTED (23-OCT-1997) Plant Industry, CSIRO, Canberra, ACT 2601, Australia

FEATURES
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1. 1788
Location/Qualifiers
/organism="Triticum aestivum"
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/cultiivar="ET3"
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1. 1788
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121. 1530
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BASE COUNT
321 a 588 c 450 g 429 t

Query Match
Best Local Similarity 93.7%; Pred. No. 3.6e-53;
Matches 609; Conservative 0; Mismatches 31; Indels 10; Gaps 5;

QY 1 CTCCTTAACAACCTCCGCTGCTGTTTAAAGATCCATTCCTCCCTTCCCTCCCTCC 60
DB 7 CTAAACAAACAACTCCGCTGCTGTTTAAAGATCCATTCCTCCCTTCCCTCCCTCC 66
QY 61 CTTCCTCTGAGTCTGACCAACCCCTCTCGCGCTCCAGCTAAATCCAGCCCACTG 120
DB 67 CCTC--CCTTCTCTGACCAACCCCTCTCTGCGCTCCAGCTAAATCCAGCCCACTG 124
QY 121 CCGGCAAGGCTTTCGCGGACGCAACGCGCGGAGCGGACGCAATGCCGCGCGCAGCA 180
DB 125 CCGGCAAGGCTTCGCGGACGCAACGCGCGCGGAGCGGACGCAATGCCGCGCGCAGCA 184
QY 181 AGAAGCGCGCGGACGCTCCGATATCTCCACCAAGAGCTGCGAGCGCGCGCGG 240
DB 185 AGAAGCGCGCGGACGCTCCGATATCTCCACCAAGAGCTGCGAGCGCGCGCGG 244
QY 241 AGAAGCTTGAGATCTCATCTCCGCGGAGCTTACAGAGCTCAGCGCTGCTGCGGACC 300
DB 245 AGAAGCTTGAGATCTCATCTCCGCGGAGCTTACAGAGCTCAGCGCTGCTGCGGACC 304
QY 301 ACCGCGGCGGAGGATCCGCTCATCACCTTCGCGGCGAGGACGCGACGCGCTTCA 360
DB 305 ACCGCGGCGGAGGATCCGCTCATCACCTTCGCGGCGGAGGACGCGACGCGCTTCA 364
QY 361 TGGCTTACACCGCGCTTCCGTGCGCGCGCTCTCCGCGCTTCTTGTGCGCGCGCTCA 420
DB 365 TGGCTTACACCGCGCTTCCGTGCGCGCGCTCTCCGCGCTTCTTGTGCGCGCGCTCA 424
QY 421 CGAGTACATGTGCCCCCGCGCTCGCGGAGCTTCCGCGCGCTCTGCGGAGCTCTCCCT 480
DB 425 CGAGTACATGTGCCCCCGCGCTCGCGGAGCTTCCGCGCGCTCTGCGGAGCTCTCCCT 484
QY 481 CGCGGCGCTCTTGAAGCGGCTCGG--CACACCCCAAGTTCGTGCTGTCGCAAGTCNG 539

DB 485 CCGCGGCGCTCTTGAAGCGGCTCGCGGACGCGGACGCGGACGCGGACGCGGCTCGG 544
QY 540 TGGCTTACACCGCGCTTCTGCGCGCGCTTCTCCGCGCTTCTTGTGCGCGCGCTCA 596
DB 545 TGGCTTACACCGCGCTTCTGCGCGCGCTTCTCCGCGCTTCTTGTGCGCGCGCTCA 604
QY 597 TCGCGGCGGCTCATTCG---CTTATCTGTCAGTTCGCGGCTGATTCGCG 642
DB 605 TCGCGGCGGCTCATTCGCTTCATCTGATTCAGTCAGTCGCGGCTGATTCGCG 654

RESULT 2
AP005554
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) chromosome 9 clone OJ118_A10, *** SEQUENCING IN PROGRESS ***
ACCESSION
AP005554
VERSION
AP005554.1 GI:21952922
KEYWORDS
HTG; HTGS PHASE2.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
SUBMITTED (23-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Sasaki, T., Matsumoto, T., Hattori, M., Sasaki, Y. and Katayose, Y.
Published Only in Database (2002)
Direct Submission
Submitted (23-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel:81-298-38-7441, Fax:81-298-38-7468
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source
1. 96312
Location/Qualifiers
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BASE COUNT
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Query Match
Best Local Similarity 71.3%; Pred. No. 1.5e-23;
Matches 415; Conservative 0; Mismatches 158; Indels 9; Gaps 4;

QY 26 TTTAAGATCCGATCTCCCTTCCGCTTCCCTTCCCTTCTGAGTCTGACACCCC 85
DB 88027 TTTAAGATCCGATCTCCCTTCCGCTTCCCTTCCCTTCTGAGTCTGACACCCC 88086
QY 86 TCTTGGCGCTTCAAGCTTAATTCACGCGCAGATGCGCGGAGGCTTGGCGGACCGCAAC 145
DB 88087 ATCCCGC-CGCAAT 88145
QY 146 GCGCGCGGAGCGGAGCGGCATGAT 205

BASE COUNT	353 a	445 c	404 g	479 t
ORIGIN	<p>14.6%; Score 120.4; DB 8; Length 1681; Best Local Similarity 62.1%; Pred. No. 2.5e-05; Matches 223; Conservative 0; Mismatches 132; Indels 4; Gaps 2; HG"</p>			
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Db	89	ATAACCGACTCAAGACCTGGAAGCCACAMCAAGGACAGTACCATATGATATCAATCAT	148	
QY	264	GGGGAAGCTTACGACGCGACGCCCTGGCTCGGCACACCCGGCGGAGTCCGCTC	323	
Db	149	GGGCAAGCTTACGACGCTCTCTGTGGCGCGCCCTTATCCGGGGGACCGCCCCCTC	208	
QY	324	ATGACCTCGCGCGGACGAGCGCACGCGCCTTACGAGCTTACACACCGCCCTCGTG	383	
Db	209	ATGGCCTCGCAGGACACGACGAGCGAGCTTCTTCTTACATATCCCTTCCACC	268	
QY	384	CGCCCGCTCTCGCGCGCTTCTTGTGCGCGGCTCACCG--ACTACACTGTCCTCC	440	
Db	269	GCCGCTCTCTCCCTCTCTCTCGGCACACTCTCTTACAACTACTCGTCTCCCC	328	
QY	441	GCTTCGCGGACCTTTCGCGCGCTCTGCGGAGCTCTCTCCGGGGCTTGTGAG-CG	499	
Db	329	ACCTCTCGGACGACGCAAACTCTTCACAACTTCATTAACCTGCAGCTTTTCCAGCC	388	
QY	500	CGTCGACACACCCCAAGTCTCGCTCGTCGCAAGTCNGTCTTCTGTGATCGGCT	558	
Db	389	AAATCCACACACACGCTCTTACGTTCTGTGCCATGTATGTTCTTCTCTACGCT	447	
RESULT 4	AY234126 1385 bp mRNA linear PLN 04-MAY-2003			
LOCUS	AY234126			
DEFINITION	Primula vitalii sphingolipid delta-8 desaturase mRNA, complete cds.			
ACCESSION	AY234126			
VERSION	AY234126.1 GI:30350278			
KEYWORDS				
SOURCE				
ORGANISM	Primula vitalii Primula vitalii Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Primulaceae; Primula. 1 (bases 1 to 1385) Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A. Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences(1) FEBS Lett. 542 (1-3), 100-104 (2003) 2 (bases 1 to 1385) Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A. Direct Submission Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK Location/Qualifiers 1..1385 /organism="Primula vitalii" /mol_type="mRNA" /db_xref="taxon:175103" 27..1385 /note="cytochrome b5 fusion desaturase" /codon_start=1 /product="sphingolipid delta-8 desaturase"			
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SOURCE				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
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 LFSRKVPDRFOELFGIGFVPMVPLVSCLPWMSGERIMFVASFVYGIQHPFCIL
 HFSAEVYLGPEGNDMEKOTAGTLNISCSPAMDMEFHGLQFOEHLPLRDLPSOLR
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 HG"

BASE COUNT 294 a 392 c 341 g 358 t

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 Best Local Similarity 60.3%; Pred. No. 0.00015;
 Matches 223; Conservative 0; Mismatches 143; Indels 4; Gaps 2;

QY 204 ATCTCCACCAAGAGCTGACGAGCGCCGCGGACGACCTTGATCTCCATCTCC 263
 DB 63 ATACACGCTCAGACCTGAAAGGCAACAAGGCAAGAAACCTATGATATCAATCCAC 122
 QY 264 GGGGACCTTACGACGCTGAGCCCTGGCTGGCCACACCCGGGCGGAGTCCGCTC 323
 DB 123 GGGGAGGTATACGACGCTGCTCTCGGGCGGCTTCAACCGGGGCGGAGTCCGCTC 182
 QY 324 ATACACCTGCGCGGCGGACGAGCGGCGCTTCAATGAGCTACACCGGCTCTCC 380
 DB 183 ATGGCCCTCGAGACGACGAGTACGAGCTTTCTAGGATATCAATCTCTTCAAC 242
 QY 381 GTGGGCGGCTCTCGCGCGCTTCTGATGCGGCGCTTCAACGACTACATGTCCTCC 440
 DB 243 GCGCGCT 302
 QY 441 GCCTCGCGGCT 499
 DB 303 ACCCTCTCTGACTACCGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 362
 QY 500 CGTGGGACACCCCGCAAGTCTGCTGAGGCAAGTCTCTCTCTCTCTCTCTCTCT 559
 DB 363 AATCCACACCTATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
 QY 560 TACTGCTCTCT 569
 DB 423 TACGGGCTCT 432

RESULT 5
 AY234127 1618 bp DNA linear PLN 04-MAY-2003
 LOCUS Primula viatii fatty acid delta-6 desaturase gene, complete cds.
 DEFINITION AY234127
 ACCESSION AY234127.1 GI:30350280
 VERSION
 KEYWORDS
 ORGANISM
 SOURCE
 Prunella viatii
 Prunella viatii
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Ericales; Primulaceae; Primula.
 1 (bases 1 to 1618)
 Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
 Napier,J.A.
 Identification of Prunella fatty acid Delta(6)-desaturases with n-3
 substrate preferences(1)
 FEBS Lett. 542 (1-3), 100-104 (2003)
 JOURNAL MEDLINE 22615586
 PUBMED 12729906
 2 (bases 1 to 1618)
 Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
 Napier,J.A.
 Direct Submission
 Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
 Research Station, Long Ashton, Bristol BS41 9AF, UK

FEATURES
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 Location/Qualifiers
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 LGHDSGHYRIMSDRKINRFQVLSGNLAI SIAMWNNNAHHLACNSLDYDPLQ
 YIPLVVSDFPNSLTSRFDYRKLFDSVSFLVSYQMSFVPMCLARIMLFAQSPML
 TLFSSREVGRAOEIPLAVFPMVPLVSCLPWMSGERIMFVASFVYGIQHPFCIL
 NHSSDYVGGPVDNMEKOTAGTLNISCSPAMDMEFHGLQFOEHLPLRDLPSOLR
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 THG"

BASE COUNT 396 a 425 c 367 g 430 t

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 Best Local Similarity 65.2%; Pred. No. 0.00091;
 Matches 174; Conservative 0; Mismatches 90; Indels 3; Gaps 1;

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 DB 75 ATACACGCTCAGACCTGAAAGGCAACAAGGCAAGAACTATGATATCAATCCAC 134
 QY 264 GGGGACCTTACGACGCTGAGCCCTGGCTGGCCACACCCGGGCGGAGTCCGCTC 323
 DB 135 GGGGAGGTATACGACGCTGCTCTGAGGCGGCTTCAACCGGGGCGGAGTCCGCTC 194
 QY 324 ATACCTGCGCGGCGGACGAGCGGACGAGCTTCAATGAGCTTCAACCGGCTCT 380
 DB 195 ATGGCCCTCGACGACGACGAGCTGAGCTTCTGAGCTATATCTCTCTCTAC 254
 QY 381 GTGGGCGGCT 440
 DB 255 GCGCGCT 314
 QY 441 GCCTCGCGGACTTCT 467
 DB 315 ACCTCTCTGACTACCGCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 341

RESULT 6
 AR200409 1702 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 26 from patent US 6355861.
 DEFINITION AR200409
 ACCESSION AR200409.1 GI:20250483
 VERSION
 KEYWORDS
 SOURCE
 Unknown.
 ORGANISM
 Unclassified.
 1 (bases 1 to 1702)
 Thomas,T.L.
 Production of gamma linolenic acid by a DELTA-6-desaturase
 Patent: US 6355861-A 26 12-MAR-2002;
 Location/Qualifiers
 1..1702
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BASE COUNT 358 a 471 c 446 g 427 t

RESULT	7
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LOCUS	AY234125
DEFINITION	Primula farinosa fatty acid delta-6 desaturase mRNA, complete cds.
ACCESSION	AY234125
VERSION	AY234125.1 GI:30350276
KEYWORDS	
SOURCE	Primula farinosa
ORGANISM	

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49_1410
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NHFSDDVYVGPVGNDMFKKOTAGTNISGCAWMDPFGGILQPOVEHTLPRMRGCG
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TLG"

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RESULT 8
RMS2A06_00
WPCOMMIT
Sequence split into 10 fragments LOCUS RMS2A06 Accession BX511200

LOCUS	DEFINITION	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
RM52206	1002253 bp	DNA	linear	HTG 23-MAY-2003		
	Rattus norvegicus chromosome 1 clone R932-52A6, *** SEQUENCING IN PROGRESS ***, 721 unordered pieces.					
EX511200	GI:31074747					
EX511200.1	GI:31074747					
HTG; HTGS PHASE1; HTGS DRAFT.						
Rattus norvegicus (Norway rat)						
Rattus norvegicus						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
1 (bases 1 to 1002253)						
Schoen, O., Conrad, A., Hornischer, K., Loehner, T. H., Thies, S., Scharte, M. and Bloeker, H.						
Direct Submission						
Submitted (23-MAY-2003) GBF, Dept. of Genome Analysis, Mascheroder Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de						
All annotations in this database entry are developed by computational tools. It is therefore not explicitly noted in the feature lines that evidence is not experimental.						
----- Genome Center						
Center: GBF, Braunschweig						
Center code: GBF						
Web site: http://genome.gbf.de/						
Contact: info.genome@gbf.de						
----- Project Information						
Center project name:						
Center clone name: Rp32-52A06						
----- Summary Statistics						
Sequencing vector: ###;						
Chemistry: Dye-terminator-amersham: ### of reads						

Chemistry: Dye-primer-amersham: ## of reads
Assembly program: #
Consensus quality: 276318 bases at least Q40
Consensus quality: 315218 bases at least Q30
Consensus quality: 355218 bases at least Q20
Estimated insert size: ##; agarose-fp estimation
Estimated insert size: 930153; sum-of-ctrls estimation

PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
+-----+
+ Analysis and annotation were performed with the automatic +
+ 'first-pass' annotation and submission tool +
+ 'AnnotMitter' (Hornischer & Bloeker). +
+ Programs used by 'AnnotMitter': +
+-----+
* NOTE: This is a 'working draft' sequence. It currently
* consists of 721 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
+-----+
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* 101 1688: contig of 1588 bp in length
* 1689 1788: gap of 100 bp
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* 3165 4800: contig of 1636 bp in length
* 4801 4900: gap of 100 bp
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* 6240 7377: contig of 1138 bp in length
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* 7478 8502: contig of 1025 bp in length
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* 8603 9759: contig of 1157 bp in length
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PUBMED 9786850
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 AUTHORS Sperling P.
 TITLE Direct Submission
 JOURNAL Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer
 Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18,
 D-22609 Hamburg, GERMANY.
 COMMENT Related sequence: X87143.
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 DB 76 TCATTACAGCGATGATCTGAAAAACACAAACCAACCGGAGATTATGATCTCAATCC 135
 QY 262 CCGGGAGAGCTTACGACGCGCTGCTGCGCCACCAACCGGGCGGAGAGTCCCGC 321
 DB 136 AAGGCAAGCTACGACGCTCCACCTGGGTCAATCCATCCCGGAGGGAAGCAGCA 195
 QY 322 TCATCACTCGCGGCGGAGAGCAACCGCTTACGCTTACCAACCC--GCCCT 378
 DB 196 TCTTAACCTCGCGGTCAAGACGTCACGACGCGTTACGCTTACCAACCCGGAACG 255
 QY 379 CCGTGGCGCGCTCTCCCGCGCTTCTGCTGCGCGCGCTCACCAGTACCTGTCGCC 438
 DB 256 CATGGCGCACTCGAAACCTTCACACGCGCTACCACTGAAAGACCAACAGTGTCCG 315
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 DB 316 AGCTGCGGTGCTACCGCTGTTAGCGCGGAGTTTTCAAACGCGAGACTCTTCCA 373

RESULT 11
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 LOCUS AC084799 Mus musculus chromosome 16 clone RP23-197M9, WORKING DRAFT
 DEFINITION SEQUENCE, 101 unordered pieces.
 ACCESSION AC084799

VERSION AC084799.1 GI:11922127
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS 1 (bases 1 to 303091)
 TITLE DOE Joint Genome Institute.
 JOURNAL Sequencing of Human Chromosome 16
 REFERENCE 2 (bases 1 to 303091)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (17-NOV-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>
 Project Information
 Center Project Name: 0
 Center Clone name: RPCT-23_197M9
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 Consensus quality: 152568 bases at least Q40
 Consensus quality: 175579 bases at least Q30
 Consensus quality: 186949 bases at least Q20
 Estimated insert size: 198300; agarose-fp estimation
 Estimated insert size: 293091; sum-of-coverage estimation
 Quality coverage: 4.85 in Q20 bases; agarose-fp estimation
 Quality coverage: 3.28 in Q20 bases; sum-of-coverage estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 101 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 1217 1216: gap of unknown length
 2537 2536: contig of 1320 bp in length
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 16780 16879: gap of unknown length
 16880 18278: contig of 1399 bp in length
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 19553 21012: contig of 1460 bp in length
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 21113 22169: contig of 1057 bp in length

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25826	25925:	gap of unknown length
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30984	33125:	contig of 1142 bp in length
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33226	33397:	contig of 1172 bp in length
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Matches 247;	Conservative 0;	Mismatches 321;	Indels 0;	Gaps 0;

[illegible]

Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L3944
Center clone name: 20_N_19

* NOTE: This record contains 138 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overall relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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 DSIPTIAQLRIRDESIVRAIEKQSHQYVLARVNSKEPALQAVKQDASAMV
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AC074307
AC074307.1 GI:9454523
VERSION
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
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ORGANISM
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DOE Joint Genome Institute.
TITLE
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DOE Joint Genome Institute.
REFERENCE
Direct Submission
Submitted (26-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 0
Center clone name: RP21-2_6K21

Summary Statistics
Consensus quality: 156592 bases at least Q40
Consensus quality: 179034 bases at least Q30
Consensus quality: 187032 bases at least Q20
Estimated insert size: 236300; agarose-fp estimation
Baited insert size: 216369; sum-of-contigs estimation
Quality coverage: 3.09 in Q20 bases; agarose-fp estimation
Quality coverage: 3.37 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 42 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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FEATURES
source

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:38:37 ; Search time 156.169 Seconds
(without alignments)
14225.873 Million cell updates/sec

Title: US-09-857-524B-16

Perfect score: 823

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Maximum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	74.4	9.0	1465	21	AA042244
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17	72	8.7	125401	22	AAD17186
18	71.4	8.7	1606	21	AA244851
19	71.2	8.7	600	24	ABQ52496
20	70.8	8.6	77536	21	AA014651
21	69.4	8.4	1687	25	ABT23249
22	68.6	8.3	1881	24	AA18436
23	68.4	8.3	4403765	22	AA199683
24	67.6	8.2	4403765	22	AA199683
25	67.6	8.2	4411529	22	AA199682
26	67.4	8.2	1380	24	AAD35090
27	67.2	8.2	1350	24	AB213753
28	67.2	8.2	1650	21	AA033846
29	67.2	8.2	1650	21	AA033846
30	67.2	8.2	1650	21	AA033846
31	67.2	8.2	1678	21	AA244833
32	66.8	8.1	5802	24	ABT78696
33	66.4	8.1	3453	21	AAA79709
34	66.2	8.0	3849	22	AA068452
35	65.8	8.0	1327	24	AB068452
36	65	7.9	4488	17	AAT35520
37	64.8	7.9	1218	21	AAA02488
38	63.8	7.8	1471	21	AAD01349
39	63.4	7.7	58857	21	AAA58471
40	63.2	7.7	3320	21	AAA38185
41	63.2	7.7	88421	24	AA140781
42	63	7.7	1362	25	AAD49064
43	63	7.7	24379	18	AAT93095
44	63	7.7	24379	19	AAV25925
45	63	7.7	44377	18	AAT78508

ALIGNMENTS

RESULT 1	
ID	AAD01354 standard; cDNA; 823 BP.
XX	
AC	AAD01354;
XX	
DT	12-OCT-2000 (first entry)
XX	
DE	Wheat sphingolipid desaturase cDNA #2.
XX	
KW	Wheat; sphingolipid desaturase; membrane-bound desaturase;
KW	transgenic plant; fatty acid; ss.
XX	
OS	Triticum aestivum.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	165..506
FT	/tag= a
FT	/product= "sphingolipid desaturase"
FT	/note= "Does not include stop codon"
FT	/partial
XX	
XX	
XX	WO200032790-A2.
XX	
XX	08-JUN-2000.
PD	
XX	
PF	02-DEC-1999; 99WO-US26589.
XX	
XX	03-DEC-1998; 98US-0110784.
PR	
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.

Human gene express
Soybean sphingolip
Human colon cancer
Human PAL-18 polyn
Mycobacterium tube
Arabidopsis thalia
Human PAL-18 polyn
Streptomyces nous
Streptomyces nous
Sphingolipid desat
Oligonucleotide fo
Oligonucleotide fo
Nucleotide sequenc
Seed development e
Contig 109 DNA enc
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
Pythium irregulare
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
A. thaliana sidi D
S. karthausensis D
Eucahyptus grandis
S. chrysomallus ac
Listeria monocytog
Human thrombopoiet
Human colon cancer
Florida blueberry
Nucleotide sequenc
Primer used in the
88422nt genomic DN
Saprolegnia dictin
Streptomyces fireo
Streptomyces roseo
Platenolide syntha

XX Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 PI WPI: 2000-412336/35.
 DR P-PSDB; AA71556.
 XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries -
 XX
 PS Claim 2; Page 56-57; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone wrel.pk0004.c7 isolated from wheat etiolated
 CC seedling root cDNA library; wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 823 BP; 133 A; 329 C; 194 G; 153 T; 14 other;
 Query Match 98.3%; Score 809; DB 21; Length 823;
 Best Local Similarity 100.0%; Pred. No. 3.4e-133;
 Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCCTTAACAAACCTCGTGTGTTTAAAGATCCGATTCCTCCCTCCCTCC 60
 DB 1 CTCCTTAACAAACCTCGTGTGTTTAAAGATCCGATTCCTCCCTCCCTCC 60
 QY 61 CTTCTCTAGTCTGACCAACCCCTCGCGCTCGACGATTAATCAACGCAACGATG 120
 DB 61 CTTCTCTAGTCTGACCAACCCCTCGCGCTCGACGATTAATCAACGCAACGATG 120
 QY 121 CCGGCAAGGGCTTCGCGAGCAAGCGCGGAGGCAAGCGCAATGCGCGCGCAGCA 180
 DB 121 CCGGCAAGGGCTTCGCGAGCAAGCGCGGAGGCAAGCGCAATGCGCGCGCAGCA 180
 QY 121 CCGGCAAGGGCTTCGCGAGCAAGCGCGGAGGCAAGCGCAATGCGCGCGCAGCA 180
 DB 121 CCGGCAAGGGCTTCGCGAGCAAGCGCGGAGGCAAGCGCAATGCGCGCGCAGCA 180
 QY 181 AGAAGCGCGCGATCGATGATCTCCACCAAGAGAGCGAGCGCGCGCGG 240
 DB 181 AGAAGCGCGCGATCGATGATCTCCACCAAGAGAGCGAGCGCGCGCGG 240
 QY 181 AGAAGCGCGCGATCGATGATCTCCACCAAGAGAGCGAGCGCGCGCGG 240
 DB 181 AGAAGCGCGCGATCGATGATCTCCACCAAGAGAGCGAGCGCGCGCGG 240
 QY 241 AGCACTCTGATCTCCATCTCCGCGGAGCGCTACGACGCTGCTGCGTCCACC 300
 DB 241 AGCACTCTGATCTCCATCTCCGCGGAGCGCTACGACGCTGCTGCGTCCACC 300
 QY 301 ACCCGGCGGAGAGTCCCGCTCATCACTCGCGCGGCGAGAGCGACGCGCTTCA 360
 DB 301 ACCCGGCGGAGAGTCCCGCTCATCACTCGCGCGGCGAGAGCGACGCGCTTCA 360
 QY 301 ACCCGGCGGAGAGTCCCGCTCATCACTCGCGCGGCGAGAGCGACGCGCTTCA 360
 DB 301 ACCCGGCGGAGAGTCCCGCTCATCACTCGCGCGGCGAGAGCGACGCGCTTCA 360
 QY 361 TGGCTTACACACCGCGCTCGGTGCGCGCTCTCGCGCGCTTCTTGTCGCGCGCTCA 420
 DB 361 TGGCTTACACACCGCGCTCGGTGCGCGCTCTCGCGCGCTTCTTGTCGCGCGCTCA 420
 QY 421 TGGCTTACACACCGCGCTCGGTGCGCGCTCTCGCGCGCTTCTTGTCGCGCGCTCA 420
 DB 421 TGGCTTACACACCGCGCTCGGTGCGCGCTCTCGCGCGCTTCTTGTCGCGCGCTCA 420
 QY 421 CGCACTACATGTCCTCCCGCGCTCGCGAGCTTCCCGCTCTGCGAGCTTCTCT 480
 DB 421 CGCACTACATGTCCTCCCGCGCTCGCGAGCTTCCCGCTCTGCGAGCTTCTCT 480
 QY 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAATTTCTGCTGCTGCAAGTNGT 540
 DB 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAATTTCTGCTGCTGCAAGTNGT 540
 QY 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAATTTCTGCTGCTGCAAGTNGT 540
 DB 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAATTTCTGCTGCTGCAAGTNGT 540
 QY 541 GCTCTTCTGATCGGCTCTACTAGTCTCTGCTGCTCAACACCGGAGCGACATGTCG 600
 DB 541 GCTCTTCTGATCGGCTCTACTAGTCTCTGCTGCTCAACACCGGAGCGACATGTCG 600
 QY 541 GCTCTTCTGATCGGCTCTACTAGTCTCTGCTGCTCAACACCGGAGCGACATGTCG 600
 DB 541 GCTCTTCTGATCGGCTCTACTAGTCTCTGCTGCTCAACACCGGAGCGACATGTCG 600
 QY 601 CCGGCGGCTCATTTGGCTTATCTGTCAGATCGGCGGATGTCATCTCCGACACAAAT 660
 DB 601 CCGGCGGCTCATTTGGCTTATCTGTCAGATCGGCGGATGTCATCTCCGACACAAAT 660
 QY 661 CACAGGCACTGCTCAACGCTCGNAGTGGCTCGGAAATGCTTACGGCTCGGATGCTG 720

DB 661 CACAGGCACTGCTCAACGCTCGNAGTGGCTCGGAAATGCTTACGGCTCGGATGCTG 720
 QY 721 GGGAGTANACACCAANACANATTTGAANNNGCACATACCTACCTCANATTCGNTTCG 780
 DB 721 GGGAGTANACACCAANACANATTTGAANNNGCACATACCTACCTCANATTCGNTTCG 780
 QY 781 GGTACAGTCTAAACTTGCATCGTAAAGACTTGGTTAGCAT 823
 DB 781 GGTACAGTCTAAACTTGCATCGTAAAGACTTGGTTAGCAT 823
 RESULT 2
 AAD01353
 ID AAD01353 standard; cDNA; 1972 BP.
 XX
 AC AAD01353;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Wheat sphingolipid desaturase cDNA #1.
 XX
 KW Wheat; sphingolipid desaturase; membrane-bound desaturase;
 KM transgenic plant; fatty acid; ss.
 XX
 OS Triticum aestivum.
 XX
 FH Key Location/Qualifiers
 FT CDS 124..1533
 FT /*tag= a
 FT /product= "sphingolipid desaturase"
 XX
 PN W0200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99MO-US28589.
 XX
 PR 03-DEC-1998; 98US-0110784.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 DR P-PSDB; AA71555.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries -
 XX
 PS Disclosure; Page 48-49; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone wrel.pk0004.c7:is isolated from wheat etiolated
 CC seedling root cDNA library; wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 other;
 Query Match 67.1%; Score 552; DB 21; Length 1972;
 Best Local Similarity 94.6%; Pred. No. 3.5e-88;
 Matches 615; Conservative 0; Mismatches 27; Indels 8; Gaps 4;
 QY 1 CTCCTTAACAAACCTCGTGTGTTTAAAGATCCGATTCCTCCCTCCCTCCCTCC 60
 DB 8 CTCCTTAACAAACCTCGTGTGTTTAAAGATCCGATTCCTCCCTCCCTCCCTCC 67

QY	61	TTTCTCTCTGAGTCTGAGCAACCCCTCTGGGCTCAGCTAAATCAGCCACGATGG	120
Db	68	CTTCTCTTGAGTCTTGACCAACCCCTCTGGGCTCAGCTAAATCAGCCACGATGG	127
QY	121	CCCGCAGCGGCTTTCGCGAGCAACGCGCGGAGACCAAGCATATGCGGCGCGAGA	180
Db	128	CCCGCAGCGGCTTTCGCGAGCGAACGCGCGGAGACCAAGCATATGCGGCGCGAGA	187
QY	181	AGAGCGCGCGAGCTCCGATGATCTCCACCAAGAGCTGCAGGCGCACGCGCGCGG	240
Db	188	AGGAGCGCGCGAGCTCCGATGATCTCCACCAAGAGAGTGCAGGCGCGCACGCGCGG	247
QY	241	ACGACCTCTGAGTCTTCATCTCCGGGAGGTCTACGACGTCAGCCCTGGCTGGCGAC	300
Db	248	ACGACCTCTGAGTCTTCATCTCCGGGAGGTCTACGACGTCAGCCGTGGCTGGCGAC	307
QY	301	ACCGCGGCGGCGAGGTCCTCGCTCATACCTCGCGCGGACGAGACCGACCGACCTTCA	360
Db	308	ACCGCGGCGGCGAGGTCCTCGCTCATACCTCGCGCGGACGAGACCGACCGACCTTCA	367
QY	361	TGGCTTACCAACCCGCTTCCTCGTGGCGCGCTCTCTCGCGCTTCTTTCGTGGCGCTCA	420
Db	368	TGGCTTACCAACCCGCTTCCTCGTGGCGCGCTCTCTCGCGCTTCTTTCGTGGCGCTCA	427
QY	421	CCGATACATCTCCCCCGCGCTCCGCGGACATTCCGCGCGCTCTCTCCGCGACCTCTCT	480
Db	428	CCGATACATCTCCCCCGCGCTCCGCGGACATTCCGCGCGCTCTCTCCGCGACCTCTCT	487
QY	481	CCGCGGCGCTCTTCGAGCGCGCTCG-CACACCCCAAGTTCCTGCTCGTGCAGAACTCG	539
Db	488	CCGCGGCGCTCTTCGAGCGCGCTCGAGCAACCCCAAGTTCCTGCTCGTGCAGATGCG	547
QY	540	TGCTCTTTCGATCGGCTCTTACTG-CCTTGCTCTGTCAA--CACCGGAGGCACATGT	596
Db	548	TGCTCTTTCGATCGGCTCTTACTGCTCTGCTCTGTCTACACACCGGAGGCACATGT	607
QY	597	TGCGCGGCGGCTCATTTGG----CTTATCTGTGATGTCGGGCTGGATTTGGC	642
Db	608	TGCGCGGCGGCTCATTTGGCTTTCATCTGATTCAGTTCAGTTCGGGCTGGATTTGGC	657

RESULT 3	
AA001350	AA001350 standard; cDNA; 1764 BP.
XX	
AC	AA001350;
XX	
DT	12-OCT-2000 (first entry)
XX	
DE	Corn sphingolipid desaturase cDNA.
XX	
KW	Corn; sphingolipid desaturase; membrane-bound desaturase;
KW	transgenic plant; fatty acid; ss.
XX	
OS	Zea mays.
XX	
XX	
FH	Location/Qualifiers
FT	89..1477
CDS	/*tag= a
FT	/product= "Sphingolipid desaturase"
XX	
PN	W0200032790-A2.
XX	
PD	08-JUN-2000.
XX	
PF	02-DEC-1999; 99WO-US28589.
XX	
PR	03-DEC-1998; 98US-0110784.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	
PI	Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

DR WPI : 2000-412336/35.
DR P-RSDB: NAY71552.
XX
XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries -
XX
XX
PS Claim 2; Page 41-42; 57pp; English.
XX
XX The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone cdelc.pX001.08.f16 isolated from corn developing
CC embryo cDNA library, cdelc. The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
XX
XX Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 other;

Query Match	Similarity	38.3%	Score 314.8	/DB 21	Length 1764
Best Local	Similarity	78.2%	Pred. No. 1.3e-46		
Matches	417	Conservative	0	Mismatches	108
				Indels	8
				Gaps	3
QY	82	CCCTCTCTCGCGCTCCAGCTPAATCCAGCGCCACCGATGCGCCCGACGGGCTTGGCGAGC	141		
Db	27	CTCTCCCGCGCTCCCTTACCAAAATCAGACACACCCAGGCGAGATCCAGGCACACGCGCGC	86		
QY	142	CAACGGGCGCGGAAAGCGAGATGCGCGCGCGCAAGCA-----GGAGCGCGCGAGC	195		
Db	87	CAATGCGCGCTCTGTGTGATGCAATGCGCGCGCGCGCGAGCGCGCGCGCGCGAGC	146		
QY	196	TCGCGATGATCTCCACCAAGAGCTGAGCGCGCACGCGCGCGCGAGACGACTTGTGATCT	255		
Db	147	TGGCGATGATCTCTCCAAAGAGCTCGCGCTCAGCGTTTCGCGCGAGACCTCTGATCT	206		
QY	256	CCATCTCCGGGAGCGTTCAGCGCTCAGCGCTTGGCTGCGCACATCCCGGCGGCGAGG	315		
Db	207	CCATCTCCGGGAGCGTTCAGCGCTCAGCGCTTGGCTGCGCACATCCCGGCGGCGAGC	266		
QY	316	TCGCGCTATCACCTTCGCGCGCGCGCACAGCGCACAGCGCTTCATGCGCTACACCGCG	375		
Db	267	TCGCGCTTCTACCTTCGCGCGGAGGAGCGCACAGCGCTTTCGCGCTACACCGCGC	326		
QY	376	CCTCGTGGCGCGCGCTCTCCGCGCGCTTCTTCGTGCGCGCGCTCACCGACTACACTGTC	435		
Db	327	CCTCGGCGCGCGCGCTCTCCGCGCGCTTCTTCGTGCGCGCGCTCTCGACTACGCGCGCT	386		
QY	436	CCCCCGCTTCGCGCGAGCTTCGCGCGCTCTTCGCGAGCTCTCTCTCGCGGCGCTTTGG	495		
Db	387	CCCCCGGCTTCGCGCGAGCTTCGCGCGCTCTTCGCGAGCTCTCTCTCGCGGCGCTTTGG	446		
QY	496	AGCGCGCTTCGCGCGAGCTTCGCGCGCTTCGCGCGAGCTCTCTCTCGCGGCGCTTTGG	554		
Db	447	AACCGCTTCGCGCGAGCTTCGCGCGCTTCGCGCGAGCTCTCTCTCGCGGCGCTTTGG	506		
QY	555	GCTCTCTA-CTGCTCTCTGCGCTCTCAACACCGGCGCGACATGTTGCGCGGCGG	606		
Db	507	CGCTGATCTCTCTCTGCGATGCGCGACGCGCTTGGCGCGACCTCTCTCGCGGCGG	559		
RESULT 4					
ABK49503					
ID ABK49503 standard; DNA; 1702 BP.					
XX ABK49503;					
XX 15-JUL-2002 (first entry)					
XX DNA encoding Evening primrose delta6-deaturase.					
XX delta6-deaturase; sunflower; soybean; maize; tobacco;					
KW peanut; carrot; oil seed rape; gamma linolenic acid; GLA;					

KW	chilling tolerance; gene; de; evening primrose.
XX	
OS	Oenothera biennis.
XX	
FH	Key Location/Qualifiers
FT	CDS 48..1406
FT	/tag= a
FT	/product= "delta6-desaturase"
XX	
PN	US6355861-B1.
XX	
PD	12-MAR-2002.
XX	
PF	19-SEP-1997; 97US-0934254.
XX	
PR	13-OCT-1992; 92US-0959952.
PR	10-OCT-1991; 91US-0774475.
PR	08-JAN-1992; 92US-0817919.
PR	14-SEP-1994; 94US-0307382.
PR	28-JAN-1997; 97US-0789936.
XX	
PA	(RHON) RHONE-POULENC AGROCHIMIE.
XX	
P1	Thomas TL;
XX	
DR	WPI: 2002-380944/41.
DR	P-PSDB; AAU79851.
XX	
PT	Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria -
PS	Claim 2; Column 41-46; 53pp; English.
XX	
CC	The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the evening primrose delta6 desaturase involved in the production of gamma linolenic acid.
SQ	Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
Query Match	13.0%; Score 106.8; DB 24; Length 1702;
Best Local Similarity	62.3%; Pred. No. 3.4e-10;
Matches 187; Conservative	0; Mismatches 107; Indels 6; Gaps 1
QY	204 ATCTCCACCAAGAGACTGACGGCGCAGCCGCCGGGAGAGACTGTGCATCTTCC 263 DB 72 ATCAGCGGGAGGAGACTTCGGCGCACAAAGTCCGGGATCTTGATCTCCATCCAG 131
QY	264 GGGAGCGTTACGAGCTACGCGCTTGGCTGCCACACCCGGGGGGGAGTCCGCTC 323
DB	132 GGCAAGGCTTACGACTGCTCTTCGGGGCGGGGAGCAACCCGGCGGAGGTCCGCTC 191
QY	324 ATCAACCTCCGGCGGAGAGCGCACCGACGCTTACATGAGCTTACCACCGCCCTCCGTG 383
DB	192 CTCAGTCTGGSCGGGACGAGAGCTACCGACGCTTATTGCTTACCATCCCGGACAGGG 251
QY	384 CGCCGCTCTCTCCGCGGCTTCTCTTCTGCG-----CGGCTACCGACTACATGTCGCC 437
DB	252 TGGGGGAATCTGAGATCCGCTCTTACCGGCTACTACTACAGAATTGCAAGTGTGCG 311
QY	438 CCCGCTTCGCGGCACTTCGCGGCTCTCTCGGAGCTTCCTCCGGGAGCTTTCGAG 497
DB	312 GAGATCTCCAGGAGTAACCGAGGCTTTGAACGAGATGTGCGGCTCCGGATCTTCGAG 371

ID	ABX15367standard; cDNA; 1702 BP.
XX	
XX	ABX15367;
XX	
DT	16-APR-2003 (first entry)
XX	
DE	Evening primrose delta-6-desaturase #1 cDNA.
XX	
KW	Dela-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
KM	maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KW	octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
KM	evening primrose.
XX	
OS	Oenothera biennis.
XX	
FT	Key
FI	Location/Qualifiers
FT	48..1406
CDS	/tag= a
FT	/product= "Evening primrose delta-6-desaturase #1"
XX	
PN	US2002108147-A1.
XX	
PD	08-AUG-2002.
XX	
PF	21-DEC-2001; 2001US-0029756.
XX	
PR	13-OCT-1992; 92US-0959952.
PR	19-SEP-1997; 97US-0934254.
PR	10-OCT-1991; 91US-0774475.
PR	08-JAN-1992; 92US-0817919.
PR	14-SEP-1994; 94US-0307382.
PR	28-JAN-1997; 97US-0789936.
XX	
PA	(THOM/) THOMAS T L.
PI	Thomas TL;
XX	
DR	WPI; 2003-066659/06.
DR	P-PSDB; ABG73416.
XX	
PT	Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
PT	for producing plant with increased gamma linolenic acid content, and
XX	for inducing octadecatetraenoic acid production in plant -
PS	Claim 2; Fig 10; 55pp; English.
CC	The invention relates to a nucleic acid encoding an evening primrose
CC	delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC	nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC	for producing a plant (such as sunflower, soybean, maize, tobacco,
CC	peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC	acid (GLA) content by transforming a plant cell with the nucleic acid or
CC	vector and regenerating a plant with increased GLA content from the plant
CC	cell, for inducing or increasing production of GLA in an organism lacking
CC	in or producing low levels of GLA and for inducing production of
CC	octadecatetraenoic acid in at least one of a plant deficient or lacking
CC	in or producing low levels of octadecatetraenoic acid, a bacterium which
CC	produces alpha-linolenic acid or a bacterium which exhibits a
CC	delta-15-desaturase activity on a GLA substrate. This sequence represents
CC	cDNA encoding an evening primrose delta-6-desaturase polypeptide.
XX	
SQ	Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
Query Match	13.0%; Score 106.8; DB 25; Length 1702;
Best Local Similarity	62.3%; Pred. No. 3.4e-10;
Matches 187; Conservative	0; Mismatches 107; Indels 6; Gaps 1
0y	ATTCACCAAGAGACTGCAGCGCAGCCGCCGGAGAGACCTGTGATCTCCATCTCC 263
Db	72 ATCACGGGAGAGACCTCCGCCGCACAACAAGTCCGGCATCTTGATCTCCATCCAG 131
0y	GAGGAGCTTACGACGTCACGCGCTGTGCTGCACACACCCGGGGGAGAGTCCGCTC 323

DB 132 GCGAAGTCTACACTGCTCTCGTGAGGCGGAGACCCCGGCGGAGGTCCGCTC 191
 QY 324 ATCACCCTGCGCGGCGGAGGAGCGGAGCGGCTTCATGAGCTACACCGCGGCTTCGAG 383
 DB 192 CTGAGCTGCGGCGGAGGAGCGGAGCGGCTTCATGAGCTACACCGCGGCGGAGG 251
 QY 384 CGCGGCTCTCGCGGCGGCTTCGAGG-----CGGCTCAGCGGAGTACAGTGTCCG 437
 DB 252 TGGCGGAGTCTGAGTCCGCTTCACCGGCTACTACTCAAGAGCTTCGAGGTGCG 311
 QY 438 CGCGGCTCGGCGGAGTCTTCGCGGCTTCGCGGAGTCTTCGCGGCGGCTTCGAG 497
 DB 312 GAGATCTCCAGAGTACCGGAGGCTTTGAAAGAGATGTGCGGCTTCGAGGTTCGAG 371

RESULT 6
 ID AAZ44832 standard; DNA; 1594 BP.
 XX
 AC AAZ44832;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE B. napus sld1 DNA.
 XX
 KM Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material; ds.
 XX
 OS Brassica napus.
 XX
 FH Key Location/Qualifiers
 FT 51..1400
 FT /*tag= a
 FT /product= "sld1"
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E, Zaehrlinger U, Schmidt H, Sperling P;
 DR P-PSDB; AAY51333.
 DR WPI; 2000-127549/12.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 PS Claim 11; Fig 1; 62pp; German.
 XX

CC materials. This sequence encodes the Brassica napus sphingolipid
 CC desaturase sld1 protein described in the method of the invention.
 XX
 SO Sequence 1594 BP; 382 A; 369 C; 375 G; 468 T; 0 other;
 Query Match 11.5%; Score 94.8; DB 21; Length 1594;
 Best Local Similarity 59.7%; Pred. No. 4,4e-08;
 Matches 178; Conservative 0; Mismatches 117; Indels 3; Gaps 1;
 QY 202 TGATCTCCAGAGAGTGCAGGCGGAGCGGCGGAGGAGCTTCGATTCATCT 261
 DB 76 TCAATTAAGAGCATATGTAAGAAAAACACACCAACCGGAGATTATGATCTCAATCC 135
 QY 262 CGGAGGAGCTTACGAGAGTGCAGGCGGCTTCGCGGAGGAGCGGAGGAGGAGG 321
 DB 136 AAGGCAAGTCTACGAGAGTGCAGGCGGCTTCGCGGAGGAGGAGGAGGAGG 195
 QY 322 TCATCACTCTCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 378
 DB 196 TCTTAAGCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255
 QY 379 CGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 438
 DB 256 CATGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 315
 QY 439 CGGCTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 496
 DB 316 AGCTGTGCGTACATCCGCTTTAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 373

RESULT 7
 ID ABR98631/C
 XX ABR98631 standard; DNA; 12733 BP.
 XX
 AC ABR98631;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Vector pPERF14 containing L. lactis derived promoter sequence.
 XX
 KM ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
 KM P59; P1P2; PL; xylO; tefO; trpO; malO; lambdaclac; cellular proliferation;
 KM antibiotic; vector.
 XX
 OS Lactococcus lactis.
 OS Synthetic.
 OS Staphylococcus aureus.
 OS Leuconostoc mesenteroides.
 XX
 PN WO200251982-A2.
 XX
 PD 04-JUL-2002.
 XX
 PF 21-DEC-2001; 2001WO-US50250.
 XX
 PR 27-DEC-2000; 2000US-259434P.
 PR 06-SEP-2001; 2001US-0948993.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Wall D, Gross M;
 DR WPI; 2002-575374/61.
 XX
 PT Isolated nucleic acid comprises bacterial promoters modified to have
 PT altered activity in at least one gram-positive organism, e.g. Bacillus
 PT anthracis or Clostridium botulinum, useful for regulating gene
 PT expression in bacteria -
 XX
 PS Example 3; Page 224-227; 246pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising a fusion
 CC promoter comprising at least one promoter that is modified to have

CC altered activity in at least one gram-positive organism, or comprising
CC 15, CP25, P32, P59 Plp2 or Pl, linked to at least one operator consisting
CC of xylo, tecto, rypO, malO or lambdaciO, where at least one operator is
CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors
CC transcribed from the fusion promoters. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector. a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in *Enterococcus*
CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-regulated genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is vector (or fragment)
CC incorporating a fusion promoter sequence of the invention.
XX

Sequence 12733 BP, 3549 A, 2567 C, 3207 G, 3409 T, 1 other;

Query Match	10.4%	Score 85.6	DB 24	Length 12733
Best Local Similarity	47.0%	Pred. NO. 1.7e-06		
Matches 262, Conservative	0	Mismatches 296	Indels 0	Gaps 0

QY	35	CGATTCCTCCCTTNCNCCCTCCGCTCCCTTCCCTCGTAGTCCGACACACCCCTCCGAGG	94
Db	5351	CGACCC	5292
QY	95	TCGAGCTAAATCCAGCGCCAGATGACCAGACGGGCTTTGGGAGACGGACGGCCGGA	154
Db	5291	CC	5233
QY	155	AGCCGAGCAATGCTCGGCGCCGAGACGAGAGCGCCGCGACGTCCGATGATTCACCA	214
Db	5231	CC	5172
QY	215	GGAGCTGAGGCGACGCGCGCGCGGAGACGACTCGATCTGCATCTCCGGAGAGCTA	274
Db	5171	CC	5112
QY	275	CGAGCTACGCGCTTGGCTGCGCACACCGGGGCGAGGATCCGCTATCAACCTGAC	334
Db	5111	CC	5055
QY	335	CGGCGAGGACGCCACCGAGCGCTTCATGCGCTTACACCGCGCTTCGATGCGCGCTCT	394
Db	5051	CC	4992
QY	395	CCGCGGCTTTCGTCGCGCGGCTCACCGGACATACATCTCCCCCGGCTCCGCGACTT	454
Db	4991	CC	4932
QY	455	CCGCGGCTCTCTCGGAGCTCTCTCGCGGAGCTTTTCGAGGCGATCGGACACCCCC	514
Db	4931	CC	4872
QY	515	AAGTTCCTGCTCGTCGCAAACTCAGTCTTTCGATCGGACCTTACTGCTTCGCGCT	574
Db	4871	CC	4812
QY	575	GCTCAGACGGGGGAC 592	
Db	4811	CCCCCCCCCCCCCCCC 4794	

RESULT .8
ABK98592/c
ID ABK98592 standard; DNA; 12739 BP.

XX ABK98592;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Vector pBEPE1 containing XylR/Xy10/CP25 sequences.
DE
XX
XX ds1 promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; Xy10; tetrO; trpO; malO; lambdaclO; cellular proliferation;
KW antibiotic; vector.
XX
XX Bacillus.
OS Bacteriophage lambda.
OS Escherichia coli.
OS Synthetic.
XX
XX WO200251982-A2.
PN
XX
XX 04-JUL-2002.
PD
XX
XX 21-DEC-2001; 2001WO-US50250.
XX
XX 27-DEC-2000; 2000US-259434P.
XX
XX 06-SEP-2001; 2001US-0948993.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haseelbeck R, Wall D, Gross M;
P1
XX
XX WPI; 2002-575374/61.
DR
XX
XX
XX Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene
PT expression in bacteria
PT
XX
XX Example 1; Page 206-209; 246pp; English.

	Query Match	10.4%	Score 85.6	DB 24	Length 12739;
	Best Local Similarity	47.0%	Pred. No. 1.7e-05:		
	Matches 26;	Conservative	0; Mismatches 226;	Indels	Gaps 0;
OY	35 CGATCTCCCTTGNCCCCCTCCTGCTCTCTGTAGTCCTGCACACCCTCTCGGGC	94			
Dd	5357 CCAcccccccccctcc	5239B			

QY 95 TCCAGCTAAATTCACGCGACCGATGCGCGACGAGGCTTCGCGAGCAACGCGCGCGA 154
 Db 5297 CC 5238
 QY 155 AGCCGACGCAATGCGCGCGCGCGCGAGAGAGCGCGCGAGCTCGCATGATTCACCA 214
 Db 5237 CC 5178
 QY 215 GGAGCTGACAGGCGACGCGCGCGCGAGACGCTGATGCTGATGCTGATGCTGATGCTGAT 274
 Db 5177 CC 5118
 QY 275 CGAGCTGACAGGCGCGCGCGCGCGAGAGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCG 334
 Db 5117 CC 5058
 QY 335 CGGCGAGAGCG 394
 Db 5057 CC 4998
 QY 395 CGGCGCGCTTCTGTCG 454
 Db 4997 CC 4938
 QY 455 CGGCGCGCTTCTGTCG 514
 Db 4937 CC 4878
 QY 515 AAGTTCTGCTGCTGCGCAAGTNGTGTCTTTCGATGCGCTTCTGCTGCTGCTGCTGCT 574
 Db 4877 CC 4818
 QY 575 GCTCAACACCGGCGCGAC 592
 Db 4817 CCCCCCCCCCCCCCCCCCCC 4800

RESULT 9
 AA217263
 ID AA217263 standard; cDNA; 1337 BP.
 XX AA217263;
 AC
 XX
 DT 12-OCT-1999 (first entry)
 XX
 DE Human gene expression product cDNA sequence SEQ ID NO:4735.
 XX
 KW Human; gene; gene expression product; diagnosis; therapy; probe;
 KW detection; mapping; tissue typing; profiling; forensic; cancer;
 KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
 XX
 OS Homo sapiens.
 PN WO9318972-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 28-JAN-1999; 99WO-US01619.
 XX
 PR 03-APR-1998; 98US-0080666.
 PR 28-JAN-1998; 98US-0072910.
 PR 24-FEB-1998; 98US-0075954.
 PR 31-MAR-1998; 98US-0080114.
 PR 03-APR-1998; 98US-0080515.
 XX
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 PI Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
 PI Escobedo J, Garcia PD, Garcia V, Glase K, Imle MA,
 PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I,
 PI Lamsen G, Leshkowitz D, Pot D, Randazzo F, Reinhard C,
 PI Stache-Crain B, Sudduth-Klinger J, Williams LT;

XX WPI; 1999-494092/41.
 DR
 XX Novel human genes and their expression products which are
 PT differentially expressed in different cell types
 PS Claim 1; Page 2250-2251; 2479pp; English.
 XX
 CC The present invention describes a library of human polynucleotides
 CC comprising the sequences given in AA212512 to AA21779. Also described is
 CC a method of detecting differentially expressed genes correlated with the
 CC cancerous state of a mammalian cell, comprising detecting at least one
 CC differentially expressed gene product in a test sample from a cell
 CC suspected of being cancerous, where the gene product is encoded by one
 CC of the 5248 polynucleotide sequences given in AA212512 to AA21779. The
 CC polynucleotides can be used as a source of primers and probes, which can
 CC be used for a variety of purposes, e.g. detection of expression levels,
 CC mapping, tissue typing or profiling, forensics, genetic analysis and
 CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
 CC can be used for raising antibodies for experimental, diagnostic and
 CC therapeutic purposes. The polynucleotides may also be used to construct
 CC arrays for diagnostics (which may be used to determine function of an
 CC encoded protein); and to detect differences in expression levels between
 CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
 CC identify a genetic predisposition or susceptibility to a disease such as
 CC cancer). The polynucleotides of the invention are especially used in the
 CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
 CC and lung cancer. The polynucleotides can also be used to screen for
 CC peptide analogues and antagonists.
 XX
 SQ Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;

Query Match 10.0%; Score 82.2; DB 20; Length 1337;
 Best Local Similarity 31.2%; Pred. No. 7.1e-06;
 Matches 181; Conservative 0; Mismatches 400; Indels 0; Gaps 0;

QY 1 CTCCTTAACAACCTCCGTTGCTGTTTAAATGCGATCTCCCTCCCTCCCTCC 60
 Db 378 CCCCCNN 437
 QY 61 CTTCTCTGAGTCTGACCACTCTCTGCGCTTCAGCTAAATTCACGCGACGCGATG 120
 Db 438 NNN 497
 QY 121 CCGCGACGCGCTTCGCGAGCGCAAGCGCGCGGAGCGCATGCGCGCGCGAGCA 180
 Db 498 CCCCCNN 557
 QY 181 AGAGCGCGCGAGCTGCGATGATCTCCACCAAGAGCTGAGGCGAGCGCGCGG 240
 Db 558 CCCCCNN 617
 QY 241 ACGACTCTGATCTTCATCTCCGCGAGAGCTTACGACGTACGCGCTGCTGCGCAC 300
 Db 618 CCCCCNN 677
 QY 301 ACCCGGCGGAGAGTCCCGCTCATCATCTCGCGCGCGAGAGCGCACCGACTTCA 360
 Db 678 CCCCCNN 737
 QY 361 TGGCTTACACCGCGCGCTCGTGGCGCGCTCTCGCGCGCTTCTTCTTCTTCTTCTTCT 420
 Db 738 NNN 797
 QY 421 CCGACTACACTGCTCCCGCGCTCGCGACTTCCGCGCGCTCTCTGCGCGACTTCT 480
 Db 798 CCCCCNN 857
 QY 481 CCGCGGCGCTTCTTTCAGAGCGCTGCGACACCGCGCAAGTTCTGCTGCTGCGCAAGTCT 540
 Db 858 NNN 917
 QY 541 GCTTTCTGACATGCGGCTTCTACTGCTCTCGGCTGCTCAAC 581


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XX US6294328-B1.
PN
XX
PD 25-SEP-2001.
XX
XX 24-JUN-1998; 98US-0103840.
XX
XX 24-JUN-1998; 98US-0103840.
XX
XX (GENO-) INST GENOMIC RES.
XX
XX Fieleschmann RD, White OR, Fraser CM, Venter JC;
XX WPI; 2001-647261/74.
XX
XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
XX determining the nucleotide sequence of the strain at positions in the
XX genome corresponding to positions where M. tuberculosis strains CDC
XX 1551 and H37Rv differ
XX
XX Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
XX
XX The invention relates to evaluating strain variation within and between
XX different populations of the tuberculosis bacterial pathogen,
XX Mycobacterium tuberculosis or related Mycobacterium by determining the
XX nucleotide sequence of the first strain at positions in the complete
XX sequence of the genome that correspond to positions that differ in the
XX nucleotide sequences of M. tuberculosis strains CDC 1551 (H37Rv) and
XX H37Rv (H37Rv). The method is useful for evaluating strain variation of
XX M. tuberculosis and has valuable application in the fields of
XX tuberculosis genetics, epidemiology, patient treatment and epidemic
XX monitoring.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?docID=6294328B1.
XX
XX Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
SQ
Query Match 9.1%; Score 75.2; DB 22; Length 4411529;
Best Local Similarity 45.5%; Pred. No. 9.4e-05;
Matches 263; Conservative 0; Mismatches 315; Indels 0; Gaps 0;
QY 13 CCTCCGTTGCTTTTAAAGATCCGATCTCCCTTCCCTCCCTCCCTCTCTCTCTGAG 72
Db 1218100 CCGCGCTGCGCGCATGCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCG 1218041
QY 73 TCCTGACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 132
Db 1218040 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217981
QY 133 TCCTGACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 192
Db 1217980 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217921
QY 193 ACCTGCGCATGATCTCTCAACCAAGAGCTGAGGCGGCGCGCGCGCGCGCGCGCG 252
Db 1217920 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217861
QY 253 TCTCCATCTCTCGGAGAGCTGACGCTCAAGCTGCGCGCGCGCGCGCGCGCGCG 312
Db 1217860 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217801
QY 313 AGGTCCCGCTCAATCACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 372
Db 1217800 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217741
QY 373 CGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 432
Db 1217740 CCGTGGCGCTTACCGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217681
QY 433 TCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 492
Db 1217680 TCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217621
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QY 493 TCGAGCGCGTGGCGACACCCCAAGTTCTGCTCTGCGAAGTCNGTGTCTTTCAT 552
Db 1217620 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217561
QY 553 CGGCGCTTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 590
Db 1217560 CTGACCGCATTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217523

RESULT 14
AAC42244
ID AAC42244 standard; DNA; 1465 BP.
XX
XX AAC42244;
AC
XX 17-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-01231825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
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PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135253.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140891.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
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PR 22-JUL-1999; 99US-0145192.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.

PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0148368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0158294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161923.
PR 29-OCT-1999; 99US-0162142.

Query Match 9.0%; Score 74.4; DB 21; Length 1465;
Best Local Similarity 55.8%; Pred. No. 0.00016;
Matches 163; Conservative 0; Mismatches 126; Indels 3; Gaps 1;
QY 208 CCACCAAGAGCTGACGCGCACGCGCGCGGACCTGTGATCTCATCTCGGGG 267

Db 147 CAAGCGAGATTGAAAAACACAACAACTGGAGATTGATTGATTCAAGTA 206
Qy 268 ACCTTACGACGTCAGCGCCCTGGTGGCCACCAACCGGGGAGAGTCCCGTATCA 327
Db 207 AAGTTTACGACGTTTCCGATTGGTTAAATCTATCTCCGAGAGGAGACGCGATTCTCA 266
Qy 328 CCCTGCGCGGCGAGAGCGACGCGCTTCATGCGCTTACCAACCGCCCTCGTGGCC 387
Db 267 ATCTGCGCGGCGAGAGCGACGCGCTTCATGCGCTTACCAACCGCGAATGGC 326
Qy 388 CGCTTCCGCGCGCTTCTTGTGGC---CGCTCACCGACTACACTGTCCCCCGGCT 444
Db 327 ACACCTTAGAAAAGCTTCAACATGGCTATCAGCGAGACACACAGCTGTCAAGCTCT 386
Qy 445 CCGCGGACTTCCGCGCGCTCTCGCGGCGCTCTCTCCGCGGCGCTTTCGA 496
Db 387 CAGCTGACTACCGTCTTTAGCGCGAGTTCTCAACGCGGCGCTTTCGA 438

RESULT 15

ABT09682
ID ABT09682 standard; DNA; 1065 BP.

AC ABT09682;

DT 02-DEC-2002 (first entry)

DE Human PAL-18 polynucleotide SEQ ID NO: 33.

KW Human; PAL-18; cancer; chromosome 1q41; prostate cancer; colon cancer;

KW breast cancer; cytostatic; gene; ds.

OS Homo sapiens.

PN US2002106765-A1.

PD 08-AUG-2002.

PF 12-MAR-2001; 2001US-0804682.

PR 10-MAR-2000; 2000US-188586P.

PA (KIND/) KINDERS R J.

PA (CORE/) COREY M J.

PI Kinders RJ, Corey MJ;

DR WPI; 2002-697869/75.

PT New isolated PAL-18 polypeptide, useful for diagnosing, characterizing,

PT and treating disease and in determining disease susceptibility -

PS Claim 1; Page 50-51; 150pp; English.

CC The present invention relates to human PAL-18 polypeptides and

CC polynucleotides. The PAL-18 gene is found on chromosome 1q41. The

CC sequences can be used to diagnose, monitor and treat cancers,

CC particularly breast, colon and prostate cancers. The present sequence is

CC a PAL-18 polynucleotide shown in the invention.

SQ Sequence 1065 BP; 98 A; 606 C; 36 G; 210 T; 115 other;

Query Match 8.8%; Score 72.4; DB 24; Length 1065;

Best Local Similarity 43.8%; Pred. No. 0.00037;

Matches 218; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

Qy 3 CCCTAACAACTCCGCTGCTTTTAAGATCGATCTCCCTTCNCCCTCCCTCCCT 62
Db 472 CCNCTNCACCCCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 531
Qy 63 TCCTCTGAGTCTGACCACTCTCTCGGCTTCAGTAATTCACGCGCATGGCC 122
Db 532 CTCCTTNNCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 591

Qy 123 CGCAGGAGCTTCGCGGACCAACGCGCGGAGAGCCGACGATGCGGCGCCAGCAAG 182
Db 592 CTCNCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 651
Qy 183 GACGCGGAGAGCTCCGATGATCTTCACCAAGAGCTGAGGCGACGCGCGGAG 242
Db 652 TNNCNCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 711
Qy 243 GACCTTGATCTGCATCTCCGAGGAGCTTCAGAGTACAGGCGCTGGTGGCGAC 302
Db 712 CNAFTCCCNCTTCNCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 771
Qy 303 CCGGCGGAGAGTCCGCTCATCACTTCGCGGCGGAGAGCGACCGA-----CGCC 356
Db 772 CCCCNNNNCCNCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 831
Qy 357 TTGATGAGCTTACCAACCGGCTTCGCGGCGGCTTCGCGGCTTCTTCTGCGCG 416
Db 832 CTCACCTNCCNCCNCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 891
Qy 417 CTCACGACTACACTGTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 476
Db 892 CCCCCCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 951
Qy 477 TCCTCCGCGGCGCTCTTC 494
Db 952 TCCCCCCCAACCCCTTC 969

Search completed: December 31, 2003, 16:16:56
Job time : 167.169 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:48:07 ; Search time 1254.26 Seconds
(without alignments)
15947.709 Million cell updates/sec

Title: US-09-857-524B-16

Perfect score: 823

Sequence: 1 ccccccaaacaccctccgtc.....cgtnaagacttggttagcat 823

Scoring table: IDENTITY_NUC

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: Listing first 45 summaries

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_estro:*
9: gb_estc1:*
10: gb_estc2:*
11: gb_estc3:*
12: gb_estc4:*
13: gb_estc5:*
14: gb_estc6:*
15: em_estcun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_png:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	76.4	642	14	CA633913 wleln.pk0
2	484.4	58.9	679	13	BQ788546 WHE4151 B
3	466.6	56.7	563	13	BQ606843 BRY 271B
4	448	54.4	665	14	CA502522 WHE4048_E

5	438.6	53.3	674	10	BE414354 SCU008.G0
6	426.2	51.8	500	14	CA030713 HX07011r
7	412	50.1	493	14	CA637422 wrel.pk0
8	394.2	47.9	453	13	BQ238994 TAF05038F
9	342.2	41.6	453	13	BQ605802 BRY_1370
10	314.8	38.3	1764	11	AY103762 Zee mays
11	308.4	37.5	634	12	BI075898 IP1_22.F1
12	306.8	37.3	744	14	CD463185 ETH1_42.C
13	289.8	35.2	576	29	CC344270 OGM060TV
14	285.4	34.7	4708	14	CA710447 wdk2c.pk0
15	283.6	34.5	400	10	BG158998 RH122_41
16	253	30.7	436	13	BQ239011 TAE05038D
17	195.2	23.7	558	14	CD230432 SS1_43.D0
18	178.6	21.7	257	10	BG158990 RH122_41
19	172	20.9	222	13	BQ998888 H12H15
20	141.2	17.2	186	14	CB883321 HQ01N24w
21	135.4	16.5	452	29	CC011349 PUEAUS3TD
22	128.8	15.7	413	9	AM099929 gdl8e05.Y
23	121.4	14.8	468	9	A1736850 BD34d09.Y
24	105	12.8	693	28	BZ010599 oeg03d06
25	104.4	12.7	807	13	BX464554 BX464554
26	98.6	12.0	1177	29	CC193928 CH261-95J
27	97.8	11.9	670	29	AG126228 Pan trog1
28	96.4	11.7	558	28	BH442910 BOGWX55TR
29	96	11.7	1424	13	BQ720687 AGENCOURT
30	95	11.5	1686	29	CC189908 CH261-611
31	95	11.5	1695	29	CC290874 CH261-172
32	94.8	11.5	635	28	BH557089 BOHRT79TR
33	94.6	11.5	1161	12	BM912505 AGENCOURT
34	94.6	11.5	1292	29	CC208790 CH261-26P
35	94.6	11.5	1767	29	CC294031 CH261-82A
36	94.4	11.5	918	28	AO895329 HS 4832.A
37	94.4	11.5	1068	9	AL570062 AL570062
38	94.4	11.5	1700	29	CC298790 CH261-106
39	94.2	11.4	933	29	AG063086 Pan trog1
40	94.2	11.4	1100	29	CC262597 CH261-167
41	94.2	11.4	1153	29	CC294165 CH261-130
42	94	11.4	1201	9	AL563250 AL563250
43	93.8	11.4	588	29	DR102N24T
44	93.8	11.4	1116	10	BF256617 HVSMBF001
45	93.8	11.4	1156	29	CC319460 TAM32-17H

ALIGNMENTS

RESULT 1
CA633913
LOCUS
DEFINITION CA633913 642 bp mRNA linear EST 23-NOV-2002
wleln.pk0080.d7 wleln Triticum aestivum CDNA clone wleln.pk0080.d7
5' end, mRNA sequence.
ACCESSION CA633913
VERSION CA633913.1 GI:25212209
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
1 (bases 1 to 642)
REFERENCE
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanfey, M.K.
Dupont Wheat cDNA Sequence
Unpublished
Contact: Scott V. Tingey
Crop Genetics
E. I. Dupont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@usa.dupont.com
Seq primer: M13.
Location/Qualifiers

FEATURES

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source
1. .642
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wleim.pk0080.d7"
/tissue_type="leaf"
/clone_lib="wleim"
/notes="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) leaf 7 day old
etiolated seedling (normalized)"
BASE COUNT      102 a      248 c      158 g      121 t      13 others
ORIGIN
Query Match      76.4%; Score 629; DB 14; Length 642;
Best Local Similarity 100.0%; Pred. No. 5.8e-115;
Matches 642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 182 GAGCGCGCGCGCATGATCTCCACCAAGAGCTGAGCGCGCGCGCGA 241
DB 1 GAGCGCGCGCGCATGATCTCCACCAAGAGCTGAGCGCGCGCGCGA 60
QY 242 CGACCTTGATCTCCATCTCCGCGGAGCTCTAAGAGTCAAGCCCTGCGCCACCA 301
DB 61 CGACCTTGATCTCCATCTCCGCGGAGCTCTAAGAGTCAAGCCCTGCGCCACCA 120
QY 302 CCGCGCGCGGAGGTCCTGCTCATCACTCGCGCGCGAGAGCGCACCGCGCTTCAT 361
DB 121 CCGCGCGCGGAGGTCCTGCTCATCACTCGCGCGCGAGAGCGCACCGCGCTTCAT 180
QY 362 GGCCTTACACCCGCGCTCGCTGCGCGCGCTCTTCGCGCGCGCGCTCAC 421
DB 181 GGCCTTACACCCGCGCTCGCTGCGCGCGCTCTTCGCGCGCGCGCTCAC 240
QY 422 CGACTACACTGTCCCCCGCGCTCTCGCGCACTTCCGCGCTCTCGCGCACTCTCTC 481
DB 241 CGACTACACTGTCCCCCGCGCTCTCGCGCACTTCCGCGCTCTCGCGCACTCTCTC 300
QY 482 CGCGGCGCTCTTGAGAGCGCTCGGACACCGCCCAAGTTCCGCTCGTGAAGTGTG 541
DB 301 CGCGGCGCTCTTGAGAGCGCTCGGACACCGCCCAAGTTCCGCTCGTGAAGTGTG 360
QY 542 CTCTTGATCGAGCGCTCTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
DB 361 CTCTTGATCGAGCGCTCTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 602 GGGGGCTCATTTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
DB 421 GGGGGCTCATTTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 662 ACAGGACCTGCGCTCAACGCTGAGTGGCTCGGGAATGCTTAACTCCGATCCTG 721
DB 481 ACAGGACCTGCGCTCAACGCTGAGTGGCTCGGGAATGCTTAACTCCGATCCTG 540
QY 722 GAGTANACACACANACANATTTCTGAANNGTCAATACCTGAATTCGCTGTCG 781
DB 541 GAGTANACACACANACANATTTCTGAANNGTCAATACCTGAATTCGCTGTCG 600
QY 782 GTCAACAAGTCTAAAGCTTGATGCTTAAAGTGTGTTAGCAT 823
DB 601 GTCAACAAGTCTAAAGCTTGATGCTTAAAGTGTGTTAGCAT 642
RESULT 2
BO788546 679 bp mRNA linear EST 26-JUL-2002
LOCUS BO788546
DEFINITION WHE4151_B02_C03ZS Wheat CS whole plant cDNA library Triticum
aestivum cDNA clone WHE4151_B02_C03, mRNA sequence.
ACCESSION BO788546
VERSION BO788546.1 GI:21997018
KEYWORDS EST, Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

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REFERENCE
1 (bases 1 to 679)
AUTHORS Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., Deal,K., Dvorak,J.,
Lazo,G.R., Rauscher,C.J., Wilson,C. and Woo,J.
TITLE The structure and function of the expressed portion of the wheat
genomes - Chinese Spring whole plant cDNA library
JOURNAL Unpublished
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.ueda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
FEATURES
source
1. .679
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE4151_B02_C03"
/tissue_type="Roots", "leaves", "crown", "stem and sheath"
/dev_stage="Adult"
/lab_host="E. coli SOLR"
/clone_lib="Wheat CS whole plant cDNA library"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; plant
tissues from wheat cv. CS grown to full tillering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
RNA was prepared from leaves (young leaf and third leaf),
whole roots, crown, stem and sheath tissues, and then
equal quantities of RNA were pooled from the these
samples. PolyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo excised
to give pBluescript SK(-) phagemids in J. Dvorak's lab (E.
Akhunov, J. Dvorak) at the University of California,
Davis. Colony plating, plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
BASE COUNT      95 a      300 c      176 g      107 t      1 others
ORIGIN
Query Match      58.9%; Score 484.4; DB 13; Length 679;
Best Local Similarity 94.6%; Pred. No. 2.7e-86;
Matches 545; Conservative 0; Mismatches 23; Indels 8; Gaps 4;
QY 75 CTGACCAACCCCTCTGCGCTCCAGCTAAATCAAGCCACCGATGCCCCGACGGGCTTC 134
DB 13 CTGACCAACCCCTCTGCGCTCCAGCTAAATCAAGCCACCGATGCCCCGACGGGCTTC 72
QY 135 GCGGAGCAACGCGCGGGAAGCGGAGCGGCAATGCGCGCGCGGCGGAGGAGCGCGGAG 194
DB 73 GCGGAGCAACGCGCGGGAAGCGGAGCGGCAATGCGCGCGCGGCGGAGGAGCGCGGAG 132
QY 195 GTCCGATGATCTCCACCAAGAGCTGAGGCGGACGCGCGCGGAGGAGGAGGAGGAG 254
DB 133 GTCCGATGATCTCCACCAAGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 192
QY 255 TCCATCTCCGCGGAGCTTACGAGCTGACGCGCTGCTGCGGACCAACCGCGCGGAG 314
DB 193 TCCANCTCCGCGGAGCTTACGAGCTGACGCGCTGCTGCGGACCAACCGCGCGGAG 252
QY 315 GTCCGCTATACACCTCGCGCGGCGGAGCGGACCGGAGCGCTTATGCGCTTACGACCG 374
DB 253 GTCCGCTATACACCTCGCGCGGCGGAGCGGACCGGAGCGCTTATGCGCTTACGACCG 312
QY 375 CCCTCCGCGCGCGCTCTCGCGCGCTTCTTGCTGCGCGGCTTACCGACTACACTGTC 434

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Db      313 CCCTCGTGGCGCCGCTCTCCGCGCTTCTTGTCGGCGCCTCAACGACTACACTGTC 372
Qy      435 CCCCCGCGCTCCGCGCACTTCCGCGCCTCTCTCGCGAGCTCTCTCCGCGGCGCTCTTC 494
Db      373 CCCCCGCGCTCCGCGCACTTCCGCGCCTCTCTCGCGAGCTCTCTCCGCGGCGCTCTTC 432
Qy      495 GAGCGGCTGGG-CACACCCCAAGTTCTGCTCTGCGCAAGTCTGCTCTTCTGCATC 553
Db      433 GAGCGGCTGGGCAACCCCAAGTTCTGCTCTGCGCAATGTCGGTGTCTTCTGCATC 492
Qy      554 GCGCTTACTAGC-TCTCTGCTCTGTCAA--CACCGGGGCAATGTTCCGCGGCGCTCA 610
Db      493 GCGCTTACTAGCCTCTCTGCTCTGCGCAACCGGGGCAATGTTCCGCGGCGCTTC 552
Qy      611 TTGG---CTTATCTGGTCAGTGGGCTGGATTGGC 642
Db      553 ATTGGCTTACTGTGATCCAGTGGGCTGGATTGGC 588

RESULT 3
LOCUS      B0606843          563 bp      mRNA      linear      EST 25-JUN-2002
DEFINITION BRY_2718 wheat EST endosperm library Triticum aestivum cDNA 5',
            mRNA sequence.
ACCESSION  B0606843
VERSION     B0606843.1 GI:21556172
KEYWORDS   EST.
SOURCE      Triticum aestivum (bread wheat)
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
            1 (bases 1 to 563)
REFERENCE   Clarke,B., Lambrecht,M. and Rhee,S.Y.
            Arabidopsis genomic information for interpreting wheat EST
            sequences
AUTHORS     Funtc. Integr. Genomics 3 (1-2), 33-38 (2003)
TITLE       12590341
JOURNAL     MEDLINE
PUBMED      22478026
COMMENT     Contact: Lambrecht M
            The Arabidopsis Information Resource
            Carnegie Institution of Washington, Dept. of Plant Biology
            260 Panama Street, Stanford, CA 94305, USA
            Tel: 1 650 325 1521 x 251
            Fax: 1 650 325 3748
            Email: theebacom@stanford.edu.
            Location/Qualifiers
FEATURES
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                    /organism="Triticum aestivum"
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                    /db_xref="taxon:4565"
                    /tissue_type="endosperm"
                    /dev_stage="developing endosperm tissue 8, 10 and 12 DPA
                    (days post anthesis)"
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BASE COUNT      72 a      249 c      149 g      93 t
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Query Match      56.7%; Score 466.6; DB 13; Length 563;
Best Local Similarity 96.4%; Pred. No.9.1e-83;
Matches 509; Conservative 0; Mismatches 15; Indels 4; Gaps 3;

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Db      121 ATCTCCACCAAGAGCTGACGAGCGACGCTGCCGGAGACCTTGATCTTCATCTCC 180
Qy      264 GGGAGAGCTTACAGCTACAGCCCTGCTGGCGCAACACCGGGGCGGAGGATCCGCTC 323
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Qy      324 ATCACCTTGGCGGCGAGACGCCACGACGCTTCATGAGCTTACCAACCGGCTTCGTC 383
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Qy      384 CCGCGCTCTCTCCGCGCTTCTTCTGTCGGCGGCTTACGACTACATCTCCCGCGGC 443
Db      301 CCGCGCTCTCTCCGCGCTTCTTCTGTCGGCGGCTTCTCGACTACACCTCCCGCGGC 360
Qy      444 TCGCGGACTTCGGCGGCTCTCTCGGCGAGCTCTCTCGGCGGCTCTTCGAGGCGTC 503
Db      361 TTGGCGGACTTCGGCGGCTCTCTCGGCGAGCTCTCTCGGCGGCTCTTCGAGGCGTC 420
Qy      504 GG-CACACCCCAAGTCTGCTGCTGCGCAAGTCTGCTCTTCTGACTCGGCTCTTAC 562
Db      421 GGCACACCCCAAGTCTGCTGCTGCGCAAGTCTGCTCTTCTGACTCGGCTCTTAC 480
Qy      563 TGC-TCTTGCCTGCTCTCA--CACCGGGGCAATGTTCCCGGGGCGC 607
Db      481 TCGTCTCTGCTGCTGCTCCAGCACCGGGGCGCCACATGTTCCCGGGGCGC 528

RESULT 4
LOCUS      CA502522          665 bp      mRNA      linear      EST 14-NOV-2002
DEFINITION WHE4048 B08 J16ZT Wheat meiotic anther cDNA library Triticum
            aestivum cDNA clone WHE4048_B08_J16, mRNA sequence.
ACCESSION  CA502522
VERSION     CA502522.1 GI:24993482
KEYWORDS   EST.
SOURCE      Triticum aestivum (bread wheat)
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
            1 (bases 1 to 665)
REFERENCE   Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R., Pham
            J., Rausch,C.J., Sutton,T., Woo,J., and Wilson,C.
            The structure and function of the expressed portion of the wheat
            genomes - Meiotic anther cDNA library
AUTHORS     Unpublished
TITLE       Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105585773
            Fax: 5105595818
            Email: oanderson@pw.usda.gov
            Sequences have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: 77 primer.
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                    /lab_host="E. coli DH10B"
                    /clone_lib="wheat meiotic anther cDNA library"
                    /note="Vector: pSPORT1, Site 1: SalI, Site 2: NotI. Plants
                    were grown in a glasshouse. Anther meiotic stage was
                    determined by removing anthers from individual primary
                    florets. One anther was sacrificed for microscopic staging
                    , and if determined to be between (and including) meiotic
                    stages pre-meiosis and metaphase I, the remaining two

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anthers were collected and pooled for library construction. The tissue, total RNA, and poly(A) RNA were prepared, cDNA synthesised, and directionally ligated into pSPORT1 by Tim Sutton in the P Langridge lab at the Department of Plant Science, University of Adelaide, Waite Campus, Australia. Average insert size 1.5kb. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 90 a 293 c 178 g 104 t

ORIGIN

Query Match 54.4%; Score 448; DB 14; Length 665;

Best Local Similarity 93.8%; Pred. No. 4.5e-79;

Matches 511; Conservative 0; Mismatches 26; Indels 8; Gaps 4;

106 CCAAGCCACCGATGAGCCCGACCGGCTTCCGCGACGACGAGCCGCGGAGACCGACCA 165
 36 CCAAGCCACCGATGAGCCCGACCGGCTTCCGCGACGACGAGCCGCGGAGACCGACCA 95
 166 TCCGCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 225
 96 TCCGCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 155
 226 CGCAGCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 285
 156 CGCAGCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 215
 286 CTTGAGCTGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 345
 216 CTTGAGCTGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 275
 346 CCAAGCCACCGATGAGCCCGACCGGCTTCCGCGACGACGAGCCGCGGAGACCGACCA 405
 276 CCAAGCCACCGATGAGCCCGACCGGCTTCCGCGACGACGAGCCGCGGAGACCGACCA 335
 406 TCGTGGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 465
 336 TCGTGGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 395
 466 TCGGCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 524
 396 TCGGCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 455
 525 TCGGCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 581
 456 TCGTGGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 515
 582 ACCGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 637
 516 CCGGCGCGCGACGAGAGAGCGCGCGACGTCGATGATCTCCACCAAGAGCTGAGG 575
 638 TTGGC 642
 576 TTGGC 580

RESULT 5
 BE414354 674 bp mRNA linear EST 24-JUN-2000
 LOCUS SCU008.G07.R990714 ITBC SCU wheat Endosperm Library Triticum
 DEFINITION aestivum cDNA clone SCU008.G07, mRNA sequence.
 ACCESSION BE414354
 VERSION BE414354.1 GI:9412186
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 Triticaceae; Triticum.
 1 (bases 1 to 674)
 Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier,
 S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
 Hermann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,

TITLE
 JOURNAL
 COMMENT
 Contact: Holton T
 Centre for Plant Conservation Genetics, Southern Cross University
 PO Box 157, Lismore NSW 2480 AUSTRALIA
 Tel: 61 2 6622 3409
 Fax: 61 2 6622 2080
 Email: tholton@scu.edu.au
 International Triticaceae EST Cooperative (ITBC): Production of
 Unpublished Sequence tags for Species of the Triticaceae
 (2000)

FEATURES
 source
 1. 674
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cuiivar="Myuna"
 /db_xref="taxon:4565"
 /clone="SCU008.G07"
 /issue_type="endosperm"
 /clone_lib="ITBC SCU wheat Endosperm Library"
 /note="Vector: Bluescript II SK(-)"

BASE COUNT 103 a 272 c 182 g 112 t 5 others

Query Match 53.3%; Score 438.6; DB 10; Length 674;

Best Local Similarity 91.3%; Pred. No. 3.3e-77;

Matches 506; Conservative 0; Mismatches 44; Indels 4; Gaps 4;

56 CCTCCCTCCCTCTGAGTCTGACCAACCCCTCTCGCGCTCCAGCTAAATCCAGCGACC 115
 88 CCCCCGGGTGAGAGATTCGACACAGCTCTCTGCGCTTCACTAATNACAGCGACC 147
 116 GATGCGCGCGACGAGGCTTCCGCGACGCAAGCGCGGAGCGCAATGCGGCGCG 175
 148 GATGCGCGCGACGAGGCTTCCGCGACGCAAGCGCGGAGCGCAATGCGGCGCG 207
 176 CAGCAAGAGCGCGCGAGAGTCCGATGATCTTCAACCAAGAGCTCAGCGCGCGCG 235
 208 CAGCAAGAGCGCGCGAGAGTCCGATGATCTTCAACCAAGAGCTCAGCGCGCGCG 267
 236 CCGGAGAGAGCTTGGATCTCCATCTCCGAGGAGCTCTGACAGTCCAGCGCGCTGCG 295
 268 CCGGAGAGAGCTTGGATCTCCATCTCCGAGGAGCTCTGACAGTCCAGCGCGCTGCG 327
 296 CCAACACCGCGCGAGAGTCCGCTCATCAACCTCGCGCGAGAGCGCAAGCGCGCG 355
 328 CCAACACCGCGCGAGAGTCCGCTCATCAACCTCGCGCGAGAGCGCAAGCGCGCG 387
 356 CTTATGAGGCTTACCAACCGCGCTTCCGAGGCGCGCTCTCCGCGCTTCTTGTGCGCG 415
 388 CTTATGAGGCTTACCAACCGCGCTTCCGAGGCGCGCTTCCGAGGCGCGCTTCTTGTGCGCG 447
 416 CTTATGAGGCTTACCAACCGCGCTTCCGAGGCGCGCTTCCGAGGCGCGCTTCTTGTGCGCG 475
 448 NCTCTTGAGCTTACCAACCGCGCTTCCGAGGCGCGCTTCCGAGGCGCGCTTCTTGTGCGCG 505
 476 CTTCTCGCGCGGCTTTCGAGGCGCGTCCG-CACACCCCAAGTTCTCTGTCGCAAA 534
 506 CTTCTCGCGCGGCTTTCGAGGCGCGTCCG-CACACCCCAAGTTCTCTGTCGCAAA 565
 535 GTGCGGCTTTCGATGAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
 566 GTGCGGCTTTCGATGAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625
 594 TGTTCGCGCGGCGCG 607
 626 TGTTCGCGCGGCGCG 639

RESULT 6

CA030713 500 bp mRNA linear EST 24-OCT-2002
 LOCUS HX07011r HX Hordeum vulgare subsp. vulgare cDNA clone HX07011
 DEFINITION 5-PRIME mRNA sequence.
 ACCESSION CA030713
 VERSION CA030713.1 GI:24326542
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 500)
 Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
 EST sequencing and analysis in barley (2002)
 Unpublished
 Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5532
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 500 Std Error: 0.00
 Plate: 7 row: 0 column: 11
 Seq primer: M3rev.
 Location/Qualifiers
 1..500
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /db_xref="GABI:271384"
 /db_xref="taxon:112509"
 /clone="HX07011"
 /tissue_type="apex"
 /dev_stage="apex (3-5 mm in size)"
 /lab_host="Xl10-Gold"
 /clone_1ib="HX"
 /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

BASE COUNT 61 a 225 c 135 g 79 t
 ORIGIN
 Query Match 51.8%; Score 426.2; DB 14; Length 500;
 Best local Similarity 96.7%; Pred. No. 9.3e-75;
 Matches 445; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
 107 CAGCGCACCGATGCGCGCAGCGGCTTCGCGAGCGAAGCGCGGAGCGCGCAAT 166
 |||||
 30 CAGCGCACCGATGCGCGCAGCGGCTTCGCGAGCGTACCGCGCGCGCGCAAT 89
 |||||
 167 GCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226
 |||||
 90 GCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 149
 |||||
 227 GACGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 286
 |||||
 150 GACGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 209
 |||||
 287 CTGGCTGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 346
 |||||
 210 GTGGCTGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 269
 |||||
 347 CACGCGCGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406
 |||||
 270 CACGCGCGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 329
 |||||

CA637422 493 bp mRNA linear EST 23-NOV-2002
 LOCUS wrel.pK0004.c7 wrel Triticum aestivum cDNA clone wrel.pK0004.c7 5'
 DEFINITION end, mRNA sequence.
 ACCESSION CA637422
 VERSION CA637422.1 GI:25215718
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Triticum.
 1 (bases 1 to 493)
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.
 Dupont Wheat cDNA Sequence
 Unpublished
 Contact: Scott V. Tingey
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@usa.dupont.com
 Seq primer: M3.
 Location/Qualifiers
 1..493
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wrel.pK0004.c7"
 /tissue_type="root"
 /clone_1ib="wrel"
 /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; wheat (Triticum aestivum L.) root; 7 day old etiolated seedling"

BASE COUNT 72 a 218 c 119 g 81 t
 ORIGIN
 Query Match 50.1%; Score 412; DB 14; Length 493;
 Best local Similarity 95.0%; Pred. No. 6.1e-72;
 Matches 458; Conservative 0; Mismatches 21; Indels 3; Gaps 3;
 1 CTCCCTAACAACTCCGCTGCTGTTTAAAGATCCGATCTCCCTTCCCTCC 60
 |||||
 1 CTCCCTAACAACTCCGCTGCTGTTTAAAGATCCGATCTCCCTTCCCTCC 60
 |||||
 61 CTTCCTCTGAGTCTCGACCACTCCCTCTCGGCTTCAGCTAAATCAAGCCATG 120
 |||||
 61 CTTCCTCTGAGTCTCGACCACTCCCTCTCGGCTTCAGCTAAATCAAGCCATG 120
 |||||
 121 CCGGACGCGGCTTCGCGAGCGAAGCGCGCGGAGCGGAGCGGAGCGGAGCG 180
 |||||
 121 CCGGACGCGGCTTCGCGAGCGAAGCGCGCGGAGCGGAGCGGAGCGGAGCG 180
 |||||
 181 AGAGCGCGCGCGAGCTCCGATGATCTCCACCAAGAGCTGAGGCGAGCGCGCG 240
 |||||
 181 AGAGCGCGCGCGAGCTCCGATGATCTCCACCAAGAGCTGAGGCGAGCGCGCG 240
 |||||

QY 241 ACCAGCTCTGATCTCCATCTCCGGGAGCGTCTACGAGTCAAGCCCTGGGCGCCACC 300
 Db 241 ACGACCTCTGATCTCCATCTCCGGGAGCGTCTACGAGTCAAGCCCTGGGCGCCACC 300
 QY 301 -ACCCGGGCGGAGGTCCTGCTCATCACTTCGCGGCGGAGAGCGCACCGCTTC 359
 Db 301 AACCCGGGCGGAGGTCCTGCTCATCACTTCGCGGCGGAGAGCGCACCGCTTC 360
 QY 360 ATGGGCTTACC-ACCCGCTCTCCGGGCGGCGGCTCTCC-CCGCTTCTTGTGGCGCGC 417
 Db 361 ATGGGCTTACC-ACCCGCTCTCCGGGCGGCGGCTCTCC-CCGCTTCTTGTGGCGCGC 420
 QY 418 TCACCGACTACATGTCTCCCGCGCTCCGCGGACTTCGCGGCTCTCTGCGGAGCTCT 477
 Db 421 TCTCCGACTACATGTCTCCCGCGCTCCGCGGACTTCGCGGAGCTCTCTGCGGAGCTCT 480
 QY 478 CC 479
 Db 481 TC 482

RESULT 8
 BQ238994 453 bp mRNA linear EST 03-MAY-2002
 LOCUS TaE05038F05R TaE05 Triticum aestivum cDNA clone TaE05038F05R, mRNA
 DEFINITION
 ACCESSION BQ238994
 VERSION BQ238994.1 GI:20434870
 KEYWORDS
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Triticum.
 1 (bases 1 to 453)
 Cloutier,S.
 Wheat functional genomics - Glenlea developing seeds cDNA libraries
 Unpublished
 Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-Food Canada
 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@agr.ca
 was cloned directionally, not all sequences generated with reverse
 primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >2.0 kb
 Plate: 038 row: F column: 05
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..453
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="TaE05038F05R"
 /tissue_type="developing seeds"
 /dev_stage="5 days after anthesis"
 /lab_host="E. coli DH10B"
 /note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
 NotI; Site_2: MluI; mRNA obtained from wheat seeds of
 cultivar Glenlea 5 days post-anthesis"

BASE COUNT 62 a 214 c 109 g 68 t
 ORIGIN
 Query Match 47.9%; Score 394.2; DB 13; Length 453;
 Best Local Similarity 94.8%; Pred. No. 2e-68; Indels 4; Gaps 1;
 Matches 419; Conservative 0; Mismatches 19; Indels 4; Gaps 1;
 QY 17 CGTGTCTTTTAAATCGATCTCCCTTCMCCCTCCCTCTCTCTGAG--- 72
 Db 12 CGTTCCTTTTAAATCGATCTCCCTTCGCGCTCCCTCTCTCTCTCTCTCC 71

QY 73 TCTGACCAACCCCTCTCTGAGCTCCAGCTAAATCCAGCGCAACGATGACCGGAGCT 132
 Db 72 TCTGACCAACCCCTCTCTGAGCTCCAGCTAAATCCAGCGCAACGATGACCGGAGCT 131
 QY 133 TCGCGAGCGCAACGCGCGCGGAGAGCGCAATGCGCGCGCGGAGAGAGCGCGCG 192
 Db 132 TCGCGAGCGCAACGCGCGCGGAGAGCGCAATGCGCGCGCGGAGAGAGCGCGCG 191
 QY 193 ACGTCCGATGATCTTCCACCAAGAGCTGAGGCGGAGCGCGCGGAGAGAGCTTGA 252
 Db 192 ACGTCCGATGATCTTCCACCAAGAGCTGAGGCGGAGCGCGCGGAGAGAGCTTGA 251
 QY 253 TCTTCATCTCCGGGAGGAGTCTACAGATGACGCGCTGAGTGGCGGAGCGCGGAG 312
 Db 252 TCTTCATCTCCGGGAGGAGTCTACAGATGACGCGCTGAGTGGCGGAGCGCGGAG 311
 QY 313 AGGTCCGCTCATACCTTCGCGGCGGAGAGCGGAGCGGAGCGCTTCATGAGCTTAC 372
 Db 312 AGGTCCGCTCATACCTTCGCGGCGGAGAGCGGAGCGGAGCGCTTCATGAGCTTAC 371
 QY 373 CGGCTTCGCTGCGCGCGCTCTCTCCGCGCTTCTTGTGGCGGCGCTTACGACTG 432
 Db 372 CGGCTTCGCTGCGCGCGCTCTCTCCGCGCTTCTTGTGGCGGCGCTTACGACTG 431
 QY 433 TCCCGCGCGCGCTCCGCGGACTT 454
 Db 432 TACCCCGCGCTTCGAGGACTT 453

RESULT 9
 BQ605802 697 bp mRNA linear EST 25-JUN-2002
 LOCUS BRN_1370 wheat EST endosperm library Triticum aestivum cDNA 5',
 DEFINITION
 ACCESSION BQ605802
 VERSION BQ605802.1 GI:21554898
 KEYWORDS
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Triticum.
 1 (bases 1 to 697)
 Clarke,B., Lambrecht,M. and Rhee,S.Y.
 Arabidopsis genomic information for interpreting wheat EST
 sequences
 JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
 MEDLINE 22478026
 PUBMED 12590341
 CONTACT: Lambrecht M
 The Arabidopsis Information Resource
 Carnegie Institution of Washington, Dept. of Plant Biology
 260 Panama Street, Stanford, CA 94305, USA
 Tel: 1 650 325 1521 x 251
 Fax: 1 650 325 3748
 Email: rhees@coma.stanford.edu.
 Location/Qualifiers
 1..697
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Wynna"
 /db_xref="taxon:4565"
 /tissue_type="endosperm"
 /dev_stage="developing endosperm tissue 8, 10 and 12 DPA
 (days post anthesis)"
 /clone_lib="wheat EST endosperm library"

BASE COUNT 114 a 217 c 177 g 189 t
 ORIGIN
 Query Match 41.6%; Score 342.2; DB 13; Length 697;
 Best Local Similarity 86.6%; Pred. No. 4.3e-58;
 Matches 388; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

120 GCCCCAGGAGGCTTCGCGGACGCAACGCGCGCGGAAAGCCGACGCAATGCGGCGCCAGC 179
 1 GCGCCAGAGGCTTCGCGGACGCAACGCGCGCGGAAAGCCGACGCAATGCGGCGCCAGC 60
 180 AAGAGCGCGCGGAGCTTCGCGGACGCAATGCTTCACCAAGAGAGCTTCGCGGCGCGCGG 239
 61 AAGAGCGCGCGGAGCTTCGCGGACGCAATGCTTCACCAAGAGAGCTTCGCGGCGCGCGG 120
 240 GACGACCTCTGATGATCCATCTCCGCGGAGCTTCAGAGTCAAGCGGCTTCGCGGCGCGC 299
 121 GACGACCTCTGATGATCCATCTCCGCGGAGCTTCAGAGTCAAGCGGCTTCGCGGCGCGC 180
 300 CACCGCGCGGAGGAGTTCGCGGCTTCACGCTTCGCGGCGGAGAGCGGCGCGGCTTC 359
 181 CACCGCGCGGAGGAGTTCGCGGCTTCACGCTTCGCGGCGGAGAGCGGCGGCTTC 240
 360 ATGAGCTTACGACCGCGCTTCGCGGCGGCTTCGCGGCGGCTTCGCGGCGGCTTC 419
 241 ATGAGCTTACGACCGCGCTTCGCGGCGGCTTCGCGGCGGCTTCGCGGCGGCTTC 300
 420 ACCGACTACAGTCTCCCGCGGCTTCGCGGCTTCGCGGCGGCTTCGCGGCGGCTTC 479
 301 ACCGACTACAGTCTTCACGCTTCGCGGCTTCGCGGCGGCTTCGCGGCGGCTTC 360
 480 TCCGCGGCGGAGTTCGCGGAGC-GCGTGGGACACCGGCAAGTTCGCTGCGCAAGTTC 538
 361 TTCGCGGCGGCTTCGCGGAGGCGGAGGACACCTTCGCTGCTTGAATTCGCTG 420
 539 GTGCTCTTCGATCGGCGCTTCGCTGCT 566
 421 GGGCTTTTGAATAGCCCTTATTGCT 448

RESULT 10
 LOCUS AY103762 1764 bp mRNA linear HTC 16-OCT-2002
 DEFINITION Zea mays PC0087385 mRNA sequence.
 ACCESSION AY103762
 VERSION AY103762.1 GI:21206840
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1764)
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
 Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1764)
 Coe,E.H.

JOURNAL Direct Submission
 REFERENCE Submitted (25-APR-2002) Maize Mapping Project, University of
 AUTHORS Missouri, Columbia, MO 65211, USA
 TITLE If you are interested in getting corresponding physical clones,
 JOURNAL these are publicly available from ZmDB, www.zmdb.iastate.edu; B1ASR
 searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.
 FEATURES
 source
 1..1764
 location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeDB:634923"
 /db_xref="taxon:4577"
 /clone_11b="Maize Mapping Project/DuPont Consensus
 Library"
 /note="this sequence is part of a project of EST

assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

BASE COUNT 310 a 602 c 456 g 396 t
 ORIGIN
 Query Match 38.3%; Score 314.8; DB 11; Length 1764;
 Best Local Similarity 78.2%; Pred. No. 1,2e-52;
 Matches 417; Conservative 0; Mismatches 108; Indels 8; Gaps 3;

82 CCCCTCTCGCGCTCCAGTAAATCAGCCAGGAGCGGCGCTTCGCGAGC 141
 27 CCTCCCGCGCTCCCTCAATCAGCAGCCAGGCGGATCGAGCCGCGG 86
 142 CACGCGCGCGGAGCCGAGCAATGCGGCGGCGAGCA-----GAGCGCGCGAGC 195
 87 CATGCGCGCGCTTCGATGCAATGCGGCGGCGGCGAGCGCGGCGAGC 146
 136 TCCGATGATCTCCACCAAGAGCTGAGGCGGAGCGGCGGAGCACTTGGATCT 255
 147 TCGCATATCTCTTCACAGAGAGCTCCGCTCAGCTTCGCGAGCACTTGGATCT 206
 256 CCATCTCGGAGAGCTTACAGAGCTCAGCGCTGCGTGGCGGCGGCGAGC 315
 207 CCATCTCGGAGAGCTTACAGAGCTCAGCGCTGCGTGGCGGCGGCGAGC 266
 316 TCCGCTATCATCCTTCGCGGCGGAGAGCGGAGCGCTTCATGAGCTTACACCGCG 375
 267 TCCGCTATCATCCTTCGCGGCGGAGAGCGGAGCGGAGCGCTTCGCTACACCGCG 326
 376 CCTCGGAGCGGCGGCTTCGCGGCGGCTTCGCGGCGGCTTCGCTACAGCTACGCTCC 435
 327 CCTCGGAGCGGCGGCTTCGCGGCGGCTTCGCGGCGGCTTCGCTACAGCTACGCTCC 386
 436 CCGCGCGCTTCGCGGAGCTTCGCGGCGGCTTCGCGGAGCTTCGCGGCGGCTTCGCG 495
 387 CCGCGCGCTTCGCGGAGCTTCGCGGCGGCTTCGCGGAGCTTCGCGGCGGCTTCGCG 446
 447 AACGCGTGGCGGCGGAGCTTCGCGGCGGCTTCGCGGAGCTTCGCGGCGGCTTCGCG 506
 496 AGCGGCTGGG-CACACCGGCAAGTTCGCTTCGCGGAGCTTCGCGGAGCTTCGCGG 554
 555 GCGCTTA-CTGCTCTTCGCGGCTTCGCGGAGCTTCGCGGAGCTTCGCGGAGCTTCGCG 606
 507 CGCTTACTCTGCTTCGCGGAGCTTCGCGGAGCTTCGCGGAGCTTCGCGGAGCTTCGCG 559

RESULT 11
 LOCUS B1075898 634 bp mRNA linear EST 20-JUN-2001
 DEFINITION IP1 22.F11.b1 A002 Immature panicle 1 (IP1) Sorghum bicolor cDNA,
 mRNA sequence.
 ACCESSION B1075898
 VERSION B1075898.1 GI:14514555
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 634)
 Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and Pratt
 L.H.
 An EST database from Sorghum: developing preanthesis panicles
 Unpublished
 CONTACT Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210

QY 368 CCACCCGCTCCGTCGCGCCGCTCTCTCGCGCTTCTTGTGCGCGCCCTCACCGACTA 427
 Db 258 CCACCCGCTCCGTCGCGCGCCGCTCTCTCGCGCTTCTTGTGCGCGCCCTCACCGACTA 317
 QY 428 CACTGTCCCGCCGCTCCGCGACTTCCGCGCCCTCTCTCGCGAGCTTCTCTCGCGGG 487
 Db 318 CACCGCTCTCCCGCGCTCCGCGACTACCGCGCCCTCTCTCGCGAGCTTCTCTCGCGGG 377
 QY 488 CCTCTTCGAGCGGCTCGG-CAGACCCCGAAGTTCGCTCGCTCGGCAAAATCTGTCTTT 546
 Db 378 CCTCTTCGAGCGGCTCGGCCCCCAAGGTCAGCTCGCCCTCATGCGCGTCTT 437
 QY 547 CTGATCGGCTCTTA-CTGCTCTCTCGCTCTCAACACCGGCGCCACATGTTGCGCGGG 605
 Db 438 CTACCGCGGCTCTTACTGTCTCTCTGCTCGCGCACCGGCTCTCGCGCACTCTCGCGGG 497
 QY 606 G 606
 Db 498 G 498

RESULT 13
 CC344270 576 bp DNA linear GSS 16-MAY-2003
 LOCUS OGMBO60TV ZM 0.7.1.5 KB Zea mays genomic clone ZMMMA0385123,
 DEFINITION genomic survey sequence.
 ACCESSION CC344270
 VERSION CC344270.1 GI:30813676
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 576)
 Whitefaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T., Resnick
 A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek
 R.W., Nurnberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished
 TITLE TIGR
 JOURNAL 9712 Medical Center Drive, Rockville, MD 20850, USA
 COMMENT Contact: Cathy Whitefaw
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitefaw@tigr.org
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source 1..576
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_1ib="ZMMMA0385123"
 /clone_1ib="ZM 0.7.1.5 KB"
 /note="Vector: pBCK-; Site 1: HincII, 0.7-1.5 kb
 methylation filtered genomic DNA library"
 BASE COUNT 85 a 263 c 135 g 93 t
 ORIGIN

Query Match 35.2%; Score 289.8; DB 29; Length 576;
 Best Local Similarity 79.7%; Pred. No. 1e-47;
 Matches 372; Conservative 0; Mismatches 82; Indels 13; Gaps 2;

QY 57 CTCCCTTCTCTAGTCTGACACCCCTCTCTCGCGCTCAAGCTAATTCAGCCACCG 116
 Db 115 CTCCCACTTCCACATTTCTCCCGCTCTCTCGAGACCTCCAAATACAGACACCC 174
 QY 117 ATGGCCCGACGCGCTTGGCGAGCGCAACGCGCCGGAAGCGAGCGCAATGCGCGCGC 176
 Db 175 AT-----AGGGGCGACGCGCGCGCAATGCGCGCTCTGCGAGCGCAATGCGCGCGC 227

QY 177 AGCAAGA-----CGCGCCGACGTCCGACATATCTCACCAAGAGCTGACGGCGAC 230
 Db 228 GGAAGAGCGCGGTGCGCGCGGAGCGCTTGATCTCTCAAGAGAGCTCCGCGAGAC 287
 QY 221 GCGCGCGGAGACACTTGTGATCTTCATCTCGGAGAGCTTACAGAGCTCACGCCCTGG 290
 Db 288 GCGTCGCGCGGACACTGTGATCTTCATCTCGGAGAGCTTACAGAGCTGACGCCCTGG 347
 QY 291 CTGCGCCACACACCGCGGCGGAGAGTCCCGCTCATACCTTCCGCGCCACAGACGAC 350
 Db 348 CTTCGCCACACCGCGGCGGAGAGTCCCGCTCATACCTTCCGCGGAGAGACGAC 407
 QY 351 GACGCTTCATGAGCTTACACCGCGCTCCGCGCGCGCTCTCTCGCGCTTCTCTGTC 410
 Db 408 GACGCTTCGCGGCTTACACCGCGCTCTCGCGCGCGCTCTCTCGCGCTTCTCTGTC 467
 QY 411 GCGCGCTTCACCGACTACACTGTCTCCCGCGCTCTCGCGAGCTTCCGCGCTCTCTGCG 470
 Db 468 GCGCGCTTCACCGACTACACTGTCTCCCGCGCTCTCGCGAGCTTCCGCGCTCTCTGCG 527
 QY 471 CAGCTCTCTCTCGCGCGGCTCTTTCAGGCGCGTCCGACACCGCCCAAG 517
 Db 528 CAGCTCTCTCTCGCGCGGCTCTTTCAGGCGCGTCCGACACCGCCCAAG 574

RESULT 14
 CA710447 478 bp mRNA linear EST 26-NOV-2002
 LOCUS wdk2c.pk015.k22 wdk2c Triticum aestivum cDNA clone wdk2c.pk015.k22
 DEFINITION 5' end, mRNA sequence.
 ACCESSION CA710447
 VERSION CA710447.1 GI:25432240
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 1 (bases 1 to 478)
 Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
 Miao,G., Caraher,N. and Hanafey,M.K.
 Dupont Wheat cDNA Sequence
 Unpublished
 TITLE Crop Genetics
 JOURNAL E. I. Dupont de Nemours and Company
 COMMENT 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@usa.dupont.com
 Seq primer: M13.

FEATURES
 source 1..478
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
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 /clone_1ib="wdk2c"
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
 XhoI; Wheat (Triticum aestivum L.) developing kernel, 7
 days after anthesis."

BASE COUNT 67 a 199 c 111 g 78 t 23 others
 ORIGIN

Query Match 34.7%; Score 285.4; DB 14; Length 478;
 Best Local Similarity 87.8%; Pred. No. 7.7e-47;
 Matches 324; Conservative 0; Mismatches 42; Indels 3; Gaps 2;

QY 1 CTCCCTAACAACTCTCGTGTGTTTAAGATCGATCTCCCTTCNCCCTCTCCCTTC 60
 Db 14 CTCCCTAACAACTCTCGTGTGTTTAAGATCGATCTCCCTTCNCCCTCTCCCTTC 73

QY 61 CTTCTCTGAGTCTGAGCACCCTCTCTGCGCTCCAGCTAAATCCAGCCACCGATGG 120
 DB 74 CTTCTCTGAGTCTGAGCACCCTCTCTGCGCTCCAGCTAAATCCAGCCACCGATGG 133
 QY 121 CCGGCAACGGGCTTCGGGAGCAACGGCGCGGAAAGCCGACGCAATGCCCGCCAGCA 180
 DB 134 MCGGCAACGGGCTTCGGGAGCAACGGCGCGGAAAGCCGACGCAATGCCCGCCAGCA 193
 QY 181 AGGACCCCGGAGCTCCGATATCTCCACAAAGAGCTGACAGGCGCAAGCGCGCGG 240
 DB 194 AGGACCCCGGAGCTCCGATATCTCCACAAAGAGCTGACAGGCGCAAGCGCGCGG 253
 QY 241 AGGACCTTGATATCTCCATCTCCGAGAGCTGAC-GAGCTCAAGCGCTGCGCGCAC 299
 DB 254 AGGACCTTGATATCTCCATCTCCGAGAGCTGAC-GAGCTCAAGCGCTGCGCGCAC 313
 QY 300 CACCC--GGGCGGCGAGTCCCGCTCATCACCTCGCGCGGCGAGAGCCACCGAGGCT 357
 DB 314 CACCCCGGCGGAGGTCGCGCTCATCTCCTGCGCGGCGAGAGCCACCGAGGCT 373
 QY 358 TCATGGCCT 366
 DB 374 GNAAGCCTT 382

RESULT 15

BG158998 400 bp mRNA linear EST 06-FEB-2001
 LOCUS RH122_41_d11_b1_A003 Rhizome2 (RH122) Sorghum proplinguunum cDNA, mRNA
 DEFINITION sequence.

ACCESSION BG158998
 VERSION BG158998.1 GI:12692662
 KEYWORDS EST.

SOURCE Sorghum proplinguunum
 ORGANISM Sorghum proplinguunum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 400)
 Cordonnier-Pratt,M.-M., Gingle,A., Petersen,A., Sudman,M. and Pratt
 L.H.

REFERENCE An EST database from Sorghum: Sorghum proplinguunum rhizomes
 AUTHORS Unpublished
 JOURNAL Contact: Cordonnier-Pratt MM
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@prattuga.edu
 Seq primer: JEN REV
 High quality sequence stop: 297
 POLY(A)=No.

FEATURES

source Location/Qualifiers
 1..400

/organism="Sorghum proplinguunum"
 /mol_type="mRNA"
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 /clone_lib="Rhizome2 (RH122)"
 /note="Organ: Rhizome; Vector: pBluescript II from Lambda
 Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made
 from poly-A RNA in the cloning vector Lambda Zap II.
 Clones to be sequenced were prepared by mass excision."
 46 a 188 c 112 g 54 t

BASE COUNT

Query Match 34.5%; Score 283.6; DB 10; Length 400;
 Best Local Similarity 88.6%; Pred. No. 1.7e-46;
 Matches 318; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

QY 182 GGAAGCGCGGAGCTCCGATGATCTTCACCAAGAGCTGACGCGAGCGCGCGGGA 241
 DB 41 GGGCGCGGAGCTCCGATGATCTTCACCAAGAGCTCCGCGAGCGCGCGCGGGA 100

QY 242 CGACTCTGAGATCTCCATCTCCGAGAGCTTACAGAGTACAGCCCTGGCTGCGCACCA 301
 DB 101 CGACTCTGAGATCTCCATCTCCGAGAGCTTACAGAGTACAGCCCTGGCTGCGCACCA 160
 QY 302 CCGGCGCGGAGGTCCTCGCTATCACCTCGCGGCGAGAGCGCCACCGAGCTTTGAT 361
 DB 161 CCGGCGCGGAGGTCCTCGCTATCACCTCGCGGCGAGAGCGCCACCGAGCTTTGAT 220
 QY 362 GGCCTACACCGCGCTCCGATGCGCGGCTCTCCGCGGCTTTGATGAGCGCGCTCAC 421
 DB 221 GGCCTACACCGCGCTCCGATGCGCGGCTCTCCGCGGCTTTGATGAGCGCGCTCAC 280
 QY 422 CGACTACATGTCCTCCCGCGCTCCGCGAGTTCGCGCGCTCTCGCGAGCTTCCTC 481
 DB 281 CGACTACATGTCCTCCCGCGCTCCGCGAGTTCGCGCGCTCTCGCGAGCTTCCTC 340
 QY 482 CCGGCGCTCTTTCGAGCGGCTGCG-CACACCCCAAGTTCTGCTGTCGCAAAAGTCG 539
 DB 341 CCGGCGCTCTTTCGAGCGGCTGCG-CACACCCCAAGTTCTGCTGTCGCAAAAGTCG 399

Search completed: December 31, 2003, 23:59:29
 Job time: 1259.26 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:49:12 ; Search time 40.8386 Seconds
(without alignments)
8894.970 Million cell updates/sec

Title: US-09-857-524B-16

Perfect score: 823
Sequence: 1 cccctacaacaccgcgtt.....cgttaagacttggttagcat 823

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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5: /cgn2_6/prodata/2/ina/6C_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106.8	13.0	1702	4	US-08-934-254-26
2	75.2	9.1	4411529	3	US-09-103-840A-1
3	74.2	9.0	1926	4	US-09-249-585A-4
4	74.2	9.0	1931	2	US-09-130-114-2
5	73.4	8.9	7218	1	US-08-232-663-14
6	70.8	8.6	77536	4	US-09-410-551B-1
7	68.6	8.3	1881	4	US-09-434-288-5
8	68.4	8.3	4403765	3	US-09-103-840A-2
9	67.6	8.2	4403765	3	US-09-103-840A-2
10	67.6	8.2	4411529	3	US-09-103-840A-1
11	65.2	7.9	319	3	US-09-165-264-8
12	65	7.9	4488	3	US-08-406-030A-3
13	63.2	7.7	320	3	US-09-165-264-13
14	63	7.7	44377	2	US-08-804-227C-7
15	63	7.7	44377	2	US-08-804-198-1
16	62	7.5	12001	1	US-08-458-568A-11
17	61.8	7.5	833	2	US-08-403-852D-3
18	61.8	7.5	833	3	US-08-510-646B-3
19	61.8	7.5	833	3	US-09-231-818-3
20	61.8	7.5	4466	4	US-09-410-551B-20
21	61.8	7.5	4478	4	US-09-410-551B-16
22	61.8	7.5	4478	4	US-09-410-551B-22
23	61.8	7.5	4571	4	US-09-410-551B-18
24	61.8	7.5	5392	2	US-08-403-852D-1
25	61.8	7.5	5392	2	US-08-510-646B-1
26	61.8	7.5	5392	3	US-09-231-818-1
27	61.8	7.5	77536	4	US-09-410-551B-1

28	61.4	7.5	152331	3	US-09-128-155-16	Sequence 16, Appl
29	60.6	7.4	320	3	US-09-165-264-14	Sequence 14, Appl
30	60.6	7.4	1158	4	US-09-372-422A-21	Sequence 21, Appl
31	60.4	7.3	939	3	US-09-105-390-45	Sequence 45, Appl
32	60.4	7.3	1020	3	US-09-105-390-61	Sequence 61, Appl
33	60.4	7.3	1193	4	US-09-372-422A-23	Sequence 23, Appl
34	60.4	7.3	2612	3	US-09-105-390-7	Sequence 7, Appl
35	60.2	7.3	1717	4	US-09-048-888-2	Sequence 2, Appl
36	59.8	7.3	2481	4	US-09-894-998A-35	Sequence 35, Appl
37	59.8	7.3	6085	3	US-09-029-603-4	Sequence 4, Appl
38	59.6	7.2	318	3	US-09-165-264-12	Sequence 12, Appl
39	59.6	7.2	320	3	US-09-165-264-11	Sequence 11, Appl
40	59.6	7.2	675	3	US-08-998-416-723	Sequence 723, App
41	59.6	7.2	2064	1	US-08-343-428-1	Sequence 1, Appl
42	59.4	7.2	1896	4	US-09-311-626B-15	Sequence 15, Appl
43	59.2	7.2	1027	4	US-09-674-741-9	Sequence 9, Appl
44	59.2	7.2	1071	2	US-08-997-080-180	Sequence 180, Appl
45	59.2	7.2	1071	2	US-08-997-362-180	Sequence 180, App

ALIGNMENTS

RESULT 1
US-08-934-254-26
Sequence 26, Application US/08934254
Patent No. 6355861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83632XXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
US-08-934-254-26
Query Match 13.0%; Score 106.8; DB 4; Length 1702;
Best Local Similarity 62.3%; Pred. No. 3.3e-13;

Matches 187; Conservative 0; Mismatches 107; Indels 6; Gaps 1;

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QY 204 ATCTCCACCAAGAGCTGACGAGCGCGCGGACGACCTCTGATCTCCATCTCC 263
Db 72 ATACCGCGGAGGACCTCCCGCCGACACAAAGTCGCGCATCTGATCTCCATCCAG 131
QY 264 GGGGACGCTACGACGTCACGCGCTGAGCTCGCCACCAACCGGCGGAGTCCGCTC 323
Db 132 GCGAGAGTCAACGACTGCTCTCGGTGGGCGGAGAGACCCGCGCGGAGTCCGCTC 191
QY 324 ATACCTCTCCCGCGGACGACGCGCAACCGCATTCAGCTTACACCGCCCTCTG 383
Db 192 CTGAGTCTGCGCGCGCGGACGTCACCGAGCGCTTCACTTCGATCCACCGGCGAG 251
QY 384 CGCGCGCTCTCGCGCGCTCTTCTGTCG-----CGGCTCAACCGCATCTGCTCC 437
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Db 312 GAGATCTCCAGAGCTACCGGAGGCTTTGACGAGATGTCGCGGTCCGGATCTTCCAG 371

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RESULT 2

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US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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Query Match 9.1%; Score 75.2; DB 3; Length 4411529;

Best Local Similarity 45.5%; Pred. No. 1.6e-06;

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Matches 263; Conservative 0; Mismatches 315; Indels 0; Gaps 0;
QY 13 CTTCCGTTGCTGTTTAAAGATCCGATCTCCCTTCCCTCCCTCTCTCTCTGAG 72
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Db 1218040 CCGGCGCGCGCGCGCGCGCGCTTCCGCGCACCGCCGATCGCGCAACCGCGCG 1217981
QY 133 TCGCGACGCAACGCGCGCGGAAACCGACCAATGCGGCGCGCGCGCGCGCGCG 192
Db 1217980 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1217921
QY 193 ACCTCGCATGATCTCCACCAAGAGCTGACGAGCGGCGCGCGCGCGCGCGCGCG 252
Db 1217920 CGGCGCGCGACGCGCGGATGCCGTCGCGCGCGCGCGCGCGCGCGCGCGCG 1217861
QY 253 TCTCATCTCCGCGGAGCGTCAAGCGCTCAAGCGCGCTGCGCGCGCGCGCGCGCG 312
Db 1217860 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217801
QY 313 AGGTCCCGCTCATACCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 372
Db 1217800 GCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217741

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QY 373 CGGCTCTCGGCGCGCGCGCTCTCGCGCGCTTCTGTCGCGCGCGCTACCGACTAC 432

Db 1217740 CGGTCGCGTACCGCTGAGCGGACGAGCGCGCTTTCGCGCGCGCGCGCGCG 1217681

QY 433 TCCCGCGCGCTTCCGCGCATTCGCGCGCTCTCTCGCGGAGCTCTCTCGCGCGCT 492

Db 1217680 TCCCG 1217621

QY 493 TCGAGCGCGTGGCGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 552

Db 1217620 CCGGCGCGACCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217561

QY 553 CGGCTCTACTGCTCTCTCGCGCTCTGCTCAACGCGCGCGCGCGCGCGCGCGCG 590

Db 1217560 CTGACCGCATTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217523

RESULT 3

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US-09-249-585A-4
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0905
; CURRENT APPLICATION NUMBER: US/09/249.585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURES:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

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Query Match 9.0%; Score 74.2; DB 4; Length 1926;

Best Local Similarity 55.5%; Pred. No. 1.1e-06;

Matches 162; Conservative 0; Mismatches 129; Indels 1; Gaps 1;

QY 269 CGTCTACGAGCTACGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328

Db 652 CGTCTGCTGCT 711

QY 329 CTTGCG 388

Db 712 CTTGCG 771

QY 389 GCTCTCTCGCGCGCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448

Db 772 CGTCT 831

QY 449 CGACTTCTCGCGCGCT 507

Db 832 CGTCT 891

QY 508 CACCG 559

Db 892 CTTCT 943

RESULT 4

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US-09-130-114-2
; Sequence 2, Application US/09130114
; Patent No. 5978807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damej, Bassem B.
; APPLICANT: Robbins, Alan K.

```

TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
FILE REFERENCE: 0867/1D90JUS1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1931
TYPE: DNA
ORGANISM: EBNA
US-09-130-114-2

Query Match 9.0%; Score 74.2; DB: 1; Length 1931;

Best Local Similarity 55.5%; Pred. No. 1.1e-06; Mismatches 129; Indels 1; Gaps 1;

Match 162; Conservative 0;

QY 269 GGTCTACGACGTACGCGCTGCTGCGCCACCGCGGCGGAGTCCCGCTCATCAG 328
DB 652 GGTCTACGACGTACGCGCTGCTGCGCCACCGCGGCGGAGTCCCGCTCATCAG 711
QY 329 CCTGCGCGCGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 388
DB 712 CCTGCGCGCGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 771
QY 389 GGTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 448
DB 772 GGTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 831
QY 449 GGTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 507
DB 832 GGTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 891
QY 508 CACCCCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
DB 892 CACCCCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 943

RESULT 5

US-08-232-463-14

Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313

FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300

TELEFAX: (703) 683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: pTZ19-F18

US-08-232-463-14

Query Match 8.9%; Score 73.4; DB: 1; Length 7218;

Best Local Similarity 3.6%; Pred. No. 1.9e-06; Mismatches 136; Indels 0; Gaps 0;

Match 14; Conservative 234; Mismatches 136; Indels 0; Gaps 0;

QY 218 GGTGAGGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 277
DB 1042 GGTGAGGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1101
QY 278 GGTGAGGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 337
DB 1102 GGTGAGGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1161
QY 338 CAGAGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 397
DB 1162 CAGAGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1221
QY 398 CCGCTTCTGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 457
DB 1222 CCGCTTCTGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1281
QY 458 CCGCTTCTGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 517
DB 1282 CCGCTTCTGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1341
QY 518 TTCTGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 577
DB 1342 TTCTGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1401
QY 578 CAGAGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601
DB 1402 CAGAGCGGACGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1425

RESULT 6

US-09-410-551B-1/C

Sequence 1, Application US/09410551B

Patent No. 6503737

GENERAL INFORMATION:

APPLICANT: KOSAN BIOSCIENCES, INC.

APPLICANT: REEVES, CHRISTOPHER

APPLICANT: CHU, DANIEL

APPLICANT: KHOSLA, CHAITAN

APPLICANT: SANTI, DANIEL

APPLICANT: WU, KAI

TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA

FILE REFERENCE: 30062-20026.00

CURRENT APPLICATION NUMBER: US/09/410,551B

CURRENT FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: US 60/139,650

PRIOR FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: US 60/123,810

PRIOR FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: US 60/102,748

PRIOR FILING DATE: 1998-10-02

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 77536

TYPE: DNA
ORGANISM: Streptomyces hygroscopicus
FEATURE:
NAME/KEY: CDS
LOCATION: (52275) ... (71465)
US-09-410-551B-1

Query Match 8.6%; Score 70.8; DB 4; Length 77536;
Best Local Similarity 49.2%; Pred. No. 8.1e-06;
Matches 186; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 135 GCGGACGCAACGCGCGGAGCGAGCAATGCGCGCGCGCGAGCAAGAGCGCGCGAC 194
DB 14484 GTGACGACATGCGGAGGTCGCGGAGGCGCTGGCGACATGAGCGCGCGAGCAACC 14425
QY 195 GTTCGATGATCTCCACCAAGAGCTGCAAGCGCGCGCGCGAGCACTTGTGATC 254
DB 14424 GGCAGATGCTCTCAGGTCGCGCGCGCGCTGAGACCCCGAGGAGCGCTGTATCACC 14365
QY 255 TTCATCTCGGAGGAGCTTACGAGCTACGCGCTGTGCTGCGCACCGCGGCGGAG 314
DB 14364 GCGGCTTCGCGACCTTCGCGGATCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 14305
QY 315 GTCCGCTCATCACTCTCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 374
DB 14304 CTCCTCTCCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14245
QY 375 CCTCTGCTGCG 434
DB 14244 GCGGACCG 14185
QY 435 CCG 494
DB 14184 TTCCACACCG 14125
QY 495 GAGCGCGTGGCG 512
DB 14124 GACACCGTCTCAACCGC 14107

RESULT 7
US-09-434-288-5/c
Sequence 5, Application US/09434288
Patent No. 6303767
GENERAL INFORMATION:
APPLICANT: Beilich C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1881
TYPE: DNA
ORGANISM: Streptomyces narbonensis
US-09-434-288-5

Query Match 8.3%; Score 68.6; DB 4; Length 1881;
Best Local Similarity 49.8%; Pred. No. 1.5e-05;
Matches 227; Conservative 0; Mismatches 225; Indels 4; Gaps 2;

QY 156 GCGGACGCAATGCG 215
DB 955 GCGGACGCAATGCG 896
QY 216 GAGCTGACG 275
DB 895 GCGGCG 836

QY 276 GAGTACCG 335
DB 835 GAGGCACTTACTGTGATCGCAACCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 776
QY 336 GCGGACG 395
DB 775 ACCGTGCGCAACGCAAGGCTTACCGCATTTATGAGGTCCTCCGCGCGCGCGCGCG 716
QY 396 CGCGCGCTTCTGTGCG 452
DB 715 ACCATGCG 656
QY 453 TTCCG 511
DB 655 CTGACCG 596
QY 512 CCGAAGTCTGCTGCG 571
DB 595 GCG 536
QY 572 CCGTCTCAACCG 607
DB 535 CGCGCGTCACTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 500

RESULT 8
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 8.3%; Score 68.4; DB 3; Length 4403765;
Best Local Similarity 47.8%; Pred. No. 3.7e-05;
Matches 227; Conservative 0; Mismatches 247; Indels 1; Gaps 1;

QY 40 TCCCTTNCCTTCCCTTCCCTTCTCTCTGATCTGTACACACCTCTCTCGCGCTTCAG 99
DB 839794 TCCCG 839735
QY 100 CTAAATCCAGCG 159
DB 839734 GACCTTCCG 839675
QY 160 ACGCAATGCG 219
DB 839674 CCG 839616
QY 220 TCGAGCG 279
DB 839615 CACAGTCCACCG 839556
QY 280 TCACGCGCTGTGCG 339


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT95-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-3

Query Match      7.9%; Score 65; DB 3; Length 4488;
Beet Local Similarity 48.8%; Pred. No. 8,7e-05;
Matches 243; Conservative 0; Mismatches 241; Indels 14; Gaps 2;

Oy 31 GATCCGATCTCCCTTGNCCCTCCCTCCCTCTCTCTGATGACCAACCCTCTC 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2804 GCTCCCTCCCTCCCTCCCTCCCTCCCTCTCTCTCTCCCTCCCTCCCTCC 2745

Oy 91 GCCTCAGCTAAATTCAGCCACCGAT-----GACCCGACGGGCTTCCGGAAC 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2744 TCCCCAACCCGCAATCCGGGCGCTGCTGCTGGGTCCGACCCCGGGCTCAGCGCCC 2685

Oy 143 AACGGCCCGAAGCCGACCGCATGCCGCGCCGACGAAAGACGC-----GCCGACT 196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2684 TCGCCGAGCGCGCGCCGCGCCGCGCTTGGCTGAGAGAGAGGCCCCCGCGCGGCGTCCG 2625

Oy 197 CCGCATATCTCCACCAAGAGCTGCGAGGCGACACGCCGCGGAGACACCTCTGGATCTC 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2624 GCGGGGGCAATAAAACGGGCGGAGCGCGCGCCGGGGACGTAAAGCCGCTACGGGCCG 2585

Oy 257 CATCTCCGGGAGCTCTACGACGTCAAGCCCTGGCTGCGCACACCCGGGCGGAGGT 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2564 GGTAGAGCGCCCGCGCCCGCGCTCTCTCCGCGCGCTCTCTCCGCGCCCGCGCGC 2505

Oy 317 CCGGCTATCACTCTGCGCGGCGAGACGCCACGACGCTTCAATGAGCTTACACCGCGC 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2504 GCGCACTCTGGGCGCGCGCCGACGAGCCCTCTGCGGGGACATGACCCGCGCCCGGC 2445

Oy 377 CTGCTGCGCGCGCTCTCTCCGCGGCTTCTTGTGTGGCGGCTTACACGACTATGTGCC 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2444 CCGGCGCCCTCTCCGCGGACACCGCCCGCGGCGGCGCTCTCGACCTCCGACCTCC 2385

Oy 437 CCGCGGCTCCGCGGACTTTCGCGCGGCTCTCTGCGAGAGCTCTCTCCGCGGAGCTTTGCA 496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2384 CCTTCCTTCGCGCGGCTCTCGCGGCTCTCTCTCTCTCTCTCCAGAGTGTCCGTTGCG 2325

Oy 497 GCGCGTGGGACACACCCC 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2324 GTCATGCGGCGGCTCC 2307

RESULT 13
US-09-165-264-13/c
; Sequence 13, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamourthy, Thuralayah
; TITLE OF INVENTION: Multi-Local Genomic Analysis

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FILE REFERENCE: 44747
 CURRENT APPLICATION NUMBER: US/09/165,264
 CURRENT FILING DATE: 1998-10-01
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 13
 LENGTH: 320
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
 US-09-165-264-13

Query Match 7.7%; Score 63.2; DB 3; Length 320;
 Best Local Similarity 50.0%; Pred. No. 0.00015;
 Matches 158; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 199 GCATGATCTCCACCAAGAGCTGACAGCGCAGCGCGGAGCACTCTGATCTCCA 258
 DB 318 GCATGCTCTGTCACAGTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 259
 QY 259 TCTCCGGGAGCTGACAGTACGCTGCTGCGCCACACCGGCGGAGAGTCC 318
 DB 258 CC 199
 QY 319 CGCTATACCTCGCGGCGAGAGCGACGAGCTTCAATGAGCTACACCGGCGCT 378
 DB 198 CC 139
 QY 379 CGGTGCGCCGCTCTCGCGCGCTTCTGTCGCGCGCTACACGACTAGTCCCC 438
 DB 138 CC 79
 QY 439 CGGCTCGCGGACTTCCGCGCGCTCTCTGCGGAGCTTCTCGGCGGCTTGTGAGC 498
 DB 78 CC 19
 QY 499 GCGTGGGACACCCCC 514
 DB 18 CCCCCCCCCCCCCCCC 3

RESULT 14

US-08-804-227C-7

Sequence 7, Application US/08804227C
 Patent No. 5876991

GENERAL INFORMATION:
 APPLICANT: Dehoff, Bradley S.
 APPLICANT: Kuhnstoss, Stuart A.
 APPLICANT: Rosteck, Paul R., Jr.
 APPLICANT: Sutton, Kimberly L.
 TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: THOMAS G. PLANT, 1501
 STREET: LILLY CORPORATE CENTER
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: USA

ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCII(DOS) Text only
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/804,227C
 FILING DATE: February 21, 1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Plant, Thomas, G.
 REGISTRATION NUMBER: 35,784
 REFERENCE/DOCKET NUMBER: X-8231

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-276-2459
 INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
 LENGTH: 44377 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

FEATURE:
 NAME/KEY: CDS
 LOCATION: 350..14002

FEATURE:
 NAME/KEY: CDS
 LOCATION: 14046..20036

FEATURE:
 NAME/KEY: CDS
 LOCATION: 20110..31284

FEATURE:
 NAME/KEY: CDS
 LOCATION: 31329..36071

FEATURE:
 NAME/KEY: CDS
 LOCATION: 36155..41830

US-08-804-227C-7

Query Match 7.7%; Score 63; DB 2; Length 44377;
 Best Local Similarity 50.5%; Pred. No. 0.00028;
 Matches 153; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 182 GGAGCGCGCGGAGCTTCCGATGATCTCCACCAAGAGCTGACAGCGCAGCGCGCGGA 241
 DB 30714 GAGCGCGGAGCGCTGCGGAGCGCGCTGCGCGAGCGGTGGCGAGCTTCCGCGAGGA 30773
 QY 242 CGACCTTGATCTCATCTCGGAGAGCTTACAGAGCTGACGCTGAGCTGCGCGCA 301
 DB 30774 ACGCCACGACCGGCTGCTGCGGCTGCTGCGGAGAGCTGCGGCTGCTGCGG 30833
 QY 302 CCGGCGCGGAGGCTTCCGCTATACCTGCGCGGAGAGCGCAGCGAGCGCTTAT 361
 DB 30834 CTCCGCGCGGAGGCTTCCGCTATACCTGCGCGGAGAGCTTCCGCGGAGCTTAC 30893
 QY 362 GGCCTACACCGCGCTCGGCGCGCTCTCCGCGCTTCTGCTGCGCGCTGAC 421
 DB 30894 GCGCGTGAAGCTGCGGAGCGGATGCGGCTGCGGAGCTTCCGCGAGCTTCCGCG 30953
 QY 422 CGACTACAGTGTCCCGCGCTTCCGCGGAGCTTCCGCGGAGCTTCTGCTGCTC 481
 DB 30954 GGTCTTGAACACCGCAGCGCGCGGCTGCTGCTGCACTGAGCGGCTGCTGCGCC 31013
 QY 482 CGC 484
 DB 31014 GGC 31016

RESULT 15

US-08-804-198-1

Sequence 1, Application US/08804198
 Patent No. 5945320

GENERAL INFORMATION:
 APPLICANT: Burgelt, Stanley G.
 APPLICANT: Kuhnstoss, Stuart A.
 APPLICANT: Rao, Nagaraja R.
 APPLICANT: Richardson, Mark A.
 APPLICANT: Rosteck, Paul R., Jr.
 TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: PAUL R. CANTRELL, 1138
 STREET: LILLY CORPORATE CENTER
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: USA

ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002
FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036
FEATURE:
NAME/KEY: CDS
LOCATION: 20110..31284
FEATURE:
NAME/KEY: CDS
LOCATION: 31329..36071
FEATURE:
NAME/KEY: CDS
LOCATION: 36155..41830
US-08-804-198-1

Query Match 7.7%; Score 63; DB 2; Length 44377;
Best Local Similarity 50.5%; Pred. No. 0.00028;
Matches 153; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 182 GGACGGCGCGGACGTCGCGATGATCTCCACCAAGAGCTGACGGCCGACGGCGCGGCA 241
Db 30714 GGACGGCGCGGACGTCGCGGAGCGCTGCGCGAGCGGTGCGCGACTCTCCGCGAGGA 30773
QY 242 CGACTCTGGATCTCCATCTCCGGGAGCTCTTACGACGTACGCGCCCTGCTGGCCACCA 301
Db 30774 AGCCCAAGACGGGCTGCTCGGCTGCTGCGGCAACACGTGGCCGCGGTACTGGGCCACGG 30833
QY 302 CCGGGGCGGAGGTCCGCTCATTCACCTTCGCGCGCGCAGAGCGCACCGAGCGCTTCAAT 361
Db 30834 CTCGCGCGCGAGGTGCGGCGCCGACCGCGCGTTCCGCGAGGTGCGGTTGACTCGCTCAC 30893
QY 362 GGGCTACCAACCGCCCTCCGTGCGCCCGCTCTCCGCGCGCTTCTGCTCGGCCGCTCAC 421
Db 30894 GGGCGTGAACCTCGCAACCGAGTGGCGGGGTCAACGGGGTCAAGCTCCCGCACCTT 30953
QY 422 CGACTACACTGTCCCCCGCTTCGCGGCACTTCGCGCGGCTCTCGCGGAGCTTCTCTC 481
Db 30954 GGTCTTGACCACTCCACCGCGCGGCTGTCTCTGCACTTGACGCGGCTGTGGCCCC 31013
QY 482 CGC 484
Db 31014 GGC 31016

Search completed: January 1, 2004, 00:05:52
Job time: 63.8386 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 21:04:45 ; Search time 205.271 Seconds
(without alignments)
13877.414 Million cell updates/sec

Title: US-09-857-524B-16

Perfect score: 823
Sequence: 1 cccctacaacacccgcgt.....cgtnaagactgttcgatcat 823

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA.*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	106.8	13.0	1702	14	US-10-029-756-26
2	87	10.6	3163	12	US-10-292-798-1513
3	87	10.6	3163	13	US-10-017-161-1857
4	85.6	10.4	12739	15	US-10-032-393-47
5	85.6	10.4	12739	15	US-10-032-393-8
6	84.8	10.3	3133	12	US-10-292-798-1191
7	84.8	10.3	3133	13	US-10-017-161-1483
8	78.2	9.5	5452	12	US-10-292-798-1189
9	78.2	9.5	5452	13	US-10-017-161-1481
10	77.2	9.4	1064	10	US-09-804-682-29
11	76	9.2	1117	12	US-10-292-798-1141
12	76	9.2	1117	13	US-10-017-161-1403
13	72.4	8.8	1065	10	US-09-804-682-33
14	70.8	8.6	77536	13	US-09-940-316B-1
15	70.4	8.6	520	15	US-10-184-644-332

16	70.4	8.6	520	15	US-10-184-634-332	Sequence 332, App
17	69.4	8.4	1687	12	US-10-163-198-40	Sequence 40, Appl
18	69.4	8.4	1953	15	US-10-369-493-42356	Sequence 42356, A
19	68.6	8.3	1881	13	US-10-271-889-5	Sequence 5, Appl1
20	68.4	8.3	9025608	15	US-10-156-761-1	Sequence 1, Appl1
21	67.4	8.2	1380	10	US-09-967-477B-7	Sequence 7, Appl1
22	67.2	8.2	1350	10	US-09-938-842A-558	Sequence 558, App
23	66.4	8.1	3453	15	US-10-101-464A-861	Sequence 861, App
24	66	8.0	1609	10	US-09-931-457A-50	Sequence 50, Appl
25	64.4	7.8	956	13	US-10-027-632-31508	Sequence 31508, A
26	64.4	7.8	956	14	US-10-027-632-31508	Sequence 31508, A
27	63.6	7.7	825	15	US-10-156-761-4706	Sequence 4706, Ap
28	63.6	7.7	9025608	15	US-10-156-761-1	Sequence 1, Appl1
29	63.2	7.7	88421	10	US-09-976-059-1	Sequence 1, Appl1
30	63	7.7	1362	13	US-09-769-863-13	Sequence 13, Appl
31	63	7.7	1362	13	US-10-054-534B-13	Sequence 13, Appl
32	63	7.7	1362	13	US-10-431-952-13	Sequence 13, Appl
33	62.8	7.6	1440	15	US-10-156-761-6190	Sequence 6190, Ap
34	62.8	7.6	1899	15	US-10-156-761-2267	Sequence 2267, Ap
35	62.4	7.6	1230	15	US-10-156-761-6338	Sequence 6338, Ap
36	62.4	7.6	4698	15	US-10-156-761-6923	Sequence 6923, Ap
37	62.2	7.6	747	10	US-09-887-576-781	Sequence 781, App
38	62.2	7.6	3012	15	US-10-156-761-2716	Sequence 2716, Ap
39	62.2	7.6	10056	15	US-10-156-761-411	Sequence 411, App
40	62.2	7.6	100000	15	US-10-156-761-15103	Sequence 15103, A
41	62	7.5	1402	10	US-09-931-457A-44	Sequence 44, Appl
42	62	7.5	1926	15	US-10-156-761-2231	Sequence 2231, Ap
43	61.8	7.5	1428	14	US-10-108-915-33	Sequence 33, Appl
44	61.8	7.5	4466	13	US-09-940-316B-20	Sequence 20, Appl
45	61.8	7.5	4478	13	US-09-940-316B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-10-029-756-26
Sequence 26, Application US/10029756
Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029, 756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934, 254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19, 827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
SEQUENCE DESCRIPTION: SEQ ID NO: 26;
US-10-029-756-26

Query Match 13.0%; Score 106.8; DB 14; Length 1702;
Best Local Similarity 62.3%; Pred. No. 2,6e-18;
Matches 187; Conservative 0; Mismatches 107; Indels 6; Gaps 1;

QY 204 ATCTCCACCAAGAGCTGCAGCGCAGCGCGCGGAGCAGCCTGATCTCCATCTCC 263
DB 72 ATACCGCGGAGGAGCTCCCGCCGACACAGTCCGCGCATCTTGATCTCCATCAG 131
QY 264 GGGAGCTGTACGACGTACGCGCTGCTGCGCCACCAACCGCGCGGAGTCCGCTC 333
DB 132 GGCAGAGCTACGACTGCTCTCGGTGGCGCGGAGCAGCCCGCGCGAGTCCGCTC 191
QY 324 ATACCGCTGCGCGCGGAGCGGAGCGGAGCGGCTTCACTGCGCTTCACTGCGCTG 383
DB 192 CTAGTGTGCGCGGAGCGGAGCGGAGCGGCTTCACTGCGCTTCACTGCGCTG 251
QY 384 CGCGCGCTCCGCGCGCTTCTTCTGTCG-----CGCGCTCAACGACTGTCGCC 437
DB 252 TGGCGGATGTGATCGGCTCTTCAACGCGGCTACTACTCAAGAGCTTGAAGTGTG 311
QY 438 CGCGCTCGCGGAGCTTCCGCGCGCTCTTCCGCGAGCTCTTCCGCGCGCTTCTGAG 497
DB 312 GAGATCTCCAGGACTACCGGAGGCTTTGACGAGATGTGCGGCTCGGAGTCTTGAG 371

RESULT 2
US-10-292-798-1513/c
Sequence 1513, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1513
LENGTH: 3163
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1)..(3163)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2963)
FEATURE:
NAME/KEY: modified_base
LOCATION: (556)..(655)
OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:
NAME/KEY: modified base
LOCATION: (658)..(669)
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FEATURE:
NAME/KEY: modified base
LOCATION: (671)..(697)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (704)..(707)
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LOCATION: (709)..(736)
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NAME/KEY: modified base
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NAME/KEY: modified base
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (843)..(843)
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NAME/KEY: modified base
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
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FEATURE:	
NAME/KEY: modified_base	
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OTHER INFORMATION: a, t, c, g, unknown or other	
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LOCATION: (1500) ..(1500)	
OTHER INFORMATION: a, t, c, g, unknown or other	
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LOCATION: (1601) ..(1601)	
OTHER INFORMATION: a, t, c, g, unknown or other	
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NAME/KEY: modified_base	
LOCATION: (1605) ..(1605)	
OTHER INFORMATION: a, t, c, g, unknown or other	
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NAME/KEY: modified_base	
LOCATION: (1635) ..(1635)	
OTHER INFORMATION: a, t, c, g, unknown or other	
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NAME/KEY: modified_base	
LOCATION: (1637) ..(1637)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	

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	FEATURE:	
	NAME/KEY: modified_base	
	LOCATION: (1674) .. (1674)	
	OTHER INFORMATION: a, t, c, g, unknown or other	
	FEATURE:	
	NAME/KEY: modified_base	
	LOCATION: (1695) .. (1695)	
	OTHER INFORMATION: a, t, c, g, unknown or other	
	FEATURE:	
	NAME/KEY: modified_base	
	LOCATION: (1852) .. (1852)	
	OTHER INFORMATION: a, t, c, g, unknown or other	
	FEATURE:	
	NAME/KEY: modified_base	
	LOCATION: (1866) .. (1866)	
	OTHER INFORMATION: a, t, c, g, unknown or other	
	FEATURE:	
	NAME/KEY: modified_base	
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	OTHER INFORMATION: a, t, c, g, unknown or other	
Query Match	10.6%; Score 87; DB 12; Length 3163;	
Beet Local Similarity	33.3%; Pred. No. 4e-13;	
Matches 230; Conservative	0; Mismatches 461; Indels 0; Gaps 0;	
Qy	32 ATCCGATCTCCCTTCNCCCTCCCTCCCTTCCTCTGAGTCTGACCAACCCCTCTCG	91
Db	2552 ACCC	2493
Qy	92 CGTCCAGCTAAATCCACGCCACCGATGCGCCGACGAGGCTTGCGGACGCAACGCGCC	151
Db	2492 CCCCCCAAAACCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN	2433
Qy	152 GGAAGCGAGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATCTCAC	211
Db	2432 NCC	2373
Qy	212 CAAGGACCTGACGT	271
Db	2372 CCGCNCNCCCCCAACNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2313
Qy	272 CTACGACGTACGCGCTGAGTGGCGCAACCGCGGCGGAGGTCCCGCTGATCACCTT	331
Db	2312 CCC	2253
Qy	332 CGCGGCGCAGACGCCACCGACGCTTGATGACTACACCGCGCTTCGTCGCGCGCT	391
Db	2252 CNGCNCNCC	2193
Qy	392 CCTCCGCGCGCTTCGTGTCGCGCGCGCTCACGACCTACGTGCTCCCGCGCTCGCGCA	451
Db	2192 CCGCC	2133
Qy	452 CTTCGCGCGCTCTCTCGCGAGCTCTCTCGCGGCGCTTTCGAGGCGGTGCGACAC	511
Db	2132 CCGCNCNCC	2073
Qy	512 CCCAAGTTCGTGCTGTCGCAAAAGTCGTGCTTTTGCAATCGGCTCTACTGCTCTCG	571
Db	2072 NNNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC	2013
Qy	572 CTGCTCAACAACGCGGCGCACATGTTGGCGGCGGCTCATTTGGTTATCTGTGACGTGG	631
Db	2012 CCGCNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC	1953
Qy	632 GCTGATTGCACTACTCGCGCACACAATCAAGGACCTGCTCAACGCTCTGAGTGG	691
Db	1952 NNN	1893
Qy	692 CTGCGGAATGCTACGCGCTCGATCCTGGG	722

Db 1892 NNNNNNNNNNNNNNNNNNNNNNNNNNTTG3 1862

RESULT 3

US-10-017-161-1857/C

Sequence 1857, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUMA, MAKIKO

APPLICANT: ASAI, KIYOSHI

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ABURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

PRIOR FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: JP 2001/246789

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1857

LENGTH: 3163

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: source

LOCATION: (1)..(3163)

FEATURE:

NAME/KEY: CDS

LOCATION: (201)..(2963)

FEATURE:

NAME/KEY: modified_base

LOCATION: (556)..(655)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (658)..(669)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (671)..(697)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (704)..(707)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (739)..(743)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (745)..(747)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (750)

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NAME/KEY: modified_base

LOCATION: (754)..(756)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (761)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (763)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

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LOCATION: (818)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

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OTHER INFORMATION: a, t, c, g, unknown or other

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NAME/KEY: modified_base

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NAME/KEY: modified_base

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FEATURE:

NAME/KEY: modified_base

LOCATION: (1105)..(1107)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (1130)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (1147)

OTHER INFORMATION: a, t, c, g, unknown or other

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NAME/KEY: modified_base

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NAME/KEY: modified_base

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NAME/KEY: modified_base

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OTHER INFORMATION: a, t, c, g, unknown or other

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NAME/KEY: modified_base

LOCATION: (1247)..(1248)

OTHER INFORMATION: a, t, c, g, unknown or other

[illegible]

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RESULT 5
US-10-032-393-8/c
Sequence 8, Application US/10032393
Publication No. US20030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12739
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Vector pBEF1
US-10-032-393-8

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Query Match 10.4%; Score 85.6; DB 15; Length 12739;
 Best Local Similarity 47.0%; Pred. No. 1e-12;
 Matches 262; Conservative 0; Mismatches 296; Indels 0; Gaps 0.

35 CGATCTCCCCCTTCCGCCCTCCCTCCTCGAATCCTGACACACCCCTCTCGGCG 94

[illegible]

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RESULT 6
US-10-292-798-1191/c
; Sequence 1191, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABRATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1191
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(3133)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(2933)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(118)

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NAME/KEY: modified base
LOCATION: (379)..(385)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:

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Best Local Similarity	34.1%	Pred	No.1.5e-12				
Matches	219	Conservative	0	Mismatches	424	Indels	0
						Gaps	0

QY	39	CTCCGCTTCCGCGCCCTCCCTCCCTTCTCTGATGTCGACGACCGCTCTGGAGCTCA	98
Db	957	CNCCCCCNNNCCGNNCCCCCCCCCCCCCNCCGNCGNCGCCCCCCCCCCCCCN	898
QY	99	GCTAATTCACGCGCACGATGGCGCGCACGAGCTTTCGCGAGCGAACGCGCGGAGGCC	158
Db	897	NCCCCCCCCCGCNCGCCNCCCCCCCCCNNNNNCCCCCGCNCNCCCCCGCNCNCCCC	838
QY	159	GACCGAATGGCGCGCGCGAGGACGCGCGCGAGCGTCGCGATGATCTCCACGAAGAG	218
Db	837	CCCCCNNNNNCCCCCCCCCCCCCNNNNNCCCCCCCCCCCCCGCNCNCCCCCGC	778
QY	219	CTGCAGGCGCACGCGCGCGGAGCGACGCTTGATCTCATCTCCGAGGAGCGTCTACGAC	278
Db	777	NNNCCCCCGCCNCCNNNNCCCCCCCCCGCNCNCCCCCGCNCNCCNNNNNNCCNCCC	718
QY	279	GTCAAGCGCTTGCGTGGCGGACCACTCGGAGCGGAGGTCGCGCTATCACTCGCGGAG	338
Db	717	CCCCCCCCCGCNCNCCCCCNCCNCCCCCCCCCCCCCNCCNCCCCCGCNCNCCCCCCCC	658
QY	339	CAGGACGCGCACGAGCGCTTATGAGCTTACACACCGCGCCTCGTGCGGCGGCTCTCGCG	398
Db	657	CCNCCNNNNNNCCGNCNCCCCCGCNCNCCCCCCCCCNCCNCCNCCNCCCCCGCNCNCCC	598
QY	399	CGCTTCTTTCGTGCGCGCGCTCAACGACTATCACTGTCGCCCGCGCTCCGCGCATTTCCGC	458
Db	597	CCNNCCNNNNCCCCCGCCCGCCCNCCNCCGNNNNCCCCCGCCCGCNCNNNNCCCCCGCC	538
QY	459	CGCTCTCTCGGCGAGCTCTCTCGCGGAGGCTCTTGAGCGCGTGGGACACCCCGCAAGT	518
Db	537	CNCCNCCCCCGCCCNNNNNCCCCCCCCCGCCCNCCGNCNCCNCCNCCNCCNCCNCCN	478
QY	519	TCCTGCTCGTGGCAAGTCGNGGCTCTTGATGAGGCTGACTGCTCTGCGCTGCTC	578
Db	477	CCCCNCCCCCGCCCNCCNCCGNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC	418
QY	579	AACAACGGGAGCAATGTTGCGCGGAGGCTCATTTGCTTATCTGGTCACTCGGAGCTGAT	638
Db	417	CCCCCGCNCNCCCCCGCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN	358
QY	639	TGGCATACTCGGCGACACAAATCACAGGACCTGCTCAAGC	681
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1  RESULT 7
2  US-10-017-161-1483/C
3  ; Sequence 1483, Application US/10017161
4  ; Publication No. US20030143668A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: SUMA, MAKIKO
7  ; APPLICANT: ASAI, KIYOSHI
8  ; APPLICANT: AKIYAMA, YUTAKA
9  ; APPLICANT: ABRUANT, HIROYUKI
10 ; TITLE OF INVENTION: NOVEL G-PROTEIN-COUPLED RECEPTORS
11 ; FILE REFERENCE: 084335/0152
12 ; CURRENT APPLICATION NUMBER: US/10/017,161
13 ; CURRENT FILING DATE: 2002-12-18
14 ; PRIOR APPLICATION NUMBER: JP 2001/246789
15 ; PRIOR FILING DATE: 2001-06-18
16 ; NUMBER OF SEQ ID NOS: 2430
17 ; SOFTWARE: PatentIn Ver. 2.1
18 ; SEQ ID NO 1483
19 ; LENGTH: 3133
20 ; TYPE: DNA
21 ; ORGANISM: Homo sapiens
22 ; FEATURE:
23 ; LOCATION: source
24 ; FEATURE:
25 ; LOCATION: (1)..(3133)
26 ; FEATURE:
27 ; NAME/KEY: CDS
28 ; LOCATION: (201)..(2933)
29 ; FEATURE:
30 ; NAME/KEY: modified_base
31 ; LOCATION: (1)..(118)
32 ; OTHER INFORMATION: a, t, c, g, unknown or other
33 ; FEATURE:
34 ; NAME/KEY: modified_base
35 ; LOCATION: (124)..(129)
36 ; OTHER INFORMATION: a, t, c, g, unknown or other
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38 ; NAME/KEY: modified_base
39 ; LOCATION: (139)
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41 ; FEATURE:
42 ; NAME/KEY: modified_base
43 ; LOCATION: (146)..(148)
44 ; OTHER INFORMATION: a, t, c, g, unknown or other
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46 ; NAME/KEY: modified_base
47 ; LOCATION: (151)..(152)
48 ; OTHER INFORMATION: a, t, c, g, unknown or other
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50 ; NAME/KEY: modified_base
51 ; LOCATION: (155)
52 ; OTHER INFORMATION: a, t, c, g, unknown or other
53 ; FEATURE:
54 ; NAME/KEY: modified_base
55 ; LOCATION: (172)
56 ; OTHER INFORMATION: a, t, c, g, unknown or other
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58 ; NAME/KEY: modified_base
59 ; LOCATION: (179)..(180)
60 ; OTHER INFORMATION: a, t, c, g, unknown or other
61 ; FEATURE:
62 ; NAME/KEY: modified_base
63 ; LOCATION: (182)
64 ; OTHER INFORMATION: a, t, c, g, unknown or other
65 ; FEATURE:
66 ; NAME/KEY: modified_base
67 ; LOCATION: (185)..(188)
68 ; OTHER INFORMATION: a, t, c, g, unknown or other
69 ; FEATURE:
70 ; NAME/KEY: modified_base
71 ; LOCATION: (192)
72 ; OTHER INFORMATION: a, t, c, g, unknown or other
73 ; FEATURE:

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FEATURE:	
NAME/KEY : modified_base	
LOCATION : (212)	
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FEATURE:	
NAME/KEY : modified_base	
LOCATION : (222) ..(225)	
OTHER INFORMATION : a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY : modified_base	
LOCATION : (229)	
OTHER INFORMATION : a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY : modified_base	
LOCATION : (231) ..(232)	
OTHER INFORMATION : a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY : modified_base	
LOCATION : (238) ..(239)	
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FEATURE:	
NAME/KEY : modified_base	
LOCATION : (242)	
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FEATURE:	
NAME/KEY : modified_base	
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FEATURE:	
NAME/KEY : modified_base	
LOCATION : (248) ..(260)	
OTHER INFORMATION : a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY : modified_base	
LOCATION : (265) ..(270)	
OTHER INFORMATION : a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY : modified_base	
LOCATION : (272) ..(276)	
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FEATURE:	
NAME/KEY : modified_base	
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FEATURE:	
NAME/KEY : modified_base	
LOCATION : (282) ..(283)	
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FEATURE:	
NAME/KEY : modified_base	
LOCATION : (287) ..(290)	
OTHER INFORMATION : a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY : modified_base	
LOCATION : (302) ..(306)	
OTHER INFORMATION : a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY : modified_base	

LOCATION: (311) ..(313)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (323) ..(334)
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
LOCATION: (400) ..(402)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (409)
OTHER INFORMATION: a, t, c, g, unknown or other
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Query Match	10.3%	Score 84.8	DB 13	Length 3133
Best Local Similarity	34.1%	Pred. No.1.5e-12		
Matches 219; Conservative	0;	Mismatches 424;	Indels 0;	Gaps 0;

[illegible]

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FEATURE:	
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LOCATION:	(265) ..(266)
OTHER INFORMATION:	a, t, c, g, unknown or other
FEATURE:	
NAME/KEY:	modified base
LOCATION:	(271) ..(273)
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NAME/KEY:	modified base
LOCATION:	(276) ..(277)
OTHER INFORMATION:	a, t, c, g, unknown or other
FEATURE:	
NAME/KEY:	modified base
LOCATION:	(283) ..(285)
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NAME/KEY:	modified base
LOCATION:	(296) ..(296)
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NAME/KEY:	modified base
LOCATION:	(298) ..(300)
OTHER INFORMATION:	a, t, c, g, unknown or other
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NAME/KEY:	modified base
LOCATION:	(307) ..(307)
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NAME/KEY:	modified base
LOCATION:	(314) ..(315)
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FEATURE:	
NAME/KEY:	modified base
LOCATION:	(334) ..(334)
OTHER INFORMATION:	a, t, c, g, unknown or other
FEATURE:	
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LOCATION:	(339) ..(339)
OTHER INFORMATION:	a, t, c, g, unknown or other
FEATURE:	
NAME/KEY:	modified base
LOCATION:	(343) ..(343)
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FEATURE:	
NAME/KEY:	modified base
LOCATION:	(345) ..(348)
OTHER INFORMATION:	a, t, c, g, unknown or other
FEATURE:	
NAME/KEY:	modified base
LOCATION:	(351) ..(352)
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FEATURE:	
NAME/KEY:	modified base
LOCATION:	(357) ..(357)
OTHER INFORMATION:	a, t, c, g, unknown or other
FEATURE:	
NAME/KEY:	modified base
LOCATION:	(359) ..(359)
OTHER INFORMATION:	a, t, c, g, unknown or other
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OTHER INFORMATION:	a, t, c, g, unknown or other

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FEATURE:
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FEATURE:
NAME/KEY: modified_base
LOCATION: (370)..(373)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (376)..(378)
OTHER INFORMATION: a, t, c, g, unknown or other

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Query Match	9.5%	Score 78.2	DB 11	Length 5452
Best Local Similarity	35.1%	Pred. No. 8	2e-11	
Matches 189, Conservative	0	Mismatches 345	Indels 0	Gaps 0

OY	47	CNCCCTCCCCCTCGCTTCCTGAGTCTGACCAACCCTCTGGGCTCAGCTAAATC	106
Db	4857	CCCCCNCCCCCCCCCCCNCNNNNCCCCCCCCCCNCNCCCCCCCCCCCCCNCNNCCC	4799
OY	107	CAGGCCACGATGAGCCCGCACGGGCTTGCGGAGCGAACGGCGCGGAGCCGACAAT	166
Db	4797	CNNNCCCCCCCCCCCCCNCNNNNCNCNCCCCCCCCCNCNCCGNCCCCCCCCCCCCCN	4738
OY	167	GCCGGCCGCCAAGACGCGCGCCGACGTCCGATGATTCCACCAAAGA GTTCAGGC	226
Db	4737	NCCNNNCNNNNCCNCCCNCCCCCNCNNCCCCCCCCCNCNNCCNCCNCCCCC	4678
OY	227	GCACGGCGCGCGGAGAGACTGTGGATCTCATCTCCGGGAGAGTTACAGAGTCAGGC	286
Db	4677	NCCNCCCCCCCCCCCCCNCNNCCNCCCCCCCCCCCCCNCNNCCNCCNNTTTTCCCCC	4618
OY	287	CTGAGCTCGGCACCAACCGGAGGCGAGATCCGCTATCATCCTCGCGGCGCAGAGCG	346
Db	4617	CCCCCNCCCCCCCCCCCCCNCNNCCCCCCCCCNCNNCCNCCCCCCCCCNCNNCC	4555
OY	347	CACGACGCTTCATGAGCTAACCAACCGGCTTCGTGCGCCCGCTCTCGCGCGTTCTT	406
Db	4557	CCCCCNCNNNNCNCNCCNCCCCCCCCCCCCCNCNNNNCCCCCNCNNCCNCCN	4498
OY	407	CGTGGCCGCTACAGGACTATGTCCCCCGGCTCGCGGCACTTCGCGGCTCTCT	466
Db	4497	NCNCCCCCNCNCCCCCCCCCNCNCCNCNNNNCNCNNNNCCCCCCCCCCCCCNCNN	4438
OY	467	CGCGAGCTCTCTCGCGGAGGCTTTTCGAGCGGTGGGACACCCCCCAATTCTGTCT	526
Db	4437	CNCNCCNNNNCCNCCCCCCCCCCCCCNCNNCCNCCCCCNCNNCCNCCNCCNCC	4378
OY	527	GTGCAAAAGTCNGTCTTCTGTGATCGGCTCTACTGCTCTCGGCTGCTCAACAC	584
Db	4377	CCCCCNCNNNNNNNNCCCCCNCNCCCCCCCCCNCNCCNCCNNNNCCNCCNCCNCC	4320

RESULT 9
 US-10-017-161-1481/C
 Sequence 1481, Application US/10017161
 Publication No. US2003014366A1
 GENERAL INFORMATION:
 APPLICANT: SUMA, MAKIKO
 APPLICANT: ASAI, KIYOSHI
 APPLICANT: AKIYAMA, YUTAKA
 APPLICANT: ABEURATANI, HIROYUKI
 TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 084335/0152
 CURRENT APPLICATION NUMBER: US/10/017,161
 CURRENT FILING DATE: 2002-12-18
 PRIOR APPLICATION NUMBER: JP 2001/246789
 PRIOR FILING DATE: 2001-06-18

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NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1481
LENGTH: 5452
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: modified_base
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
LOCATION: (339)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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OY	CAGACGCGCACGAGCGCTTATGAGCTAACACACCGGCCTCGGTGGCCGCTTCGCG	398
Db	B11 CTTCCCCCCCNCNCCCCCCTTCTCCCTCCCCCCTTCANCCCNCTCCCNCTCCTCTCTCAC	870
OY	CGCTTCTTTCGTGGCGCGCTCAACGACTGACTGTCCCCCGCGCTCGCGCGACTTTCGCG	458
Db	871 CTCCCCCNCTCTTNNCCCTCCCCCNCCNCTTTCCTCCCTCTTNTTCCCCCCCNCCCC	930
OY	GCGCTCTCTGGCGAGCTCCCTCGCGGAGGAGCTTTCGAGCGGCGTGAGACAACCCCAAGT	518
Db	931 CNCCTCCNCTCCCCCNCTTTTCCCNCCNCTCMCTTCTCCCCCCCCCNCCCTTCCCC	990
OY	TCTCGTCTGTGCAAAATGCTGCTCTTCTGTGATCGGCGCTCTACTGCTCTCTGCGCTGCTC	578
Db	991 NCNCTCCCTCANNCNCTCCNCTCCCCCNCTCCTCCCCCCCCCACAACCCNCTCNCNC	1058
OY	AACACCGGGGGCAC	592
Db	1051 MACNCTCTCCCCC	1064

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1 RESULT 11
2 US-10-292-798-1141/C
3 Sequence 1141, Application US/10292798
4 Publication No. US20030235833A1
5 GENERAL INFORMATION:
6 APPLICANT: SUMA, MAKIKO
7 APPLICANT: ASAI, KIYOSHI
8 APPLICANT: ASAI, KIYOSHI
9 APPLICANT: AKIYAMA, YUTAKA
10 APPLICANT: ABRARATANI, HIROYUKI
11 TITLE OF INVENTION: GABANOINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
12 FILE REFERENCE: 084335/166
13 CURRENT APPLICATION NUMBER: US/10/292,798
14 CURRENT FILING DATE: 2002-11-13
15 PRIOR APPLICATION NUMBER: 10/017,161
16 PRIOR FILING DATE: 2001-12-18
17 PRIOR APPLICATION NUMBER: JP 2001-246789
18 PRIOR FILING DATE: 2001-06-18
19 NUMBER OF SEQ ID NOS: 2070
20 SOFTWARE: PatentIn Ver. 2.1
21 SEQ ID NO 1141
22 LENGTH: 1117
23 TYPE: DNA
24 ORGANISM: Homo sapiens
25 FEATURE:
26 LOCATION: source
27 FEATURE:
28 LOCATION: (1)..(1117)
29 FEATURE:
30 NAME/KEY: CDS
31 LOCATION: (201)..(917)
32 FEATURE:
33 NAME/KEY: modified_base
34 LOCATION: (170)..(170)
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36 FEATURE:
37 NAME/KEY: modified_base
38 LOCATION: (173)..(173)
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40 FEATURE:
41 NAME/KEY: modified_base
42 LOCATION: (207)..(306)
43 OTHER INFORMATION: a, t, c, g, unknown or other
44 FEATURE:
45 NAME/KEY: modified_base
46 LOCATION: (343)..(344)
47 OTHER INFORMATION: a, t, c, g, unknown or other
48 FEATURE:
49 NAME/KEY: modified_base
50 LOCATION: (351)..(356)
51 OTHER INFORMATION: a, t, c, g, unknown or other
52 FEATURE:
53 NAME/KEY: modified_base

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FEATURE:
NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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FEATURE:

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FEATURE:
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LOCATION: (525)..(527)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (557)..(561)
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base


```

; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBP GENE OF THE FK-520 POLYKETIDE SYNTH
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275) ... (71465)
; US-09-940-316B-1

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Query Match 8.6%; Score 70.8; DB 13; Length 77536;

Best Local Similarity 49.2%; Pred. No. 8.5e-09; Matches 186; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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QY 135 GCGAGCAACGCGCGGAGAGCGCAATGCGCGCGCGCAAGAGAGCGCGCGAC 194
DB 14484 GTGACGACATGCGGAGGTCGCGGAGCGCGCGCAATGAGCGCGGAGACACAC 14425
QY 195 GTCCGATGATCTTCACCAAGAGCTGAGCGCGCGCGCGGAGACCTTGATC 254
DB 14424 GCGAAGATCTCTCAGCGGTCGCGCGCGCGCGCGGAGCGCGCGCTGATCACC 14365
QY 255 TCATCTCCGCGGAGCTCTAGAGCTGACGCGCGCGCGCGCGCGCGCGAG 314
DB 14364 GCGGCTCCGCGACCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14305
QY 315 GTCCGCTCATCACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 374
DB 14304 CTCCTCTCCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14245
QY 375 CCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 434
DB 14244 GCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14185
QY 435 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 494
DB 14184 TTCCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14125
QY 495 GAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 512
DB 14124 GACACCGCTCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14107

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RESULT 15

US-10-184-644-332/c

; Sequence 332, Application US/10184644

; Publication No. US20030044930A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

```

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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 332
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-184-644-332

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Query Match 8.6%; Score 70.4; DB 15; Length 520;

Best Local Similarity 26.9%; Pred. No. 7.5e-09; Matches 84; Conservative 61; Mismatches 167; Indels 0; Gaps 0;

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QY 211 CCAAGAGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 270
DB 434 YCYNSSGB.YBBSN.CY.CM.CMBC.CSSCMBC.HCM.CT.C.TCM.CT.C.SC.CM 375
QY 271 TCTAGAGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
DB 374 BCT.C.BCS.CMYC.C.CAHCMSCM.CATC.SC.SC.CTYC.SCTSC.CMTC.DCB 315
QY 331 TCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 390
DB 314 TC..C.BC..C.C.HCMTC..CT.C.C.YC.HCMSC.TC.CKCTHMKCYHMSC. 255
QY 391 TCTCCGCGCGCTTCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 450
DB 254 .C.HCM.CMCA.CM.C.CCHCMSCM.C.C.ACMTC.MC.TC..C.CT.CMBC..C. 195
QY 451 ACTTCCGCGCGCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
DB 194 .CS.CATCHYCKTMTCM.T..C..C.TC.KCTCMD.C..TC..CM.Y.KC.N.A.NH 135
QY 511 CCGCACTTCT 522
DB 134 BY..D.DSBYB 123

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Search completed: January 1, 2004, 05:19:45
Job time : 216.271 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 : Search time 10.4957 Seconds
(without alignments)
1724.030 Million cell updates/sec

Title: US-09-857-524B-17

Perfect score: 592

Sequence: 1 MPAAKADADVMISTKEIQ.....ADFRLLAQLSSAGHFERYG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: A.Geneseq.19Jun03.*
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3: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1981.DAT.*
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24: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2002.DAT.*
25: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2003.DAT.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	length	DB	ID	Description
1	592	100.0	114	21	AAV71556	wheat sphingolipidic
2	588	99.3	469	21	AAV71555	wheat sphingolipidic
3	501	84.6	462	21	AAV71552	Corn sphingolipid
4	274.5	46.4	448	21	AAV71551	Florida biterbust
5	274.5	46.4	458	21	AAV51348	Sphingolipid desatur
6	271.5	45.9	450	21	AAV71554	Soybean sphingolipid
7	269.5	45.5	450	24	ABG73418	Evening primrose c
8	266	44.9	452	23	AAU79851	Evening primrose c
9	266	44.9	452	24	ABG73416	Evening primrose c

10	261	44.1	448	24	ABG73417
11	258	43.6	448	19	AAV98455
12	258	43.6	448	17	AAV67471
13	258	43.6	448	20	AAV98430
14	258	43.6	448	21	AAV51349
15	258	43.6	448	23	AAV79830
16	258	43.6	448	24	ABG73095
17	255.5	43.2	449	21	AAV51333
18	250.5	42.3	449	20	AAV51322
19	249	42.1	446	20	AAV51322
20	236.5	39.9	449	21	AAV51322
21	236.5	39.9	449	21	AAV51322
22	236.5	39.9	449	21	AAV51322
23	236.5	39.9	449	21	AAV51322
24	195	32.9	477	23	ABG73600
25	195	32.9	477	23	ABG73600
26	193.5	32.7	459	23	ABE22063
27	192	32.4	53	21	AAV83236
28	175.5	29.6	135	21	AAV83236
29	173	29.2	53	21	AAV83236
30	169.5	28.6	134	21	AAV83236
31	167.5	28.3	126	21	AAV83236
32	166.5	28.1	140	21	AAV83236
33	166.5	28.1	140	21	AAV83236
34	166.5	28.1	200	21	AAV83236
35	164	27.7	904	14	AAV83236
36	162.5	27.4	95	21	AAV83236
37	161.5	27.3	873	23	ABE6014
38	161	27.2	453	24	AAV83236
39	160.5	27.1	116	21	AAV83236
40	160.5	27.1	509	24	AAV83236
41	159.5	26.9	801	21	AAV83236
42	159.5	26.9	905	21	AAV83236
43	159.5	26.9	917	21	AAV83236
44	157.5	26.6	126	21	AAV83236
45	157.5	26.6	126	21	AAV83236

ALIGNMENTS

RESULT 1
ID AAV71556 standard; Protein; 114 AA.
AAV71556;
AC AAV71556;
XX
DT 12-OCT-2000 (first entry)
XX
DE wheat sphingolipid desaturase #2.
XX
KW wheat; sphingolipid desaturase; membrane-bound desaturase;
transgenic plant; fatty acid.
XX
OS Triticum aestivum.
XX
PN WO200032790-A2.
XX
PD 08-JUN-2000.
XX
PF 02-DEC-1999; 99WO-US26589.
XX
PR 03-DEC-1998; 98US-0110784.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
XX WPI; 2000-412336/35.
XX N-PSDB; AAD01354.
XX
PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
transgenic plants and for producing antibodies specific to which is

PT useful for screening cDNA expression libraries -
 XX
 PS Claim 10; Page 57; 57pp; English.
 XX
 CC The present sequence is a sphingolipid desaturase
 CC from clone wrel.pK004.c7 isolated from wheat etiolated
 CC seedling root cDNA library, wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 114 AA;
 Query Match 100.0%; Score 592; DB 21; Length 114;
 Best Local Similarity 100.0%; Pred. No. 5,5e-62;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASKDAADVIRMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 60
 DB 1 MPASKDAADVIRMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 60
 QY 61 ATDAFMAVHPSPVRLRRFFVGRITDYTVPPASADFRRLAQLSSAGLFEVRVG 114
 DB 61 ATDAFMAVHPSPVRLRRFFVGRITDYTVPPASADFRRLAQLSSAGLFEVRVG 114
 RESULT 2
 AA71555
 ID AA71555 standard; Protein; 469 AA.
 XX
 AC AA71555;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Wheat sphingolipid desaturase #1.
 XX
 KM Wheat; sphingolipid desaturase; membrane-bound desaturase;
 KM transgenic plant; fatty acid.
 XX
 OS Triticum aestivum.
 OS
 PN WO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PT 03-DEC-1998; 98US-0110784.
 XX
 PS (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 XX
 DR WPI; 2000-412336/35.
 XX
 DR N-PSDB; AAD01353.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries -
 XX
 PS Example 4; Page 49-50; 57pp; English.
 XX
 CC The present sequence is a sphingolipid desaturase
 CC from clone wrel.pK004.c7; isolated from wheat etiolated
 CC seedling root cDNA library, wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 469 AA;
 Query Match 99.3%; Score 588; DB 21; Length 469;
 Best Local Similarity 99.1%; Pred. No. 9,4e-61;
 Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASKDAADVIRMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 60
 DB 17 MPASKDAADVIRMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 76
 QY 61 ATDAFMAVHPSPVRLRRFFVGRITDYTVPPASADFRRLAQLSSAGLFEVRVG 114
 DB 77 ATDAFMAVHPSPVRLRRFFVGRITDYTVPPASADFRRLAQLSSAGLFEVRVG 130
 RESULT 3
 AA71552
 ID AA71552 standard; Protein; 462 AA.
 XX
 AC AA71552;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Corn sphingolipid desaturase.
 XX
 KM Corn; sphingolipid desaturase; membrane-bound desaturase;
 KM transgenic plant; fatty acid.
 XX
 OS Zea mays.
 OS
 PN WO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PT 03-DEC-1998; 98US-0110784.
 XX
 PS (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 XX
 DR WPI; 2000-412336/35.
 XX
 DR N-PSDB; AAD01350.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries -
 XX
 PS Claim 10; Page 42-43; 57pp; English.
 XX
 CC The present sequence is a sphingolipid desaturase
 CC from clone cdeic.pK001.08; isolated from corn developing
 CC embryo cDNA library, cdeic. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 462 AA;
 Query Match 84.6%; Score 501; DB 21; Length 462;
 Best Local Similarity 83.2%; Pred. No. 1,8e-50;
 Matches 94; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 2 PAASKDAADVIRMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 61
 DB 11 PGDAAGAGVIRMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 70
 QY 62 TDAFMAVHPSPVRLRRFFVGRITDYTVPPASADFRRLAQLSSAGLFEVRVG 114

Db 71 TDAFAAHPSPARPLRRFFVGRSLSDYAVSPASADYRRLAQLSSAGLFFRVG 123

RESULT 4

AA71551
ID AAY71551 standard; Protein; 448 AA.

XX AAY71551;
AC
XX

DT 12-OCT-2000 (first entry)

XX Florida bitterbush delta-6 fatty acid desaturase.

XX Florida bitterbush; delta-6 fatty acid desaturase; tariric acid;
KM transgenic plant; fatty acid; membrane-bound desaturase.

XX Picramnia pentandra.

XX WO200032790-A2.

XX 08-JUN-2000.

XX 02-DEC-1999; 99WO-US28589.

XX 03-DEC-1998; 98US-0110784.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;

XX WPI; 2000-412336/35.

XX N-PSDB; AAD01349.

XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries -

XX Claim 10; Page 40-41; 57pp; English.

XX The present sequence is a delta-6 fatty acid desaturase protein sequence
CC from clone pps.pK0011.d5, is isolated from Florida bitterbush developing
CC seed cDNA library, pps. The delta-6 desaturase enzyme catalyzes the
CC formation of tariric acid, a fatty acid that has a triple bond at the
CC delta-6 carbon. The present sequence is useful for producing
CC transgenic plants having altered levels of delta-6 desaturase which
CC in turn would alter the fatty acid composition. The enzyme is also useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.

XX Sequence 448 AA;

Query Match 46.4%; Score 274.5; DB 21; Length 448;
Best Local Similarity 51.0%; Pred. No. 9, 8e-24;

Matches 52; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

QY 14 ISTKELOAAADDLMTISISGDYDVTPLRHHGGEVPLITLAGDADAFMAVHPSPV 73

DB 8 ISQADLAKKQPDLMISIKGVYDLSKWTKEHPGELPLSPAGODVDADFIAHPGTA 67

QY 74 RPLLRFPVG-RLTDYVPPASADFRRLAQLSSAGLFFRVG 114

DB 68 WOYLDREFTGYVODYSVSEMSKDYRLVSEFSKMGLEFKTPG 109

RESULT 5

AA51348
ID AAY51348 standard; Protein; 458 AA.

XX AAY51348;
AC
XX

DT 27-APR-2000 (first entry)

XX Sphingolipid desaturase protein.

DE Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;

XX transgenic plant; crop plant; delta-8-unsaturated long-chain base;

XX tolerance; resistance; soil salinity; ion stress; toxicity; drought;

XX cold; frost; phytopathogenic microorganism; flowering time; cosmetic;

XX pharmaceutical; food; chemical raw material.

XX Unidentified.

XX DE19828850-A1.

XX 30-DEC-1999.

XX 27-JUN-1998; 98DE-1028850.

XX 27-JUN-1998; 98DE-1028850.

XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

XX Heinz E, Zaehner U, Schmidt H, Sperling P;

XX WPI; 2000-127549/12.

XX N-PSDB; AA244851.

XX New sphingolipid desaturase that selectively introduces double bond
PT into sphingolipid and capnoid -

XX Disclosure; Fig 15; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a sphingolipid desaturase protein
CC described in the method of the invention.

XX Sequence 458 AA;

Query Match 46.4%; Score 274.5; DB 21; Length 458;
Best Local Similarity 50.0%; Pred. No. 1e-23;

Matches 52; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 12 RMISTKELOAAADDLMTISISGDYDVTPLRHHGGEVPLITLAGDADAFMAVHPSPV 71

DB 17 KYTTSKELKHNPNMDLMTISIKGVYNTVMKEHPGGAPLITLAGDADAFIAHPG 76

QY 72 SVRPLLRFPVG-RLTDYVPPASADFRRLAQLSSAGLFFRVG 114

DB 77 TWMKLDKLFYGYHLKDYVSDISRDYRLASLPAKAGKFEKGG 120

RESULT 6

AA71554
ID AAY71554 standard; Protein; 450 AA.

XX AAY71554;
AC
XX

DT 12-OCT-2000 (first entry)

DE Soybean sphingolipid desaturase #2.

```

XX Soybean; sphingolipid desaturase; membrane-bound desaturase;
KW transgenic plant; fatty acid.
OS Glycine max.
PN WO200032790-A2.
XX PD 08-JUN-2000.
XX PP 02-DEC-1999; 99WO-US28589.
XX PR 03-DEC-1998; 98US-0110784.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
RX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
PI MPI: 2000-412336/35.
DR N-PADB: AAD01352.
XX PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries -
XX PS Claim 10; Page 47-48; 57pp; English.
CC The present sequence is a sphingolipid desaturase
CC from clone ssl.pK0017.b4:fls isolated from soybean seedling cDNA
CC library, ssl. The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is also useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
SQ Sequence 450 AA;
Query Match 45.9%; Score 271.5; DB 21; Length 450;
Best Local Similarity 48.1%; Pred.No. 2,2e-23;
Matches 50; Conservative 21; Mismatches 32; Indels 1; Gaps 1.
OY 12 RMISKEIQAHAAADDLMWISGDVDDTPMLRHHPGSEVPILITAGDAPAFMAHYPP 71
DY :::|||:|||||||:|||:|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 9 KYTSEELEKHNGKEGDLMSIQKYNNVDWKHEHFGSDVPSINLAGODVTDAFTAYHG 68
OY 72 SVRPILRRFPVG-RLTDYTVPASADPRLALQLSSAGLFERVG 114
DY ::|||:|||||:|||:|::|::|::|::|::|::|::|::|::|::|
DB 69 TAWSHLEKFPTGYHLSDPKVSFVSKDYRKLADEFKGLFDYTG 112
RESULT 7
ABG73418 ID ABG73418 standard; Protein; 450 AA.
AC ABG73418;
XX XX
DT 16-APR-2003 (first entry)
DE Evening primrose delta-6-desaturase #2.
XX XX
KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KW octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
evening primrose.
OS Oenothera biennis.
XX XX
FN US2002108147-A1.
PD 08-AUG-2002.
XX XX
PF 21-DEC-2001; 2001US-0029756.
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PR 13-OCT-1992; 92US-0959952.
PR 19-SEP-1987; 97US-0934254.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
XX (THOM/) THOMAS T L.
XX
XX Thomas TL;
XX
XX WPI; 2003-066659/06.
XX
XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
XX for producing plant with increased gamma linolenic acid content, and
XX for inducing octadecatetraenoic acid production in plant
XX
XX Example 15; Fig 11; 55pp; English.
XX
XX The invention relates to a nucleic acid encoding an evening primrose
XX delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
XX nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
XX for producing a plant (such as sunflower, soybean, maize, tobacco,
XX peanut, carrot or oil seed rape plant) with increased gamma-linolenic
XX acid (GLA) content by transforming a plant cell with the nucleic acid or
XX vector and regenerating a plant with increased GLA content from the plant
XX cell, for inducing or increasing production of GLA in an organism lacking
XX in or producing low levels of GLA and for inducing production of
XX octadecatetraenoic acid in at least one of a plant deficient or lacking
XX in or producing low levels of octadecatetraenoic acid, a bacterium which
XX produces alpha-linolenic acid or a bacterium which exhibits a
XX delta-15-desaturase activity on a GLA substrate. This sequence represents
XX an evening primrose delta-6-desaturase polypeptide.
XX
XX Sequence 450 AA;
XX
XX Query Match 45.5%; Score 269.5; DB 24; Length 450;
XX Best Local Similarity 51.0%; Pred. NO. 3.8e-23;
XX Matches 53; Conservative 17; Mismatches 33; Indels 1; Gaps 1;
XX
XX 12 RMISTKELQAAADDLWISGVDVDTPLRAHPGSEVPLTLTAGODATDAFMAVHP 71
XX :|:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 7 KYTIAEDRRRNKSGDWISIQGVYDSRRAAHPGSEVPLMLLAGODVTDATFIAPRG 66
XX
XX 72 SVRPLRRFFVG-RLTDYVPPASADRRRLTAQLSSAGLPERVG 114
XX :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 67 TAWHLDPLFTGYGLKDFEVEISEKDVRRLLNEMSRSGIFPKKG 110
XX
XX RESULT 8
XX ID AUA79851 standard; Protein: 452 AA.
XX AC AUA79851;
XX
XX 15-JUL-2002 (first entry)
XX
XX Evening primrose delta-6-desaturase.
XX
XX delta-6-desaturase; sunflower; soybean; maize; tobacco;
XX peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
XX chilling tolerance; evening primrose.
XX
XX Oenothera biennis.
XX
XX US6355861-B1.
XX
XX 12-MAR-2002.
XX
XX 19-SEP-1997; 97US-0934254.
XX
XX 13-OCT-1992; 92US-0959952.
XX

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PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
PA (RHON ) RHONE-POULENC AGROCHIMIE.
XX
PI Thomas TL;
XX
DR WPI: 2002-380944/41.
DR N-PSDB; ABX49503.
XX
PT Novel nucleic acid encoding evening primrose delta6-desaturase which
PT converts linoleic acid to gamma linolenic acid useful for producing
PT gamma linolenic acid in transgenic plant or bacteria
XX
PS Claim 3; Column 45-48; 53pp; English.
XX
CC The invention describes an isolated nucleic acid encoding an evening
CC primrose delta6-desaturase. The nucleic acid and a vector expressing the
CC nucleic acid are useful for producing a plant such as sunflower, soybean,
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC gamma linolenic acid (GLA) content, and also for inducing or increasing
CC production of GLA in a bacteria or plant deficient, lacking in or
CC producing low levels of GLA. The nucleic acid is also useful for inducing
CC chilling tolerance in plants. This is the amino acid sequence of the
CC evening primrose delta6 desaturase involved in the production of gamma
CC linoleic acid.
XX
SQ Sequence 452 AA;

```

Query Match 44.9%; Score 266; DB 23; Length 452;
 Best Local Similarity 49.5%; Pred. No. 1e-22; Mismatches 33; Indels 2; Gaps 1;
 Matches 52; Conservative 18;

```

QY 12 RMISTKELOAHAAADLWISISGVDYVTPMLRHHHGGEVPLTTLAGODATDAFMAYHPP 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 KTTMEDLRHHKSGDLWISIGKYYDCSRMAEHGGEVPLSLAGQVDTAFIYHNG 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 SVRPLLRFFVG-RITDYTPPASADPFRLLAQSSAGLPERVG 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 TWMRHLDPLFTGYYYLKDFEVEISKDYRRLNEMSRSGIFPKKG 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 9
 ABG73416
 ID ABG73416 standard; Protein; 452 AA.
 AC ABG73416;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DB Evening primrose delta-6-desaturase #1.
 XX
 KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
 KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KW octadecetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 KW evening primrose.
 XX
 OS Oenochera biennis.
 XX
 PN US2002108147-A1.
 PD 08-AUG-2002.
 PF 21-DEC-2001; 2001US-0029756.
 PR 13-OCT-1992; 92US-0959952.
 PR 19-SEP-1997; 97US-0934254.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.

```

XX
PA (THOM/) THOMAS T L.
XX
PI Thomas TL;
XX
DR WPI: 2003-06659/06.
DR N-PSDB; ABX15367.
XX
PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
PT for producing plant with increased gamma linolenic acid content, and
PT for inducing octadecetraenoic acid production in plant
XX
PS Claim 3; Fig 10; 55pp; English.
XX
CC The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GLA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GLA content from the plant
CC cell, for inducing or increasing production of GLA in an organism lacking
CC in or producing low levels of GLA and for inducing production of
CC octadecetraenoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecetraenoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GLA substrate. This sequence represents
CC an evening primrose delta-6-desaturase polypeptide.
XX
SQ Sequence 452 AA;

```

Query Match 44.9%; Score 266; DB 24; Length 452;
 Best Local Similarity 49.5%; Pred. No. 1e-22; Mismatches 33; Indels 2; Gaps 1;
 Matches 52; Conservative 18;

```

QY 12 RMISTKELOAHAAADLWISISGVDYVTPMLRHHHGGEVPLTTLAGODATDAFMAYHPP 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 KTTMEDLRHHKSGDLWISIGKYYDCSRMAEHGGEVPLSLAGQVDTAFIYHNG 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 SVRPLLRFFVG-RITDYTPPASADPFRLLAQSSAGLPERVG 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 TWMRHLDPLFTGYYYLKDFEVEISKDYRRLNEMSRSGIFPKKG 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 10
 ABG73417
 ID ABG73417 standard; Protein; 448 AA.
 AC ABG73417;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DB Borage delta-6-desaturase #2.
 XX
 KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
 KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KW octadecetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 KW borage.
 XX
 OS Borage officinalis.
 XX
 PN US2002108147-A1.
 PD 08-AUG-2002.
 PF 21-DEC-2001; 2001US-0029756.
 PR 13-OCT-1992; 92US-0959952.
 PR 19-SEP-1997; 97US-0934254.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.

XX (THOM/) THOMAS T L.
 XX Thomas TL;
 XX WPI; 2003-066659/06.
 XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant -
 XX Example 15; Fig 11; 55pp; English.
 XX The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC a borage delta-6-desaturase polypeptide.
 XX Sequence 448 AA;
 SQ
 Query Match 44.1%; Score 261; DB 24; Length 448;
 Best Local Similarity 47.7%; Pred. No. 3.9e-22;
 Matches 52; Conservative 20; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKEIQAAADDLWISISGDVYDTPWLRHHPGSEVPLITLAGODATDAPM 66
 DB 2 AAQIKKYYITSDIKNDKPGDLWISIQKAYDVSDWKHPGSGFPLKSLAGOEVTDAV 61
 QY 67 AYHPSPVRLRRFPVG-RLTDYTPPASADFRRLAQLSSAGLFEVRV 114
 DB 62 AFHPASTWKNLDKFFTGYYLKYDYSVEVSKDVKRLVFEFSKGLYDKG 110
 RESULT 11
 AAR98455 standard; Protein; 448 AA.
 AC AAR98455;
 DT 15-SEP-1996 (first entry)
 XX Borage delta-6-desaturase.
 DE Borage delta-6-desaturase.
 XX Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KW polyunsaturated fatty acid; octadecatetraenoic acid;
 KM chilling resistance; oilseed.
 XX Borage officinalis.
 OS Borage officinalis.
 FH Key Location/Qualifiers
 FT Region 156..163
 FT /label= Lipid_box
 FT Region 196..200
 FT /label= Metal_box-1
 FT /label= Metal_box-2
 FT /label= Metal_box-2
 XX MO9621022-A2.
 XX 11-JUL-1996.
 XX 28-DEC-1995; 95MO-IB01167.

PR 30-DEC-1994; 94US-0366779.
 XX (RHON) RHONE POULENC AGROCHIMIE.
 PA Freyessinet GL, Nuccio M, Numborg AN, Reddy AS, Thomas TL;
 XX WPI; 1996-333997/33.
 DR N-PSDB; AAT30395.
 XX Transgenic plants comprising the borage delta-6-desaturase gene -
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 XX Claim 3; Page 52-53; 75pp; English.
 PS Borage delta-6-desaturase (AAR98455) catalyses the conversion of
 CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
 CC deduced from that of the delta-6-desaturase gene (AAT30395) isolated
 CC from a borage membrane-bound polysomal library. The sequence is
 CC distinct from that of Synchocystis delta-6-desaturase (AAR9456).
 CC Expression of the desaturase in transgenic plants, esp. sunflower,
 CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
 CC increased GLA prodn. Alteration of the plant membrane lipids as a
 CC result of expression of the desaturase may also result in increased
 CC resistance to chilling.
 XX Sequence 448 AA;
 SQ
 Query Match 43.6%; Score 258; DB 17; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKEIQAAADDLWISISGDVYDTPWLRHHPGSEVPLITLAGODATDAPM 66
 DB 2 AAQIKKYYITSDIKNDKPGDLWISIQKAYDVSDWKHPGSGFPLKSLAGOEVTDAV 61
 QY 67 AYHPSPVRLRRFPVG-RLTDYTPPASADFRRLAQLSSAGLFEVRV 114
 DB 62 AFHPASTWKNLDKFFTGYYLKYDYSVEVSKDVKRLVFEFSKGLYDKG 110
 RESULT 12
 AAM67471 standard; Protein; 448 AA.
 ID AAM67471;
 AC AAM67471;
 DT 02-MAR-1999 (first entry)
 XX Borage delta-6 desaturase protein.
 DE Borage delta-6 desaturase protein.
 XX Upstream region; regulatory region; sunflower; albumin; seed; expression;
 KW lipid metabolism; delta-6 desaturase; transgenic plant.
 OS Borage officinalis.
 FH Key Location/Qualifiers
 FT Region 40..44
 FT /note= "cytochrome b5 haem-binding motif"
 FT Domain 156..163
 FT /note= "His-rich metal binding motif"
 FT Domain 196..200
 FT /note= "His-rich metal binding motif"
 FT Domain 373..377
 FT /note= "His-rich metal binding motif"
 XX MO9845460-A1.
 XX 15-OCT-1998.
 XX 09-APR-1998; 98MO-US07178.
 XX 09-APR-1997; 97US-0831570.

XX (RHON) RHONE-POULENC AGROCHIMIE.
 PA Beremand PD, Nunberg AN, Thomas TL;
 PI WPI, 1998-583201/49.
 DR N-PSDB; AAV34398.
 XX
 PT New sunflower albumin 5' regulatory region - useful for directing
 altered lipid metabolism in plant seeds
 XX Example 2; Fig 1; 38pp; English.
 PS This sequence corresponds to the borage (*Borago officinalis*) delta-6
 CC desaturase enzyme. The encoding lipid metabolism gene is an example
 CC of a heterologous gene which can be expressed at high levels in a
 CC seed-specific manner in transgenic plants, when placed under control
 CC of the sunflower albumin gene 5' regulatory region (AAV34397).
 CC
 SQ Sequence 448 AA;
 Query Match 43.6%; Score 258; DB 19; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELQAAADLWISISGVYDTPMLRHHPGSEVPLITLAGODATDAM 66
 DB 2 AAQIKYITSDLEKNDKPGDLWISIQKAYVSDWVKDHPGSPFLKSLAGOEVTDAV 61
 QY 67 AVHPSPVRLRRFFVG-RLTDYTPPASADFRRLAQLSAGLPERVG 114
 DB 62 AFHPASTWKNLDKFPFGYLLKDYSEVSKDYRKLVFERSKMGLYDKG 110
 RESULT 13
 AAV98130
 ID AAV98130 standard; Protein; 448 AA.
 XX AAV98130;
 AC
 XX 21-JUN-1999 (first entry)
 DT
 XX
 DE Borage delta-6 desaturase.
 XX
 KW Delta-6 desaturase; borage; oleosin; AtGS21; promoter;
 KW transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 KW gamma-linolenic acid; octadecatetraenoic acid.
 XX
 OS Borago officinalis.
 XX
 PH Key Location/Qualifiers
 FT Binding-site 40..44 /note= "cytochrome b5 haem-binding motif"
 FT Binding-site 156..163 /note= "metal binding, histidine-rich motif"
 FT Binding-site 196..200 /note= "metal binding, histidine-rich motif"
 FT Binding-site 373..377 /note= "metal binding, histidine-rich motif"
 FT Binding-site /note= "metal binding, histidine-rich motif"
 XX
 PN WO9845461-A1.
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07179.
 XX
 PR 09-APR-1997; 97US-0831575.
 XX
 XX (RHON) RHONE-POULENC AGROCHIMIE.
 PI Li Z, Thomas TL;
 XX WPI; 1999-180333/15.
 DR

DR N-PSDB; AAX24917.
 XX
 PT Nucleic acid containing oleosin 5'-regulatory region - useful for
 PT modulating fatty acid synthesis and lipid metabolism in plants,
 PT particularly to increase content of gamma-linolenic acid
 XX
 PS Example 2; Page 61; 101pp; English.
 CC The present sequence is borage delta-6 desaturase, an enzyme that
 CC catalyses the conversion of linoleic acid to gamma-linolenic acid
 CC (GLA). Delta-6 desaturase cDNA (see AAX24917) was isolated from a
 CC borage membrane-bound polyosomal cDNA library using a partial clone,
 CC obtained from an EST database search, as probe. The borage delta-6
 CC desaturase nucleic acid can be operably linked to the seed-specific
 CC 5' regulatory region (see AAX24916) of the Arabidopsis thaliana
 CC oleosin AtGS21 gene in claimed expression cassettes of the invention.
 CC Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton,
 CC peanut, oilseed rape or Arabidopsis are obtained that show increased
 CC levels of GLA or octadecatetraenoic acid. The levels of desirable
 CC fatty acids in oilseed crops can be manipulated to provide seed
 CC oils of use in human health and industrial applications.
 CC
 SQ Sequence 448 AA;
 Query Match 43.6%; Score 258; DB 20; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELQAAADLWISISGVYDTPMLRHHPGSEVPLITLAGODATDAM 66
 DB 2 AAQIKYITSDLEKNDKPGDLWISIQKAYVSDWVKDHPGSPFLKSLAGOEVTDAV 61
 QY 67 AVHPSPVRLRRFFVG-RLTDYTPPASADFRRLAQLSAGLPERVG 114
 DB 62 AFHPASTWKNLDKFPFGYLLKDYSEVSKDYRKLVFERSKMGLYDKG 110
 RESULT 14
 AAY51349
 ID AAY51349 standard; Protein; 448 AA.
 XX AAY51349;
 AC
 XX 27-APR-2000 (first entry)
 DT
 XX
 DE Sunflower HADES protein.
 XX
 KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Helianthus annuus.
 XX
 PN DE19828850-A1.
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 PA Heinz B, Zaehrlinger U, Schmidt H, Sperling P;
 XX WPI; 2000-127549/12.
 DR
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 PS Disclosure; Page 33-34; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoid with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a desaturase protein, HADS, isolated
 CC from *Helianthus annuus* (sunflower) which is used in the method of the
 CC invention.

XX
 SQ Sequence 448 AA;

Query Match 43.6%; Score 258; DB 21; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-EMISTKEIQAHAAADDLMWISGDVYDTPWLRHHPGGEVPLITLAGDADTAFM 66
 DB 2 AAQIKKYITSDELKNDKPGDLMWISIQKAYDVSDWKDHPGSPFLKSLAGGEVTDADFV 61
 QY 67 AYHPPSVRLRLRRFVG-RLTDYTPPASADPFRLLAQLSSAGLPERVG 114
 DB 62 AFHPASTWKLDKFFFTGYLYLKDVSVSEVSKDYRKLVFEFSKMGLYDKKG 110

RESULT 15
 AAU79830

ID AAU79830 standard; Protein; 448 AA.

XX AAU79830;

DT 15-JUL-2002 (first entry)

DE Borago officinalis delta6-desaturase.

KW delta6-desaturase; sunflower; soybean; maize; tobacco;
 KW peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
 KW chilling tolerance; borage.

XX Borago officinalis.

OS

FT Key Location/Qualifiers

FT Region 156..163 /label= Lipid_box

FT Region 196..200 /label= Metal_box_1

FT Region 372..377 /label= Metal_box_2

XX US6355861-B1.

PD 12-MAR-2002.

PF 19-SEP-1997; 97US-0934254.

PR 13-OCT-1992; 92US-0959952.

PR 10-OCT-1991; 91US-0774475.

PR 08-JAN-1992; 92US-0817919.

PR 14-SEP-1994; 94US-0307382.

PR 28-JAN-1997; 97US-0789936.

XX (RHON) RHONE-POULENC AGROCHIMIE.

PI Thomas TL;

DR WPI: 2002-380944/41.

DR N-PSDB; ABR49502.

XX Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linolenic acid to gamma linolenic acid useful for producing
 PT gamma linolenic acid in transgenic plant or bacteria

XX Example 9; Column 31-34; 53pp; English.

XX The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This is the amino acid sequence of the
 CC borage delta6 desaturase involved in the production of gamma linoleic
 CC acid.

XX Sequence 448 AA;

Query Match 43.6%; Score 258; DB 23; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-EMISTKEIQAHAAADDLMWISGDVYDTPWLRHHPGGEVPLITLAGDADTAFM 66
 DB 2 AAQIKKYITSDELKNDKPGDLMWISIQKAYDVSDWKDHPGSPFLKSLAGGEVTDADFV 61
 QY 67 AYHPPSVRLRLRRFVG-RLTDYTPPASADPFRLLAQLSSAGLPERVG 114
 DB 62 AFHPASTWKLDKFFFTGYLYLKDVSVSEVSKDYRKLVFEFSKMGLYDKKG 110

Search completed: January 1, 2004, 06:36:55
 Job time : 11.4957 secs

A;Gene: At2g46210

Nature 408, 816-820, 2000
 A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Malt, R.; Marshall,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schatz, G.; Schatz, G.; Schatz, G.;
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A86390
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-135 <STO>
 A:Cross-references: GB:AE005172; NID:g9797763; PIDN:AAF98581.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein
 F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 29.6%; Score 175.5; DB 2; Length 135;
 Best Local Similarity 35.1%; Pred. No. 3 6e-11;
 Matches 40; Conservative 22; Mismatches 43; Indels 9; Gaps 3;

Qy 1 MPASKDAADVEMISTKELQAAADLWISGVYDVTPLRHHGGEVPLITLAGOD 60
 Db 1 MPTLTK-----LYSWEBAATHNKQDDCWVVIDGKYDVSSVWDEHGGDDVLLAVAGKD 54

Qy 61 ATDAFM-AVHPSVRLRRFVGRITDVTVP--PASAPFRLLADLSAGLFE 111
 Db 55 ATDDFEDAGSKDARLMEKYFGEIDBSLPELPIELKTKYKQDPQDSVQKLF 108

RESULT 7
 SS2857
 nitrate reductase (NADH) (EC 1.7.1.1) - *Beauveria baasiana*
 C:Species: *Beauveria baasiana*
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C:Accession: SS2857
 R:Maurer, P.
 submitted to the EMBL Data Library, February 1995
 A:Reference number: SS2857
 A:Accession: SS2857
 A:Molecule type: DNA
 A:Residues: 1-894 <MAU>
 A:Cross-references: EMBL:X84950; NID:g693925; PIDN:CAA59336.1; PID:g693926
 C:Genetics:
 A:introns: 593/1
 C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
 C:Keywords: heme; iron; metalloprotein; molybdenum; molybdopterin; oxidoreductase; phosph
 F:62-467/Domain: molybdopterin-binding domain homology <PCO>
 F:535-609/Domain: cytochrome b5 core homology <CB5>
 F:645-894/Domain: cytochrome-b5 reductase homology <CBR>
 F:169/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F:570,593/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 29.4%; Score 174; DB 2; Length 894;
 Best Local Similarity 40.3%; Pred. No. 4.3e-10;
 Matches 31; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

Qy 11 VEMISTKELQAAADLWISGVYDVTPLRHHGGEVPLITLAGODATDAFMAYVP 70
 Db 535 VAIISLEELKAHGEHMEPFVYVNGHYNGTPYLDNHPGATSIINAAADATDEEFTTIS 594

Qy 71 PSVRLRRFVGRITD 87
 Db 595 ENAKAMMPQYHIGTLND 611

RESULT 8
 TS2469
 cytochrome b5 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000

C:Accession: TS2469
 R:Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
 Plant Physiol. 119, 353-361, 1999
 A:Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterologous Expressi
 A:Reference number: Z525274
 A:Accession: TS2469
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-134 <FUK>
 A:Cross-references: EMBL:AB007801; PIDN:CA817231.1
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein
 F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 28.6%; Score 169.5; DB 2; Length 134;
 Best Local Similarity 36.5%; Pred. No. 1.5e-10;
 Matches 31; Conservative 23; Mismatches 30; Indels 1; Gaps 1;

Qy 8 AADVEMISTKELQAAADLWISGVYDVTPLRHHGGEVPLITLAGODATDAFM- 66
 Db 2 SDRKVLSPFEVSKNKKTKDCWLIISGKYDVTTPMDHPRGDEVLLSTGKDATNDFED 61

Qy 67 AVHPSVRLRRFVGRITDVTVP 91
 Db 62 VGHSDTARDMDKYPFGEIDSSSV 86

RESULT 9
 T14454
 cytochrome b5 - wild cabbage
 C:Species: *Brassica oleracea* (wild cabbage)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
 C:Accession: T14454
 R:Kearns, E.V.; Keck, P.; Somerville, C.R.
 submitted to the EMBL Data Library, March 1992
 A:Description: Nucleotide sequence of cDNA for cytochrome b5 from cauliflower (*Brassica*
 A:Reference number: Z18100
 A:Accession: T14454
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-134 <KEA>
 A:Cross-references: EMBL:M87514; NID:g167139; PID:g167140
 C:Function:
 A:Description: acts as electron carrier for membrane-bound oxygenases
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: electron transfer; heme; iron; membrane protein; metalloprotein
 F:5-80/Domain: cytochrome b5 core homology <CB5>
 F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 28.5%; Score 168.5; DB 2; Length 134;
 Best Local Similarity 35.3%; Pred. No. 1.9e-10;
 Matches 30; Conservative 23; Mismatches 31; Indels 1; Gaps 1;

Qy 8 AADVEMISTKELQAAADLWISGVYDVTPLRHHGGEVPLITLAGODATDAFM- 66
 Db 2 ABEKYLGRFESQNKTKDCWLIISGKYDVTTPMDHPRGDEVLLSTGKDATNDFED 61

Qy 67 AVHPSVRLRRFVGRITDVTVP 91
 Db 62 VGHSDTARDMDKYPFGEIDSSVP 86

RESULT 10
 RDNTNT
 nitrate reductase (NADH) (EC 1.7.1.1) nia-1 - common tobacco
 C:Species: *Nicotiana tabacum* (common tobacco)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002
 C:Accession: S04838; S05696
 R:Vaucheret, H.; Kromerberger, J.; Rouze, P.; Caboche, M.
 Plant Mol. Biol. 12, 597-600, 1989
 A:Title: Complete nucleotide sequence of the two homologous tobacco nitrate reductase ge
 A:Reference number: S04838
 A:Accession: S04838

A/Molecule type: DNA
 A/Residues: 1-904 <VAV>
 A/Cross-references: EMBL:X14058
 R/Rouse, P.
 submitted to the EMBL Data Library, January 1989
 A/Reference number: S05696
 A/Accession: S05696
 A/Molecule type: DNA
 A/Residues: 1-35, 'P', 37-904 <ROU>
 A/Cross-references: EMBL:X14058; NID:g19888; PIDN:CAA32216.1; PID:g19889
 C/Genetics:
 A/Gene: nia-1
 A/Intons: 338/1; 385/1; 462/3
 C/Complex: homodimer
 C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
 C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
 F/9-411/Domain: molybdopterin-binding domain homology <PCO>
 F/531-605/Domain: cytochrome b5 core homology <CB5>
 F/554-904/Domain: cytochrome-b5 reductase homology <CBR>
 F/183/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F/422/Dissulfide bonds: interchain #status predicted
 F/565-589/Binding site: heme iron (His) (axial ligands) #status predicted
 F/118-876/Binding site: NAD (Lys, Cys) #status predicted
 F/158/Binding site: FAD (Tyr) #status predicted

Query Match 28.2%; Score 167; DB 1; Length 904;
 Best Local Similarity 35.7%; Pred. No. 2, 4e-09;
 Matches 40; Conservative 15; Mismatches 43; Indels 14; Gaps 3;

QY 1 MPASADADVNMISTKELQAAADDLMTISGDVYVTPMLRHHGGEVPLITLAGOD 60
 DB 527 MNTASK-----MYSMEVSKHSSADSAMITVGHYDAPFKDHPGSDSLINAGTD 580
 QY 61 AUDAFAVYHPPSVRLRRFVGRLL--TDYVTPP-----ASADFRLIAQL 104
 DB 581 CIEEPFHIHSDKAKKLEFRIGELLTGTGTSPPGNSVHGSSSFSLAPI 632

RESULT 11
 T52468
 cytochrome b5 (imported) - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000
 C/Accession: T52468
 R/Pukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
 Plant Physiol. 119, 353-361, 1999
 A/Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterologous Expression
 A/Reference number: Z25274
 A/Accession: T52468
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-140 <FK>
 A/Cross-references: EMBL:AB007802; PIDN:CAB17232.1
 C/Superfamily: cytochrome b5; cytochrome b5 core homology
 C/Keywords: heme; iron; metalloprotein
 F/40-64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 28.1%; Score 166.5; DB 2; Length 140;
 Best Local Similarity 39.8%; Pred. No. 3, 3e-10;
 Matches 33; Conservative 17; Mismatches 32; Indels 1; Gaps 1;
 QY 10 DVAMISTKELQAAADDLMTISGDVYVTPMLRHHGGEVPLITLAGODATDAM-AV 68
 DB 4 DGVFLTSEVSGHSSAKDCWIVDGKYYDVTKFLDHPGSDVILSTGKDATDDEVDG 63
 QY 69 HPPSVRLRRFVGRLLTDYVTP 91
 DB 64 HSSAKAMLDYVVGIDTATVP 86

RESULT 12
 S46306
 cytochrome b5 - common tobacco

C/Species: Nicotiana tabacum (common tobacco)
 C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-May-2000
 C/Accession: S46306; S33157
 R/Smith, M.A.; Stobart, A.K.; Shewry, P.R.; Napier, J.A.
 Plant Mol. Biol. 25, 527-537, 1994
 A/Title: Tobacco cytochrome b(5): cDNA isolation, expression analysis and in vitro proteolysis
 A/Reference number: S46306; M01D:94325476; PMID:8049375
 A/Accession: S46306
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-139 <SMI>
 A/Cross-references: EMBL:X71441; NID:g296385; PIDN:CAA50575.1; PID:g296386
 C/Superfamily: cytochrome b5; cytochrome b5 core homology
 C/Keywords: heme; iron; metalloprotein
 F/8-83/Domain: cytochrome b5 core homology <CB5>
 F/43-67/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 28.0%; Score 165.5; DB 2; Length 139;
 Best Local Similarity 39.8%; Pred. No. 4, 1e-10;
 Matches 33; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

QY 10 DVAMISTKELQAAADDLMTISGDVYVTPMLRHHGGEVPLITLAGODATDAM-AV 68
 DB 7 ETKVFLTAEVSGHNNKDCWLVSGKYYDVTKFLDHPGSDVILSTGKDATDDEVDG 66
 QY 69 HPPSVRLRRFVGRLLTDYVTP 91
 DB 67 HSSAKAMLDYVVGIDTATVP 89

RESULT 13
 S16292
 nitrate reductase (NADPH) (EC 1.7.1.3) - Neurospora crassa
 C/Species: Neurospora crassa
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
 C/Accession: S16292; S07176; S34796; S37298
 R/Okamoto, P.M.; Fu, Y.H.; Marzluf, G.A.
 Mol. Gen. Genet. 227, 213-223, 1991
 A/Title: Nit-3, the structural gene of nitrate reductase in Neurospora crassa: nucleotide sequence and characterization
 A/Reference number: S16292; M01D:91287699; PMID:1829499
 A/Accession: S16292
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-982 <MOL>
 A/Note: the authors translated the codon CCG for residue 140 as pro
 R/Je, K.H.D.; Lederer, F.
 EMBO J. 2, 1909-1914, 1983
 A/Title: On the presence of a heme-binding domain homologous to cytochrome b5 in Neurospora crassa
 A/Reference number: S07176
 A/Accession: S07176
 A/Molecule type: protein
 A/Residues: 1-622-623, 'Y', 624, 'IK', 627, 'Y', 628, 'XNKKY', 635, 'LIHKK', 643, 'DL', 646, 'K',
 C/Genetics:
 A/Gene: nit-3
 A/Intons: 675/1
 C/Complex: homodimer
 C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
 C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
 F/121-548/Domain: molybdopterin-binding domain homology <PCO>
 F/617-691/Domain: cytochrome b5 core homology <CB5>
 F/728-982/Domain: cytochrome-b5 reductase homology <CBR>
 F/240/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F/499/Dissulfide bonds: interchain #status predicted
 F/552-675/Binding site: heme iron (His) (axial ligands) #status predicted
 F/796-956/Binding site: NADP (Lys, Cys) #status predicted
 F/835/Binding site: FAD (Tyr) #status predicted

Query Match 28.0%; Score 165.5; DB 1; Length 982;
 Best Local Similarity 33.3%; Pred. No. 3, 8e-09;
 Matches 33; Conservative 19; Mismatches 38; Indels 9; Gaps 1;
 QY 7 DVAMISTKELQAAADDLMTISGDVYVTPMLRHHGGEVPLITLAGODATDAM 66

Db 613 DEKVTLLITLLELRQHDGEEEPFVYVNGYVNGTPTLEHGGGAASITGAGQDVTDEFL 672
 QY 67 AYHPSPVPLRLRRPFVGRLT-----DYTVPPASAD 96
 Db 673 AIHSENAKAMMPYTHIGTLTPSPAPALAKSSSTSDPALSD 711

RESULT 14

RDNTNS

nitrate reductase (NADH) (EC 1.7.1.1) nia-2 - common tobacco

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002

C/Accession: S04839; S25375; S22779

R/Voucher: H.; Kronenberger, J.; Rouze, P.; Caboche, M.

Plant Mol. Biol. 12, 597-600, 1989

A/Title: Complete nucleotide sequence of the two homeologous tobacco nitrate reductase g

A/Reference number: S04838

A/Accession: S04839

A/Molecule type: DNA

A/Residues: 1-904 <NAU>

A/Cross-references: EMBL:X14059; NID:G19890; PIDN:CAA2217.1; PID:G19891

R/Galangau, F.; Cherel, I.; Deng, M.; Meyer, C.; Moutaux, T.; Rouze, P.; Vaucheret, H.;

Curr. Top. Plant Biochem. Physiol. 7, 26-34, 1988

A/Title: Nitrate reductase expression in tobacco and tomato.

A/Reference number: S25375

A/Accession: S25375

A/Molecule type: DNA

A/Residues: 1-904 <CAL>

R/Galangau, F.; Hutterer, E.; Vincenz, M.; Rouze, P.; Galangau, F.; Vaucheret, H.; Cherel,

Mol. Gen. Genet. 209, 552-562, 1987

A/Title: Cloning of DNA fragments complementary to tobacco nitrate reductase mRNA and en

A/Reference number: S22779

A/Accession: S22779

A/Molecule type: mRNA

A/Residues: 171-724 <CAL>

A/Cross-references: EMBL:X06134; NID:G19894; PIDN:CAA29497.1; PID:G929750

C/Genetics:

A/Genes: nia-2

A/Introns: 338/1; 385/1; 462/3

C/Complex: homodimer

C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red

C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;

F/79-471/Domain: molybdopterin-binding domain homology <PCO>

F/531-605/Domain: cytochrome b5 core homology <CBS>

F/554-904/Domain: cytochrome-b5 reductase homology <CBR>

F/483/Binding site: molybdopterin (Cys) (covalent) #status predicted

F/422/Disulfide bonds: interchain #status predicted

F/566,589/Binding site: heme iron (His) (axial ligands) #status predicted

F/718,876/Binding site: NAD (Lys, Cys) #status predicted

F/758/Binding site: FAD (Tyr) #status predicted

Query Match 27.7%; Score 164; DB 1; Length 904;

Best Local Similarity 35.7%; Pred. No. 4.9e-09;

Matches 40; Conservative 15; Mismatches 43; Indels 14; Gaps 3;

QY 1 MPASADADVWRISTKEQAAHAAADDLMISIGDVYVDTWPLRHHPGCVPLITLACQD 60
 Db 527 KNTASK-----WYSSEVAKSHSSADSAMITVHGHIYDATRFKDHGGTSTLINAGTD 580
 QY 61 ATDAFMAVHPSPVPLRRPFVGRLT--TDYTVPP-----ASADFRLLAQL 104
 Db 581 CTEEFPAIHSDKAKKLEDPRIEGLITGTSTSDSPNSVHGSSSFSSFLAPI 632

RESULT 15

T00796

cytochrome b5 At2g32720 [similarity] - Arabidopsis thaliana

N/Alternate names: protein F24L7.14

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Mar-2001

C/Accession: T00796; F84736

R/Rounaley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, February 1998

A/Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence.

A/Reference number: Z14204

A/Accession: T00796

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-134 <ROU>

A/Cross-references: EMBL:AC003974; NID:G2914688; PIDN:AAC04491.1; PID:G2914701

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;

Enus, D.; Nieman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: F84736

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-134 <STO>

A/Cross-references: GB:A8002093; NID:G2914701; PIDN:AAC04491.1; GSPDB:GN00139

C/Genetics:

A/Genes: F24L7.14; At2g32720

A/Map position: 2

A/Introns: 29/3; 52/1

C/Superfamily: cytochrome b5; cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein

F/5-80/Domain: cytochrome b5 core homology <CBS>

F/40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 27.6%; Score 163.5; DB 2; Length 134;

Best Local Similarity 37.3%; Pred. No. 6.4e-10;

Matches 31; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 10 DYRMISTKELQAAHAAADDLMISIGDVYVDTWPLRHHPGCVPLITLACQDAPDAFM-AY 68
 Db 4 EAKIFLSEVSRHNOAHDPCWIVNGKVYVTKFLBDHPGGDVLSTSGKDATDPEDVG 63
 QY 69 HPPSVPLRLRRPFVGRLTDTYVP 91
 Db 64 HSESAREMMEQYVGEIDPTIP 86

Search completed: January 1, 2004, 06:39:43
 Job time : 4.29068 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 2.5084 Seconds

(without alignments)
2137.240 Million cell updates/sec

Title: US-09-857-524B-17

Sequence: 1 MPASADADVMISTKEIQ.....ADFRLLAQLSAGLFRVVG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	177	29.9	905	1 NIA_FUSOX	P39863 fusarium ox
2	174	29.4	894	1 NIA_BEABA	P43100 beauveria b
3	169.5	28.6	134	1 CYB5_1ARATH	Q42342 arabidopsis
4	168.5	28.5	134	1 CYB5_BRAOL	P40934 brassica ol
5	167	28.2	904	1 NIA1_TORAC	P11605 nicotiana t
6	165.5	28.0	136	1 CYB5_TORAC	P49098 nicotiana t
7	165.5	28.0	982	1 NIA_NEUCR	P08619 neucospora
8	164	27.7	904	1 NIA2_TORAC	P08509 nicotiana t
9	163.5	27.6	134	1 CYB2_1ARATH	Q48845 arabidopsis
10	161.5	27.3	891	1 NIA7_HORVU	P27968 hordeum vul
11	161	27.2	318	1 NIA_CHLVU	Q01170 chlorella v
12	159.5	26.9	909	1 NIA_PETRY	P36859 petunia hyb
13	159.5	26.9	917	1 NIA1_1ARATH	P11832 arabidopsis
14	159	26.9	881	1 NIA1_P1HAVU	P39865 phaseolus v
15	158.5	26.8	444	1 FAD5_BRAPE	Q0867 brachydanio
16	157	26.5	890	1 NIA2_P1HAVU	P39866 phaseolus v
17	157	26.5	926	1 NIA_SP1OL	P23312 spinacia ol
18	156	26.4	864	1 NIA_VOLCA	P36841 volvox cart
19	155.5	26.3	135	1 CYB5_TORAC	P49099 nicotiana t
20	153	25.8	900	1 NIA_LOTJA	P39869 lotus japon
21	152.5	25.8	893	1 NIA_T1EPMC	P36842 leptophaea
22	152	25.7	911	1 NIA1_BRANA	P39867 brassica na
23	152	25.7	911	1 NIA_LYCES	P17570 lycopersico
24	151	25.5	917	1 NIA2_1ARATH	P11035 arabidopsis
25	150.5	25.4	132	1 CYB5_BOROF	Q04334 borago offi
26	149.5	25.3	137	1 CYB5_ORYSA	P49100 oryza sativ
27	149.5	25.3	146	1 CYM5_RAT	P04166 rattus norv
28	148	25.0	920	1 NIA_T1CTIN	P43101 echinorium i
29	147	24.8	573	1 CYB2_HANAN	P09437 hansenula a
30	147	24.8	911	1 NIA2_BRANA	P39868 brassica na
31	146.5	24.7	916	1 NIA1_ORYSA	P16081 oryza sativ
32	145	24.5	890	1 NIA2_SOYBN	P39870 glycine max
33	145	24.5	898	1 NIA_1BEYVE	P27783 betula verr

ALIGNMENTS

RESULT 1	NIA_FUSOX	STANDARD;	PRT;	905 AA.
ID	NIA_FUSOX			
AC	P39863,			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).			
GN	NIA.			
OS	Fusarium oxysporum.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.			
OX	NCBI_TaxId=5507;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=F0M24;			
RC	MEDLINE=93380674; PubMed=8370541;			
RA	Dirolez A., Langin T., Gerlinger C., Brygoo Y., Daboussi M.-J.;			
RT	"The nia gene of Fusarium oxysporum: isolation, sequence and development of a homologous transformation system.";			
RL	Gene 131:61-67(1993).			
CC	- FUNCTION: Nitrate reductase is a key enzyme involved in the first			
CC	step of nitrate assimilation in plants, fungi and bacteria.			
CC	- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2O) = nitrate + NADPH.			
CC	- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)			
CC	AND ONE MOLYBDENUM ATOM.			
CC	- SUBUNIT: Homodimer (by similarity).			
CC	- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE			
CC	N-TERMINAL DOMAIN.			
CC	- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.			
CC	- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE			
CC	C-TERMINAL DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; Z22549; CAA80270.1; -			
DR	PIR; J08803; J08803.			
DR	HSSP; P04166; 1EUR.			
DR	InterPro; IPR001199; Cyt_B5.			
DR	InterPro; IPR001834; Cyt_B5_reductase.			
DR	InterPro; IPR000572; Burk_Mb_oxred.			
DR	InterPro; IPR001709; PPN_Cyt_reductase.			
DR	InterPro; IPR005066; Mo-co dimer.			
DR	InterPro; IPR001433; Oxred_FAD/NAD(P).			
DR	Pfam; PF00970; FAD_binding_6; 1.			
DR	Pfam; PF00173; heme_1; 1.			
DR	Pfam; PF03404; Mo-co_dimer; 1.			
DR	Pfam; PF00175; NAD_binding_1; 1.			
DR	Pfam; PF00174; oxidored_mol_yb; 1.			
DR	PRINTS; PR00406; CYTB5RDYASE.			

Q9um6 schizosacch
Q9hf1 rhizopus st
Q1032 schizosacch
Q0531 utrilago ma
Q9y706 mortierella
P54233 glycine max
P49102 zea mays (m
P49097 cuscutea ref
P49050 pichia angu
Q9v4n3 drosophila
P17571 zea mays (m
P27969 hordeum vul


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DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KM Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
Nitrates assimilation..
KW DOMAIN 3
FT METAL 179 179 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 230 230 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 428 428 INTERCHAIN (POTENTIAL).
FT DOMAIN 550 620 HEME-BINDING (BY SIMILARITY).
FT METAL 581 581 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 604 604 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT DOMAIN 645 905 FLAVIN-BINDING DOMAIN (BY SIMILARITY).
FT NP BIND 875 884 NADP (BY SIMILARITY).
SQ SEQUENCE 905 AA; 101898 MW; D5DE23F7971ACDA CRC64;

Query Match 29.9%; Score 177; DB 1; Length 905;
Best Local Similarity 38.8%; Pred. No. 4.8e-11;
Matches 33; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

QY 12 RMISTKELQAAADLMISGQVYDVTPMLRHHHPGGEVPLITLAGODATDAFMAVHP 71
DB 547 RKTIELKXHGSEEPVVKGEVYDCTPLSGPGASIFGAGQDATERMALHSE 606
QY 72 SVRPLRRFFVGRITDYTPPASAD 96
DB 607 NAKAMLPYHIGLDESRALISGD 631

RESULT 2
NIA_BEABA STANDARD; PRT; 894 AA.
ID NIA_BEABA
AC P43100;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase (NADPH) (EC 1.7.1.3) (NR).
GN NIA.
OS Beauveria bassiana (Trichothecium shioteae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocnemycetidae; Hypocreales; Clavicipitaceae; Cordycaps.
OX NCBI_TaxID=162975;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BB147;
RA Maurer P.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H2O = nitrate + NADPH.
CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC AND ONE MOLYBDENUM ATOM.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X84950; CAAS936.1; -.
CC PIR; S52857; S52857.

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DR HSSP; P04166; 1EUE.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR001834; Cyt B5 reductase.
DR InterPro; IPR000572; Euk_Mb_oxred.
DR InterPro; IPR001709; FPN_cyt_reductase.
DR InterPro; IPR005066; Mo-co_dimer.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00173; heme 1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF00174; oxidored_mol/b; 1.
DR PRINTS; PR00406; CYTB5RDYASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRODOM; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KM Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
Nitrates assimilation..
KW METAL 169 169 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 220 220 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 418 418 INTERCHAIN (POTENTIAL).
FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 894 AA; 99934 MW; D0ED234FB1B1322B CRC64;

Query Match 29.4%; Score 174; DB 1; Length 894;
Best Local Similarity 40.3%; Pred. No. 9.9e-11;
Matches 31; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 11 YRMISTKELQAAADLMISGQVYDVTPMLRHHHPGGEVPLITLAGODATDAFMAVHP 70
DB 535 VRLISLEELKXHGSEEPVVKGEVYDCTPLSGPGATSTINAAQDATERMALHSE 594
QY 71 PSVRPLRRFFVGRITDYTPPASAD 87
DB 595 ENAKAMPYHIGLITLND 611

RESULT 3
CYSL_ARATH STANDARD; PRT; 134 AA.
ID CYSL_ARATH
AC Q42342; Q9S805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5 isoform 1.
GN AT5G53560 OR MNC6.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA MEDLINE=99097071; PubMed=9880378;
RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.;
RT "Microsomal electron transfer in higher plants: cloning and
RT heterologous expression of NADH-cytochrome betas reductase from
RT Arabidopsis."; 119:353-361 (1999).
RL Plant Physiol. 119:353-361 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kocani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen

```

RT physically assigned P1 and TAC clones." ;
 RL DNA Res. 5:297-308(1998).
 RN [3]
 RP SEQUENCE OF 1-113 FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Cooke R., Landie M., Raynal M., Delseny M.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: MICROSOAMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB007801, BAA74839.1; -
 CC EMBL: AB015476, BAB09732.1; -
 CC EMBL: F20001, CAA23377.1; -
 CC PIR: T52469, T52469.
 CC HSSP: P00171, 1EHB.
 CC InterPro: IPR001199; Cyt B5.
 CC Pfam: PF00173, heme_1; 1.
 CC PRINTS: PR00363; CYTOCHROMEBS.
 CC PRODOM: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME B5_1; 1.
 CC PROSITE: PS02055; CYTOCHROME B5_2; 1.
 CC DR PROSITE: PS02055; CYTOCHROME B5_2; 1.
 CC DR PROSITE: PS02055; CYTOCHROME B5_2; 1.
 CC KW Multigene family; Transmembrane; Heme; Iron; Microsome;
 CC FT TRANSMEM 107 127
 CC FT METAL 40 40
 CC FT METAL 64 64
 CC FT CONFLICT 1 3
 CC FT CONFLICT 1 3
 CC MSS -> ARA (IN REF. 3).
 CC SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60F7C87FD CRC64;
 CC -----
 CC Query Match 28.6%; Score 169.5; DB 1; Length 134;
 CC Best Local Similarity 36.5%; Pred. No. 3.5e-11;
 CC Matches 31; Conservative 23; Mismatches 30; Indels 1; Gaps 1;
 CC
 CC QY 8 AADVMTSTKELOAAADDLMTISGDDYDVTPLRHHGGEVPLITLAGDADTAEM- 66
 CC DB 2 SSORXVLSFEESVSKNKTDCWLLISGKYDVTTPMDHDPGDEVLLSTGKDATNDFED 61
 CC QY 67 AYHPSVRLRRFFVGRLLDTYVP 91
 CC DB 62 VGHSDTARDMDKRYFGEIDSSVP 86
 CC
 CC RESULT 4
 CC CYB5_BRAOL STANDARD; PRT; 134 AA.
 CC AC P40934;
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Cytochrome b5.
 CC GN CYB5
 CC OS Brassica oleracea (Cauliflower).
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC OC Eurosidia II; Brassicales; Brassicaceae; Brassica.
 CC NCBI_TaxID=3712;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND SEQUENCE OF 6-47 AND 75-89.
 CC RC STRAIN=cv. Cauliflora;
 CC RA Kearns B.V., Keck P., Somerville C.R.;
 CC RT "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
 CC (Brassica oleracea L.).";

RL Plant Physiol. 99:1254-1257(1992).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases.
 CC -1- SUBCELLULAR LOCATION: MICROSOAMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M87514; AAA32990.1; -
 CC PIR: T14454, T14454.
 CC HSSP: P00171, 1EHB.
 CC InterPro: IPR001199; Cyt B5.
 CC Pfam: PF00173, heme_1; 1.
 CC PRINTS: PR00363; CYTOCHROMEBS.
 CC PRODOM: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME B5_1; 1.
 CC PROSITE: PS02055; CYTOCHROME B5_2; 1.
 CC KW Electron transport; Transmembrane; Heme; Iron; Microsome.
 CC FT TRANSMEM 107 127
 CC FT METAL 40 40
 CC FT METAL 64 64
 CC FT VARIANT 5 5
 CC FT VARIANT 5 5
 CC K -> N.
 CC SQ SEQUENCE 134 AA; 15062 MW; 764DC24A4CDD591 CRC64;
 CC -----
 CC Query Match 28.5%; Score 168.5; DB 1; Length 134;
 CC Best Local Similarity 35.3%; Pred. No. 4.4e-11;
 CC Matches 30; Conservative 23; Mismatches 31; Indels 1; Gaps 1;
 CC
 CC QY 8 AADVMTSTKELOAAADDLMTISGDDYDVTPLRHHGGEVPLITLAGDADTAEM- 66
 CC DB 2 ASKKVLSFEESVSKNKTDCWLLISGKYDVTTPMDHDPGDEVLLSTGKDATNDFED 61
 CC QY 67 AYHPSVRLRRFFVGRLLDTYVP 91
 CC DB 62 VGHSDTARDMDKRYFGEIDSSVP 86
 CC
 CC RESULT 5
 CC NIAL_TOBAC STANDARD; PRT; 904 AA.
 CC AC P11675;
 CC DT 01-OCT-1989 (Rel. 12, Created)
 CC DT 01-OCT-1989 (Rel. 12, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NRI).
 CC GN NIAL
 CC OS Nicotiana tabacum (Common tobacco).
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
 CC NCBI_TaxID=4097;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=cv. Xanthi; TISSUE=leaf;
 CC RA Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
 CC RT "Complete nucleotide sequence of the two homologous tobacco nitrate
 CC reductase genes." ;
 CC RL Plant Mol. Biol. 12:597-600(1989).
 CC CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2O) = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF PAD,
 CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
 CC BY THE CIRCADIAN RHYTHM.

CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 CC EMBL: X14058; CA332216.1; -.
 CC FIR; S04838; RDNNT.
 CC HSP; P17571; ZCND.
 CC Interpro: IPR001199; Cyt_B5.
 CC Interpro: IPR001834; Cyt_B5_reductase.
 CC Interpro: IPR000572; Btk_Mb_oxred.
 CC Interpro: IPR001709; PPN_Cyt_reductase.
 CC Interpro: IPR005066; Mo-co_dimer.
 CC Interpro: IPR001433; Oxred_FAD/NAD(P).
 CC Pfam: PF00970; FAD_binding_6; 1.
 CC Pfam: PF00173; heme_1; 1.
 CC Pfam: PF03404; Mo-co_dimer; 1.
 CC Pfam: PF00175; NAD_binding_1; 1.
 CC Pfam: PF00174; oxidored_melb; 1.
 CC PRINTS: PR00406; CYTB5RDTASE.
 CC PRINTS: PR00363; CYTOCHROMEBS.
 CC PRINTS: PR00407; EMOPTERIN.
 CC PRINTS: PR00371; FPNCR.
 CC Prodom: PD000612; Cyt_B5; 1.
 CC Prosite: PS00191; CYTOCHROME_B5_1; 1.
 CC Prosite: PS50255; CYTOCHROME_B5_2; 1.
 CC Prosite: PS00559; MOLYBDOPTERIN_EUK; 1.
 CC KX Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 CC Nitrate assimilation; Multigene family;
 CC FT METAL 183 183 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT METAL 237 237 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT DISULFID 422 422 INTERCHAIN (POTENTIAL).
 CC FT METAL 566 566 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 589 589 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 904 AA; 101907 MW; 85642BDA73EEL54 CRG64;
 CC
 CC Query Match 28.2%; Score 167; DB 1; Length 904;
 CC Best Local Similarity 35.7%; Pred. No. 5.6e-10;
 CC Matches 40; Conservative 15; Mismatches 43; Indels 14; Gaps 3;
 CC
 CC QY 1 MPASKADAVRMSTKELQAAADLMISGVDYDVTPLRHGGEVPLITLAGOD 60
 CC DB 527 MNTSK-----MSSSEVRGSSADSAWIIHGHIYDARPLDHDGSSDIINAGTD 580
 CC QY 61 ATDAFMAVHPSPVPLLRFFVGRLT--TDYTVPP-----ASADFRLLAQL 104
 CC DB 581 CTEFEADAHDKAKKLEFRIGELITGTTSDFGNSVHGSSSFSLAPI 632
 CC
 CC RESULT 6
 CC CYB5_TOBAC STANDARD; PRT; 136 AA.
 CC ID CYB5_TOBAC
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Cytochrome b5.
 CC OS Nicotiana tabacum (Common tobacco).
 CC OC Burkholderia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 CC NCBI_TaxID=4097;
 CC OX [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stebbart A.K., Shewry P.R., Napier J.A.;
 RT Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting.";
 RL Plant Mol. Biol. 25:527-537(1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
 CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
 CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOSOLIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
 CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
 CC LEVELS IN THE LEAF.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: X71441; CA50575.1; ALT_INIT.
 CC EMBL: X68140; CA448240.1; -.
 CC HSP; P04166; 1BSM.
 CC Interpro: IPR001199; Cyt_B5.
 CC Interpro: IPR00173; heme_1; 1.
 CC Pfam: PF00173; heme_1; 1.
 CC Prodom: PD000612; Cyt_B5; 1.
 CC Prosite: PS00191; CYTOCHROME_B5_1; 1.
 CC Prosite: PS50255; CYTOCHROME_B5_2; 1.
 CC DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 CC KX Electron transport; Transmembrane; Heme; Iron; Microsome;
 CC Multigene family.
 CC FT TRANSMEM 107 127 POTENTIAL.
 CC FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT CONFLICT 10 11 LA -> EF (IN REF. 1; CA448240).
 CC FT CONFLICT 105 105 MISSING (IN REF. 1; CA448240).
 CC SQ SEQUENCE 136 AA; 14979 MW; DACE9EA695B2835F CRG64;
 CC
 CC Query Match 28.0%; Score 165.5; DB 1; Length 136;
 CC Best Local Similarity 39.8%; Pred. No. 9.4e-11;
 CC Matches 33; Conservative 16; Mismatches 33; Indels 1; Gaps 1;
 CC
 CC QY 10 DVAMISTKELQAAADLMISGVDYDVTPLRHGGEVPLITLAGODATDAFM-AY 68
 CC DB 4 ETRVFTIAEVSQINNAKDCMLVYSGKYDVTYKFLDHPGDEVLATSKADTDPEVGG 63
 CC QY 69 HPSVAPPLLRFFVGRITDYTV 91
 CC DB 64 HSSSAPAMLDERYVDISATIP 86
 CC
 CC RESULT 7
 CC NIA_NEUCR STANDARD; PRT; 982 AA.
 CC ID NIA_NEUCR
 CC AC P08619;
 CC DT 01-AUG-1988 (Rel. 08, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).
 CC GN NIT-3.
 CC OS Neurospora crassa.
 CC OC Burkholderia; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 CC NCBI_TaxID=5141;
 CC OX [1]

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=91287699; PubMed=1829499;
 RA Okamoto P.M., Fu Y.-H., Marzluf G.A.;
 RT "Nlt-3, the structural gene of nitrate reductase in Neurospora
 crassa: nucleotide sequence and regulation of mRNA synthesis and
 turnover.";
 RL Mol. Genet. 227:213-223(1991).
 RN [2]
 RP PRELIMINARY PARTIAL SEQUENCE AROUND HIS-652.
 RA Le K.H.D., Lederer F.;
 RT "On the presence of a heme-binding domain homologous to cytochrome b5
 in Neurospora crassa assimilatory nitrate reductase.";
 RL EMBO J. 2:1909-1914(1983).
 RN [3]
 RP MUTANTS.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=93241176; PubMed=8479443;
 RA Okamoto P.M., Garrett R.H., Marzluf G.A.;
 RT "Molecular characterization of conventional and new repeat-induced
 mutants of nlt-3, the structural gene that encodes nitrate reductase
 in Neurospora crassa.";
 RL Mol. Genet. 238:81-90(1993).
 RN [4]
 RP MUTAGENESIS.
 RX MEDLINE=93360901; PubMed=8355655;
 RA Okamoto P.M., Marzluf G.A.;
 RT "Nitrate reductase of Neurospora crassa: the functional role of
 individual amino acids in the heme domain as examined by
 site-directed mutagenesis.";
 RL Mol. Genet. 240:221-230(1993).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NADPH(+) + H(2)O = nitrate + NADPH.
 CC -1- COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEME IRON,
 AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS
 CALLED CYTOCHROME B-557.
 CC -1- PATHWAY: Nitrate assimilation (denitrification).
 CC -1- SUBUNIT: Homodimer.
 CC -1- INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AND RESPONDS RAPIDLY
 TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 C-TERMINAL DOMAIN.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL, X61303; CAA3600.1; ..
 DR HSSP, P00171; 1F03.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR001834; Cyt B5 reductase.
 DR InterPro: IPR000572; Btk_Mb oxidred.
 DR InterPro: IPR005066; Mo-co dimer.
 DR InterPro: IPR001433; Oxired_FAD/NAD(P).
 DR Pfam: PF00970; FAD_binding_6; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR Pfam: PF03404; Mo-co dimer; 1.
 DR Pfam: PF00175; NAD binding_1; 1.
 DR Pfam: PF00174; oxidored_molyb; 1.
 DR PRINTS; PRO0406; CYTBSRTRASE.
 DR PRINTS; PRO0363; CYTOCHROMEBS.
 DR PRINTS; PRO0407; EUMOPTERIN.
 DR ProDom; PD000612; Cyt B5; 1.
 DR PROSITE, PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE, PS50255; CYTOCHROME B5_2; 1.
 DR PROSITE, PS00559; MOLYBDOPTERIN_EUK; 1.
 KM Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
 KM Nitrate assimilation.
 FT METAL 240 240
 FT METAL 295 295
 FT DISULFID 499 499
 FT DOMAIN 621 691
 FT METAL 652 652
 FT METAL 675 675
 FT METAL 718 962
 FT NP_BIND 952 961
 FT MUTAGEN 652 652
 FT MUTAGEN 675 675
 SQ SEQUENCE 982 AA; 108432 MW; B7838C031B19687F CRC64;
 Query Match 28.0%; Score 165.5; DB 1; Length 982;
 Best Local Similarity 33.3%; Pred. No. 8.9e-10;
 Matches 33; Conservative 19; Mismatches 38; Indels 9; Gaps 1;
 QY 7 DAADVMTSTKELQAAADDLWISISGVYDTPRLRHNGEVLITLAGQDADPAM 66
 DB 613 DEKVTSLTLEBLRQHDGESEFPVNVGQVNGTPELFGHFGAASITGAAGDVTDFL 672
 QY 67 AYHPSVRPLRLRRFFVGRLT-----DYTPPASAD 96
 DB 673 AIHSENAKMPTPIHIGTITPSAPALAKSSISDPALSD 711
 RESULT 8
 NIA2_TOBAC STANDARD; PRT; 904 AA.
 ID P08509;
 AC 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR2).
 GN NIA2.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxId=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Xanthi; TISSUE=Leaf;
 RA Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
 RT "Complete nucleotide sequence of the two homologous tobacco nitrate
 reductase genes.";
 RL Plant Mol. Biol. 12:597-600(1989).
 RN [2]
 RP SEQUENCE OF 171-724 FROM N.A.
 RA Calza R., Hutterer B., Vincenz M., Rouze P., Galanau F.,
 RA Vaucheret H., Cherel I., Meyer C., Kronenberger J., Caboche M.;
 RT "Cloning of DNA fragments complementary to tobacco nitrate reductase
 mRNA and encoding epitopes common to the nitrate reductases from
 higher plants.";
 RL Mol. Genet. 209:552-562(1987).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NADPH(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 GROUP IS CALLED CYTOCHROME B-557.
 CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
 BY THE CIRCADIAN RHYTHM.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 C-TERMINAL DOMAIN.
 CC -----

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CC or send an email to license@isb-sib.ch).

DR EMBL: X14059; CAA32217.1; -
DR PIR: X06134; CAA29497.1; -
DR HSP: P15771; ZCND.
DR InterPro: IPR001199; Cyt B5.
DR InterPro: IPR001834; Cyt B5 reductase.
DR InterPro: IPR000572; Bk Mb oxred.
DR InterPro: IPR001709; FPN_cyt_redctse.
DR InterPro: IPR005066; Mo-co-dimer.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00970; FAD_binding_6; 1.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co dimer; 1.
DR Pfam: PF00175; NAD binding_1; 1.
DR Pfam: PF00174; oxidored_molyb; 1.
DR PRINTS: PR00406; CYTBSRDIASE.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRINTS: PR00371; PNCR.
DR ProDom: PD000612; Cyt B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
DR OXIDOREDUCTASE; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KM Nitrate assimilation; Multigene family.
FT METAL 183 MLYBDENUM-PTERIN (POTENTIAL).
FT METAL 237 MLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 422 INTERCHAIN (POTENTIAL).
FT METAL 566 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 589 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 904 AA; 101957 MW; 7519675A3561D69 CRC64;

Query Match 27.7%; Score 164; DB 1; Length 904;
Best Local Similarity 35.7%; Pred. No. 1.2e-09;
Matches 40; Conservative 15; Mismatches 43; Indels 14; Gaps 3;

Qy 1 MPASKAADAVRMISTKELQAAADLMWISGCVYDVTPWLRHHPGSEVPLTLAAGD 60
Db 527 MNTASK-----MYSSEVKHSSADSAWIIHGCHIDATRFKDHFGDSTIIINAGTD 580
Qy 61 ATDAFMAVHPPSVRLRRFFVGRLL--TDYTVPP-----ASADFRLLAQL 104
Db 581 CTBEFPAIHSDKAKKLEDFRIGELITGYTSDPSGNSVHGSSSFLAPI 632

RESULT 9
CYS2 ARATH STANDARD; PRT; 134 AA.
AC 04885;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cytochrome b5 isoform 2.
GN ATG32720 OR F24I7.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernan W.C., White O., Eisen J.A., Salzberg S.L., Frazer C.M.,
RA Venter J.C.,
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL: AC003974; AAC0491.1; -
DR PIR: T00796; T00796.
DR HSP: P04166; 1B5M.
DR InterPro: IPR001199; Cyt B5.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR ProDom: PD000612; Cyt B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; CYTOCHROME_B5_2; 1.
KM Electron transport; Transmembrane; Heme; Iron; Mitochondrion;
KM Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 134 AA; 15016 MW; B405F5430F5716C1 CRC64;

Query Match 27.6%; Score 163.5; DB 1; Length 134;
Best Local Similarity 37.3%; Pred. No. 1.5e-10;
Matches 31; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

Qy 10 DVMISTKELQAAADLMWISGCVYDVTPWLRHHPGSEVPLTLAAGDADAFM-AV 68
Db 4 EAKITLSEVSEINQAHDCMIVNGKVVYVTFRLBHPGGDVLISSTKADATDDEVDG 63
Qy 69 HPPSVRLRRFFVGRLLTDYTVPP 91
Db 64 HSESAREMEQYVVGSDIPTTIP 86

RESULT 10
NIA7 HORVU STANDARD; PRT; 891 AA.
AC P27968;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NAD(P)H] (EC 1.7.1.2).
GN NAR-7.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya;
RX MEDLINE=91375416; PubMed=1896007;
RA Miyazaki J., Juricek M., Angelis K., Schorr K.M., Kleinhofs A.,
Warner R.L.,
RT "Characterization and sequence of a novel nitrate reductase from

```

RT barley.";
RL Mol. Genet. 228:329-334(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(P)+ + H2O = nitrate +
CC NAD(P)H.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- SUBUNIT: Homodimer.
CC -1- INDUCTION: By nitrate.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
-----
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DR EMBL: X60173; CAA42739.1; -.
DR PIR: S16895; RDBHNP.
DR HSSP: P17571; 2CND.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR001834; Cyt_B5_reductase.
DR InterPro: IPR000572; Euk_Mb_oxred.
DR InterPro: IPR001709; FPN_Mb_reductase.
DR InterPro: IPR005066; Mo-co_dimer.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR InterPro: IPR001221; Phe_hydroxylase.
DR Pfam: PF00970; Phe_hydroxylase.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co_dimer; 1.
DR Pfam: PF00175; NAD_binding_1; 1.
DR Pfam: PF00174; oxidored_molyp; 1.
DR PRINTS: PR00406; CYTBSRDYASE.
DR PRINTS: PR00363; CYTOCHROMEBS.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRINTS: PR00371; FPNCR.
DR PRINTS: PR00410; PHEHDXLYASE.
DR PRODOM: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
DR Nitrate assimilation; Multigene family.
DR METAL 168 168 MOLYBDENUM-PTERIN (POTENTIAL).
DR METAL 221 221 MOLYBDENUM-PTERIN (POTENTIAL).
DR DISULFID 406 406 INTERCHAIN (POTENTIAL).
DR METAL 550 550 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR SEQUENCE 891 AA; 96630 MW; AA47EC52FCE1FBD3 CRC64;

Query Match 27.3%; Score 161.5; DB 1; Length 891;
Best Local Similarity 35.6%; Pred. No. 2.1e-09;
Matches 37; Conservative 16; Mismatches 44; Indels 7; Gaps 2;

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ID NIA_CHLVU STANDARD; PRT; 318 AA.
AC 001170;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
OS Chlorella viridis.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=91354204; PubMed=1883330;
RA Cannon A.C., Iida N., Solomonson L.P.;
RT "Expression of a cDNA clone encoding the haem-binding domain of
RT Chlorella nitrate reductase."
RL Biochem. J. 278:203-209(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(P)+ + H2O = nitrate + NADH.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
-----
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-----
DR EMBL: X56771; CAA0090.1; -.
DR PIR: S17197; S17197.
DR HSSP: P04166; 1BSM.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR000572; Euk_Mb_oxred.
DR InterPro: IPR005066; Mo-co_dimer.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co_dimer; 1.
DR PRINTS: PR00363; CYTOCHROMEBS.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRODOM: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
DR Nitrate assimilation.
DR METAL 251 251 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR METAL 274 274 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR NON TER 318 318
DR SEQUENCE 318 AA; 34830 MW; E60D82FE1B98292A CRC64;

Query Match 27.2%; Score 161; DB 1; Length 318;
Best Local Similarity 33.0%; Pred. No. 7.5e-10;
Matches 29; Conservative 18; Mismatches 41; Indels 0; Gaps 0;

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RESULT 11
NIA_CHLVU

RESULT 12
 ID NIA_PETHY STANDARD; PRT; 909 AA.
 AC P36859;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
 GN NIA.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Petunia.
 OC NCBI_Taxid=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. TLR13; TISSUE=leaf;
 RX MEDLINE=9392981; PubMed=8514183;
 RA Salanoubat M., Ha D.B.D.;
 RT "Analysis of the petunia nitrate reductase apoenzyme-encoding gene: a
 RT first step for sequence modification analysis.";
 RL Gene 128:147-154 (1993).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
 CC BY THE CIRCADIAN RHYTHM.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION 2 HOURS AFTER SUNRISE. LOW
 CC EXPRESSION FOUND 2 HOURS BEFORE AND 8 HOURS AFTER SUNRISE.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 CC EMBL, U13691; AAA37713.1; --
 CC HSSP; P17571; 2CND.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR001834; Cyt_B5 reductase.
 DR InterPro: IPR000572; Bk_Mb_oxred.
 DR InterPro: IPR001709; FPN_Cyt_reducte.
 DR InterPro: IPR005066; Mo-co_dimer.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00970; FAD binding_6_1.
 DR Pfam: PF03473; heme_1_1.
 DR Pfam: PF03404; Mo-co_dimer; 1.
 DR Pfam: PF00175; NAD binding_1_1.
 DR Pfam: PF00174; Oxidored_molyb_1.
 DR PRINTS; PR00406; CYTB5RDYASE.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS00255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 KM Nitrate assimilation; Multigene family.
 FT METAL 187 187 MOLYBDENUM-PTERIN (POTENTIAL).
 FT METAL 241 241 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 426 426 INTERCHAIN (POTENTIAL).

FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 909 AA; 102376 MW; 502C706F6563E706 CRC64;
 Query Match 26.9%; Score 159.5; DB 1; Length 909;
 Best Local Similarity 36.3%; Pred. No. 3.6e-09;
 Matches 41; Conservative 14; Mismatches 43; Indels 15; Gaps 3;
 QY 1 MPASKADADVRMISFKELOAHAAADDLMISIGDYDTPMLRHHGGEVPLITLAGOP 60
 DB 531 MNTASK-----MYSSEVKKNSADSAMIIYGHVYDTRFLKDPGGIDSLINAGTD 584
 QY 61 ATDAFMAHPSPVPLLRFFVGRLT--TDYVPPA-----SADFRRLAQL 104
 DB 585 CTEEPDAIHSKAKKLLIEDFRIGELITTYGTSSSNNSSVHSSSFGFLAP1 637
 RESULT 13
 ID NIAI_ARATH STANDARD; PRT; 917 AA.
 AC P11832; O9CA18;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
 GN NIAI OR AT1G77760 OR T32E8.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.; VARIANT THR-198, AND HERBICIDE RESISTANCE.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=93287999; PubMed=8510658;
 RA Wilkinson J.Q., Crawford N.M.;
 RT "Identification and characterization of a chlorate-resistant mutant
 RT of Arabidopsis thaliana with mutations in both nitrate reductase
 RT structural genes NIA1 and NIA2.";
 RL M1. Gen. Genet. 239:289-297 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Becker J.R., Palm C.J., Federpspiel N.A., Kaul S.,
 RA White O., Alonso J., Alefati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Benlier E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feildlyum T.V., Feng J.-D., Feng B., Fujii C.Y.,
 RA Gali J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzler L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetskaia I., Kutz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Malt R., Marshall A.,
 RA Miltescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pail G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vayaberg W., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Frazer C.M., Ventler J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Becker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/RGEC)." ;
 RN Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 (4)
 RP SEQUENCE OF 342-360 AND 525-917 FROM N.A.
 RX MEDLINE=89091069; PubMed=2905260;

RA Cheng C., Dewdney J., Nam H., den Boer B.G.W., Goodman H.M.;
 RT "A new locus (NIA 1) in Arabidopsis thaliana encoding nitrate
 RT reductase.";
 RL EMBL J. 7:3309-3314 (1988).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- SUBUNIT: Homodimer.
 CC -1- TISSUE SPECIFICITY: ROOT, LEAF, AND SHOOT.
 CC -1- MISCELLANEOUS: WHEN MUTATED CONFERS RESISTANCE TO THE HERBICIDE
 CC CHLORATE.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J19050; CAA79494.1; -;
 DR EMBL: AC012193; AAG51627.1; -;
 DR EMBL: AY090950; AAM13997.1; -;
 DR EMBL: AF424624; AAL1617.1; -;
 DR EMBL: X13434; CAA31786.1; -;
 DR EMBL: X13436; CAA31786.1; -;
 DR PIR: E96807; E96807.
 DR PIR: S35228; S35228.
 DR HSSP: P17571; 2CND.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR001834; Cyt_B5_reductase.
 DR InterPro: IPR000572; Euk_Mb_oxred.
 DR InterPro: IPR001709; FPN_cyt_reductase.
 DR InterPro: IPR005066; Mo-co_dimer.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR InterPro: IPR001221; Phe_hydroxylase.
 DR Pfam: PF00970; FAD_binding_6; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR Pfam: PF03404; Mo-co_dimer; 1.
 DR Pfam: PF00175; NAD_binding_1; 1.
 DR Pfam: PF00174; oxidored_molyb; 1.
 DR PRINTS: PR00406; CYTB5RDTASE.
 DR PRINTS: PR00363; CYTOCHROMEBS.
 DR PRINTS: PR00407; EUMOPTERIN.
 DR PRINTS: PR00371; FPNCR.
 DR PRINTS: PR00410; PHEHYDRILASE.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR ProSITE: PS02855; CYTOCHROME_B5_2; 1.
 DR ProSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 DR Nitrate assimilation; Multigene family; Herbicide resistance.
 DR METAL: 197 197 MOLYBDENUM-PTERIN (POTENTIAL).
 DR METAL: 251 251 MOLYBDENUM-PTERIN (POTENTIAL).
 DR METAL: 436 436 INTERCHAIN (POTENTIAL).
 DR METAL: 580 580 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR METAL: 603 603 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR VARIANT: 198 198 A -> T (LOSS OF ACTIVITY).
 DR CONFLICT: 17 17 A -> R (IN REF. 1).
 DR SEQUENCE 917 AA; 103040 MW; 6F3ED46B9F63825 CR64;

QY 1 MPAAKADADVMIISTKELQAAADDLWISISGDVYDTPMLRHHGGEVPLITLAGOD 60
 DB 541 MNTASK-----MYSISEVRKNTADSAMIIYHGHITDCTRFKHPGGTDLINAGTD 594
 QY 61 ATDAFMAVHPSPVRLRRPFVGRU--TDYVPP-----ASADFRLLAQL 104
 DB 595 CEEFPAIRHSDRAKKLEDDRYGELLITGYDSSPNVSVGASNFGGLAPV 645
 RESULT 14
 NIA1_PHAVU
 ID NIA1_PHAVU STANDARD; PRT; 881 AA.
 AC P39865;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR-1).
 GN NIA1 OR NR1.
 OS Phaseolus vulgaris (kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseolae; Phaseolus.
 OX NCBI_TaxID=3885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Saxa; TISSUE=Shoot;
 RA Hoff T., Stummann B.W., Henningsen K.W.;
 RT "Cloning and expression of a gene encoding a root specific nitrate
 RT reductase in bean (Phaseolus vulgaris)."
 RL Physiol. Plantarum 82:197-204 (1991).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
 CC AND ONE MOLYBDENUM ATOM.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X53603; CAA37672.1; -;
 DR PIR: S25445; S25445.
 DR HSSP: P17571; 2CND.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR001834; Cyt_B5_reductase.
 DR InterPro: IPR000572; Euk_Mb_oxred.
 DR InterPro: IPR001709; FPN_cyt_reductase.
 DR InterPro: IPR005066; Mo-co_dimer.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00970; FAD_binding_6; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR Pfam: PF03404; Mo-co_dimer; 1.
 DR Pfam: PF00175; NAD_binding_1; 1.
 DR Pfam: PF00174; oxidored_molyb; 1.
 DR PRINTS: PR00406; CYTB5RDTASE.
 DR PRINTS: PR00363; CYTOCHROMEBS.
 DR PRINTS: PR00407; EUMOPTERIN.
 DR PRINTS: PR00371; FPNCR.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR ProSITE: PS02855; CYTOCHROME_B5_2; 1.
 DR ProSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;

Query Match 26.9%; Score 159.5; DB 1; Length 917;
 Best Local Similarity 35.1%; Pred. No. 3,6e-09;
 Matches 39; Conservative 16; Mismatches 43; Indels 13; Gaps 3;

KW Nitrate assimilation; Multigene family.
 FT METAL 167 167 MOLYBDENUM-PTERIN (POTENTIAL).
 FT METAL 221 221 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 406 406 INTERCHAIN (POTENTIAL).
 FT METAL 550 550 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 881 AA; 99222 MW; A212A12884EE661 CRC64;
 Query Match 26.8%; Score 159; DB 1; Length 881;
 Best Local Similarity 38.1%; Pred. No. 3.9e-09;
 Matches 32; Conservative 16; Mismatches 34; Indels 2; Gaps 1;
 QY 15 STEKQAHAAADLWISGVDVDTPEMLRHHPGGEVPLITLAGODATDAFMAYHPSPVR 74
 DB 519 SLSEVRRHNRDASMIIVNHVYDCTRFKLDHFGEGSILNAGCTCTEEFEALHSKAK 578
 QY 75 PLURRFFVGRLLTDTYVPPASAD 96
 DB 579 KMLEDYRIGELMTDTYSDSSSN 602
 RESULT 15
 FADS_BRARE STANDARD; PRT; 444 AA.
 ID FADS_BRARE STANDARD; PRT; 444 AA.
 AC QDEX7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).
 GN FADS2 OR FADS6.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBI_taxid=7953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21592990; PubMed=11724940;
 RA Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,
 RA Sargent J.R., Teale A.J.;
 RT "A vertebrate fatty acid desaturase with delta5 and delta6
 RT activities";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).
 CC -!- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6
 CC activities. May represent a component of the polyunsaturated fatty
 CC acid biosynthesis pathway.
 CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -----
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 CC -----
 CC DR EMBL; AF309556; AAG25710.1; -.
 DR HSSP; P00173; IJEX.
 DR ZFIN; ZDB-GENE-011212-1; fads2.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; FALSE_NEG.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; Heme.
 FT DOMAIN 18 95 HEME-BINDING.
 FT METAL 53 53 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

FT METAL 76 76 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1DC0F65 CRC64;
 Query Match 26.8%; Score 158.5; DB 1; Length 444;
 Best Local Similarity 35.2%; Pred. No. 2e-09;
 Matches 37; Conservative 18; Mismatches 39; Indels 11; Gaps 3;
 QY 17 KETQAHAAADLWISGVDVDTPEMLRHHPGGEVPLITLAGODATDAFMAYHP--PSVR 74
 DB 24 EYQKTKTGDDVYVERKYNVSCVKNHFGGLRIIGHYAGEDATFATPHNQLVR 83
 QY 75 PLURRFFVGRLLTDTYVPPAS-----ADFRLLAQLSSAGLFE 111
 DB 84 KYUKPLLIGEL-EASEPSQDRQNALVEDPRLRRLAECCFK 127
 Search completed: January 1, 2004, 06:30:57
 Job time : 3.5084 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 10.2316 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-17
Perfect score: 592
Sequence: 1 MPAAKDAADVMTSTKELQ.....ADFRRLAQSLKGLFERYG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_rvrvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	469	10	Q9ZTUB
2	306	51.7	446	10	Q81LD7
3	282.5	47.7	446	10	Q9FR82
4	274.5	46.4	458	10	Q43469
5	267.5	45.2	448	10	Q8VZ21
6	263.5	44.5	448	10	Q8VZ22
7	262.5	44.3	446	10	Q9ZTV9
8	258	43.6	448	10	Q9SAD5
9	250.5	42.3	449	10	Q9ZRP8
10	249	42.1	448	10	Q81L77
11	236.5	39.9	449	10	Q8LB96
12	236.5	39.9	449	10	Q9ZRP7
13	195	32.9	477	10	Q8RXB0
14	193.5	32.7	459	10	Q944W4
15	180	30.4	464	5	Q9Y1W0

17	178.5	30.2	929	3	Q8J259	Q8J259 tuber borch
18	177	29.9	445	13	Q90ZB9	Q90ZB9 oreochromis
19	177	29.9	907	3	Q92237	Q92237 giberella
20	175.5	29.6	135	10	Q9FDW8	Q9FDW8 arabidopsis
21	173	29.2	891	10	Q00101	Q00101 phaeosphaer
22	172.5	29.1	445	13	Q8Y644	Q8Y644 sparus aura
23	169.5	28.6	452	13	Q8UTM5	Q8UTM5 oncorhynch
24	169.5	28.6	467	5	Q96099	Q96099 dicystostei
25	169.5	28.6	870	3	Q9P942	Q9P942 hansenula a
26	168.5	28.5	444	13	Q9PEX6	Q9PEX6 cyprinus ca
27	167.5	28.3	134	10	Q8H293	Q8H293 ananas como
28	166.5	28.1	140	10	Q9ZWT2	Q9ZWT2 arabidopsis
29	165.5	28.0	134	10	Q48618	Q48618 olea europ
30	165.5	28.0	454	13	Q98SW7	Q98SW7 oncorhynch
31	161.5	27.3	873	3	Q8X1X0	Q8X1X0 monascus an
32	161	27.2	882	10	Q9SDY3	Q9SDY3 chlamydomon
33	160.5	27.1	454	13	Q90ZB8	Q90ZB8 oncorhynch
34	160	27.0	877	10	Q42497	Q42497 chlorella v
35	160	27.0	983	3	Q96V88	Q96V88 ustilago ma
36	159.5	26.9	892	3	Q13486	Q13486 metarhizium
37	159.5	26.9	915	10	Q43042	Q43042 petunia hyb
38	155.5	26.3	134	10	Q94HX5	Q94HX5 oryza sativ
39	155	26.2	914	10	Q9PFC2	Q9PFC2 ricinus com
40	154.5	26.1	89	5	Q8SY77	Q8SY77 diosiphila
41	154.5	26.1	132	10	Q24651	Q24651 olea europ
42	154.5	26.1	477	10	Q8H0N8	Q8H0N8 phytophthor
43	154	26.0	486	11	Q9EP24	Q9EP24 rattus norv
44	153.5	25.9	456	10	Q944W3	Q944W3 pythium itr
45	152.5	25.8	386	4	Q96H07	Q96H07 homo sapien

ALIGNMENTS

RESULT 1	ID	Q9ZTUB	PRELIMINARY;	PRT;	469 AA.
AC	Q9ZTUB	01-MAY-1999 (T-EMBLrel. 10, Created)			
DT	01-MAY-1999 (T-EMBLrel. 10, Last sequence update)				
DE	01-MAR-2003 (T-EMBLrel. 23, Last annotation update)				
GN	S276.				
OS	Triticum aestivum (wheat).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
CC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OX	Triticaceae; Triticum.				
RN	NCBI_TaxID=4565;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=cv. ET3;				
RA	Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;				
RT	"Aluminum tolerance in yeast conferred by over-expression of wheat				
RT	genes.";				
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE EMBL/GenBank/DBJ database.				
DR	EMBL; AF031194; AAD10250.1; -				
DR	HSSP; P00171; I150.				
DR	InterPro; IPR001199; Cyt B5.				
DR	InterPro; IPR005804; PA_decat fam.				
DR	InterPro; IPR001092; H1H_basid.				
DR	Pfam; PF00487; PA_decatase; 1.				
DR	Pfam; PF00173; heme_1; 1.				
DR	PRINTS; PR00363; CYTOCHROME B5.				
DR	ProDom; PD000612; Cyt B5; 1.				
DR	ProDom; PD001081; PA_decat fam; 1.				
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.				
DR	PROSITE; PS00038; H1H_1; 1.				
KW	Heme.				
SQ	SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;				
Query Match	100.0%;	Score 592;	DB 10;	Length 469;	
Best Local Similarity	100.0%;	Pred. NO. 3.1e-54;			

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASKDAVPMSTKEIQHAAADLMISGDVYDTPWLRHNGGEVPLTTAGOD 60
 DB 17 MPASKDAVPMSTKEIQHAAADLMISGDVYDTPWLRHNGGEVPLTTAGOD 76

QY 61 ATDAFMAVHPPSVPLRRFFVGLTDTYTPPASADFRRLAQLSSAGLPERVG 114
 DB 77 ATDAFMAVHPPSVPLRRFFVGLTDTYTPPASADFRRLAQLSSAGLPERVG 130

RESULT 2
 Q8LBD7 PRELIMINARY; PRT; 446 AA.

AC Q8LBD7
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Sphingolipid long chain base delta 8 desaturase.
 OS Aquilegia vulgaris.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Ranunculaceae; Aquilegia.
 OC NCBI_TaxID=3451;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Longman A.J., Michaelson L.V., Napier J.A.:
 "Isolation and characterization of a cDNA encoding a delta 8
 sphingolipid desaturase from Aquilegia vulgaris."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF406816; AAN03619.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KM SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;
 SQ

Query Match 51.7%; Score 306; DB 10; Length 446;
 Best Local Similarity 51.5%; Pred. No. 5.3e-24;
 Matches 53; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 12 RMISTKEIQHAAADLMISGDVYDTPWLRHNGGEVPLTTAGODATDAFMAVHPP 71
 DB 6 REITSEELKKHKKHGDWISIQGKIYVSEWIKDHPGSEAPLNLAAQDVTDAFVAFHFG 65

QY 72 SVRPLRRFFVGLTDTYTPPASADFRRLAQLSSAGLPERVG 114
 DB 66 SAMKYLDFKFIYGLDYTISEVSKDYRKLVAFESKAGLYDKKG 108

RESULT 3
 Q9FR82 PRELIMINARY; PRT; 446 AA.

AC Q9FR82
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 8-sphingolipid desaturase.
 OS SLD1.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Boraginaceae; Borago.
 OC NCBI_TaxID=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=21092516; PubMed=11162428;

RA Libisch B., Michaelson L.V., Lewis M.J., Shewry P.R., Napier J.A.:
 "Chimerase of delta6-fatty acid and delta8-sphingolipid desaturases";
 RL Biochem. Biophys. Res. Commun. 279:779-785 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21260464; PubMed=11368168;
 RA Sperling P., Libisch B., Zaehring U., Napier J.A., Heinz E.:
 "Functional identification of a delta 8-sphingolipid desaturase from
 Borago officinalis";
 RL Arch. Biochem. Biophys. 388:293-298 (2001).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF133728; AAG43277.1; -
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KM SEQUENCE 446 AA; 50926 MW; EBD579F035A3AF0C CRC64;
 SQ

Query Match 47.7%; Score 282.5; DB 10; Length 446;
 Best Local Similarity 51.9%; Pred. No. 1.6e-21;
 Matches 54; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

QY 12 RMISTKEIQHAAADLMISGDVYDTPWLRHNGGEVPLTTAGODATDAFMAVHPP 71
 DB 6 KYISVELEKHNDLGWVWISIQGKYVNVWDWIKKHGGEVPLNLAAQDVTDAFVAFHFG 65

QY 72 SVRPLRRFFVGLTDTYTPPASADFRRLAQLSSAGLPERVG 114
 DB 66 TANKNLNLFYTHLDDYLVSEISKDYRKLVAFESKAGLFEKKG 109

RESULT 4
 Q43469 PRELIMINARY; PRT; 458 AA.

AC Q43469
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 GN SLD1.
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Campanulids; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Helianthus.
 OC NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=cv. Inbred line HA89;
 RC TISSUE=Cotyledons of developing sunflower fruits;
 RX MEDLINE=96028121; PubMed=7588718;
 RA Sperling P., Schmidt H., Heinz E.:
 "A cytochrome b5-containing fusion protein similar to plant acyl lipid
 desaturases";
 RT Eur. J. Biochem. 232:798-805 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=cv. Inbred line HA89;
 RC TISSUE=Cotyledons of developing sunflower fruits;
 RX MEDLINE=21116801; PubMed=11171153;
 RA Sperling P., Blume A., Zaehring U., Heinz E.:
 "Further characterization of delta 8-sphingolipid desaturases from
 higher plants";
 RL Biochem. Soc. Trans. 28:638-641 (2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: X87143; CAA60621.1; -
 DR HSSP: P00171; 1F03.
 DR InterPro: IPR001199; Cyt_B5.

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DT      01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE      Delta-6-desaturase.
GN      D6DES.
OS      Echinium gentianoides.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC      Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; lamids; Boraginaceae; Echinium.
CX      NCBI_TaxID=173991;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
RT      "Cloning and Molecular Characterization of the D6-Desaturase from
RL      Echinium: Functional Expression in Yeast and Tobacco.";
RT      Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RL      -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC      EMBL; AY055117; AAL23580.1; -.
DR      InterPro; IPR001199; Cyt_B5.
DR      InterPro; IPR005804; FA_desat_fam.
DR      Pfam; PF00487; FA_desaturase; 1.
DR      Pfam; PF00173; heme_1; 1.
DR      ProDom; PD000612; Cyt_B5; 1.
DR      ProDom; PD001081; FA_desat_fam; 1.
DR      PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW      Heme.
SQ      SEQUENCE    448 AA;   51428 MW;  CZA937951EB7C1B3 CRC64;
Query Match          44.5%; Score 263.5; DB 10; Length 448;
Best Local Similarity 48.1%; Pred. No. 1.7e-19;
Matches     50; Conservative 20; Mismatches 33; Indels 1; Gaps 1.

Cy       12 RMISTKELQAHAAADIMWISGDVYVTWLRHHPGGEVPLITLAGODATDAPMAHYPP 71
           :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db        7 KYIAAEELKKHKDKEGDWISIGQKVYVSDWLKDHPGGKFLLSLAGGEVDADFVAFHSG 66
           :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Cy       72 SVRLLRRFPVG-RLTDTYTPPASADEFRRLLAOLSSAGLPFRVG 114
           |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db        67 STWKFLDSFPTGYLLKDIYSSEVSKDYRKLVFEFNKGLEFDKGG 110
           |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 7
O9ZTV9 PRELIMINARY; PRI; 446 AA.
ID O9ZTV9
AC O9ZTV9
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Desaturase/cytochrome b5 protein.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosoids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      TISSUE=Seed endosperm;
RC MEDLINE=97268723; PubMed=9108131;
RX Savanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
DL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC      EMBL; AF005096; AAD01240.1; -.
DR      HSPSP; P00173; 11SU.
DR      InterPro; IPR001199; Cyt_B5.
DR      InterPro; IPR005804; FA_desat_fam.
DR      Pfam; PF00487; FA_desaturase; 1.
DR      Pfam; PF00173; heme_1; 1.
DR      ProDom; PD000612; Cyt_B5; 1.
DR      ProDom; PD001081; FA_desat_fam; 1.
DR      PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW      Heme.
```

SQ SEQUENCE 446 AA; 51418 MW; A1954FDB2DB600F CRC64;
 Query Match 44.3%; Score 262.5; DB 10; Length 446;
 Best Local Similarity 50.9%; Pred. No. 2.1e-19;
 Matches 55; Conservative 15; Mismatches 35; Indels 3; Gaps 3;
 QY 9 ADVRMISTKE-LOHAAADLMISISGDVYDTPWLRHHPGGEVPLITLAGODATDAFM 67
 2 AERKYYTKRDLKHNHPPGDLMSIOGKAYDVSDWVKHFGSFPKSLAGQEVTDADFV 61
 Db 68 YHPSVRLRRFPVVG-RLTDYTPPASADFRRLAQLSSAGLFERVG 114
 62 YHGTAMQVLDKFFFTGYHLKDYVSSESKDYRRLVAFSKLG-FEKKG 108
 RESULT 8
 Q9SAUS PRELIMINARY; PRT; 448 AA.
 AC Q9SAUS; PRELIMINARY; PRT; 448 AA.
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Delta 6-desaturase.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Borago.
 NCBI_TaxID=13363;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RA Nunberg A.N., Beremand P.D., Thomas T.L.;
 RT "Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
 (GLA)."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC EMBL; AF007561; AAD01410.1; -.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase_1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 448 AA; 51626 MW; EAC370B22E0DB00 CRC64;
 Query Match 43.6%; Score 258; DB 10; Length 448;
 Best Local Similarity 46.8%; Pred. No. 6.4e-19;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELOHAAADLMISISGDVYDTPWLRHHPGGEVPLITLAGODATDAFM 66
 2 AAOIKYITTSDELKNDKDPDLMSIOGKAYDVSDWVKHFGSFPKSLAGQEVTDADFV 61
 Db 67 AYHPSVRLRRFPVVG-RLTDYTPPASADFRRLAQLSSAGLFERVG 114
 62 AFHPASTWKNLDFKFTGYHLKDYVSSESKDYRRLVAFSKLG-FEKKG 110
 RESULT 9
 Q04353 PRELIMINARY; PRT; 448 AA.
 AC Q04353; PRELIMINARY; PRT; 448 AA.
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Delta 6-desaturase.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Borago.
 NCBI_TaxID=13363;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268723; PubMed=9108131;
 RA Savyanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 cytochrome b5 domain results in the accumulation of high levels of
 RT delta6-desaturated fatty acids in transgenic tobacco."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; U79010; AAC49700.1; -.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase_1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 448 AA; 51635 MW; B62EEB701680909F CRC64;
 Query Match 43.6%; Score 258; DB 10; Length 448;
 Best Local Similarity 46.8%; Pred. No. 6.4e-19;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELOHAAADLMISISGDVYDTPWLRHHPGGEVPLITLAGODATDAFM 66
 2 AAOIKYITTSDELKNDKDPDLMSIOGKAYDVSDWVKHFGSFPKSLAGQEVTDADFV 61
 Db 67 AYHPSVRLRRFPVVG-RLTDYTPPASADFRRLAQLSSAGLFERVG 114
 62 AFHPASTWKNLDFKFTGYHLKDYVSSESKDYRRLVAFSKLG-FEKKG 110
 RESULT 10
 Q9ZRP8 PRELIMINARY; PRT; 449 AA.
 AC Q9ZRP8; PRELIMINARY; PRT; 449 AA.
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 RN SLD1.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Brassicales; Brassicaceae; Brassica.
 NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRRAIN=cy. Drakkar; TISSUE=ripening embryos;
 RX MEDLINE=99003197; PubMed=9766850;
 RA Speerling P., Zaehntinger U., Heinz B.;
 RT "A sphingolipid desaturase from Higher Plants Identification of a New
 RT Cytochrome b5 Fusion Protein."
 RL J. Biol. Chem. 273:28590-28596(1998).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; A0224160; CAA11857.1; -.
 DR HSSP; P82291; ICXY.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase_1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 449 AA; 51490 MW; FEF37AF9D390C1 CRC64;
 Query Match 42.3%; Score 250.5; DB 10; Length 449;
 Best Local Similarity 47.1%; Pred. No. 4e-18;
 Matches 49; Conservative 17; Mismatches 37; Indels 1; Gaps 1;

QY 12 RMISTKELOAHAAADDLWISISGVDYDVTWMLRHHGCEVPLITLAGODATDAFMAHYHP 71
 DB 8 RFTISDCLKKHNQPGDLKKNISIGKVVDSHWKSHSGEALAILAGQDVTAFLAVYHVG 67
 QY 72 SVAPLRRFPVVG-RLTDYTVPPASADPRLRLAQLSSAGLPERVG 114
 DB 68 TAWRHLENLHNGYVXVDHNSVDVSRDYRLAAEFKSKRGJFDKKG 111

RESULT 11

Q8L717 PRELIMINARY; PRT; 448 AA.
 AC Q8L717;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-6-desaturase.
 OS Argania spinosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Sapotaceae; Argania.
 NCBI_TaxID=85884;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA E1 Filali A., Anderson M., Abbae K.;
 RT "Characterization and cloning of delta-6-desaturase in Argania spinosa
 RT fruit.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY131238; AAM94345.1; -
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; PA_desat_fam.
 DR Pfam; PF00487; PA_desaturase_1.
 DR Pfam; PF00173; heme_1.1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; PA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29BF CRC64;

Query Match 42.1%; Score 249; DB 10; Length 448;
 Best Local Similarity 45.3%; Pred. No. 5.7e-18;
 Matches 50; Conservative 20; Mismatches 37; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELOAHAAADDLWISISGVDYDVTWMLRHHGCEVPLITLAGODATDAFMA 66
 DB 2 AAGIKYITSDCLKKHNQPGDLKKNISIGKVVDSHWKSHSGEALAILAGQDVTAFLAVY 61
 QY 67 AYHPSVRPLRRFPVVG-RLTDYTVPPASADPRLRLAQLSSAGLPERVG 114
 DB 62 AFHPASTWKNLDFFTGYIKDYSEVSKVSKLVFERSKMGLYDPAF 110

RESULT 12

Q8L896 PRELIMINARY; PRT; 449 AA.
 AC Q8L896;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volokovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation";
 RL Genome Biol. 0:0-0(2002).

RN (2)
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY087345; AAM64895.1; -
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; PA_desat_fam.
 DR Pfam; PF00487; PA_desaturase_1.
 DR Pfam; PF00173; heme_1.1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; PA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51744 MW; A1B557B8CE03E18 CRC64;

Query Match 39.9%; Score 236.5; DB 10; Length 449;
 Best Local Similarity 39.4%; Pred. No. 1.2e-16;
 Matches 43; Conservative 24; Mismatches 41; Indels 1; Gaps 1;
 QY 7 DAADV-RMISTKELOAHAAADDLWISISGVDYDVTWMLRHHGCEVPLITLAGODATDAFMA 66
 DB 3 ESTEKKYITNEDCLKKHNQSGDLWIAIGKVVNSDMIKTHPGDVLTLNAGQDVTAFLAVY 62
 QY 67 AYHPSVRPLRRFPVVG-RLTDYTVPPASADPRLRLAQLSSAGLPERVG 114
 DB 63 AFHPASTWKNLDFFTGYIKDYSEVSKVSKLVFERSKMGLYDPAF 111

RESULT 13

Q9ZRP7 PRELIMINARY; PRT; 449 AA.
 AC Q9ZRP7;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase (AT3G61580/2A19_180).
 GN SLD1 OR 2A19.180 OR AT3G61580.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Columbia; TISSUE=flower, MAINLY GREEN PARTS, and Root;
 RX MEDLINE=99003197; PubMed=9786850;
 RA Sperling P., Zaehner U., Heinz B.;
 RT "A sphingolipid desaturase from higher plants. Identification of a new
 RT cytochrome b5 fusion protein.";
 RL J. Biol. Chem. 273:28590-28596(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Queclier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natsumi M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones";

RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Gernlert P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashitaki Y., Heuan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Kawai J., Kim C.J., Natusaka M., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Shin P., Tang C.C., Toriumi M., Wallender B.K., Wong C.,
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Ecker J.,
 RA Theologis A., Davis R.W.,
 RU Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AJ224161; CA119858.1; -
 DR EMBL; AL132962; CAB71088.1; -
 DR EMBL; AF428420; AAL16189.1; -
 DR EMBL; BT000442; AAN17419.1; -
 DR HSSP; P00171; 115U.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 449 AA; 51675 MW; 145048PFDJ35964 CRC64;
 Query Match 39.9%; Score 236.5; DB 10; Length 449;
 Best Local Similarity 39.4%; Pred. No. 1.2e-16;
 Matches 43; Conservative 24; Mismatches 41; Indels 1; Gaps 1;
 QY 7 DAADVMTSTKEIQAHAAADLWISISGDYDVTPLRHHGGEVPLITLAGODATDAFM 66
 DB 3 ETEPKITTEDLDKHNKSGDLWALQKTYNVSDWKITPGSTVILNVGDVTDAFI 62
 QY 67 AYHPVSVPLLRPFVGRRLTDYTVPPASADFFRLLAQLSSAGLFEFVVG 114
 DB 63 AFPHGTAMHLDHFLFTGYHIRDFQVSVSRDYRMALEFRLLGFEKNG 111
 RESULT 14
 Q8RXB0 PRELIMINARY; PRT; 477 AA.
 AC Q8RXB0;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 6 fatty acid desaturase D6.
 GN D6.
 OS Phaeodactylum tricornutum.
 OC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
 OC Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
 OX NCBI_TaxID=2850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UTEX 646;
 RA Domeque F., Ierchl J., Zaehring U., Heinz E.,
 RA "Cloning and functional characterization of Phaeodactylum tricornutum
 RT front-end desaturases involved in eicosapentaenoic acid
 RT biosynthesis.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY082393; AAL92563.1; -
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 477 AA; 53452 MW; 2A48B830F8BDP99F CRC64;

Query Match 32.9%; Score 195; DB 10; Length 477;
 Best Local Similarity 39.5%; Pred. No. 3.2e-12;
 Matches 45; Conservative 20; Mismatches 41; Indels 8; Gaps 4;
 QY 4 ASGDADVMTSTKEIQAHAAADLWISISGDYDVTPLRHHGGEVPLITLAGODATD 63
 DB 9 ASGGSFARKISQOEKVTASPEDAWIHNNKRYDVSNW-HEHPGAV-IFTHAGDMDT 66
 QY 64 AFMAHYPSVPLLRPFVGRRLTDYTV---PPASA---DFRLLAQLSSAGLFE 111
 DB 67 IFPAFAPSGSLMKKFTIGELIPETTGKPEQOIAFEKGYRDLRSKLIMGMFK 120
 RESULT 15
 Q944W4 PRELIMINARY; PRT; 459 AA.
 AC Q944W4;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6 fatty acid desaturase.
 OS Pythium irregulare.
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Pythium.
 OX NCBI_TaxID=36331;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hong H., Datta N., Mackenzie S.L., Qiu X.,
 RA "A delta-6 fatty acid desaturase from Pythium irregulare."
 RU Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF419296; AAL13110.1; -
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR InterPro; IPR00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 459 AA; 52498 MW; 286464DA761B805 CRC64;
 Query Match 32.7%; Score 193.5; DB 10; Length 459;
 Best Local Similarity 37.0%; Pred. No. 4.4e-12;
 Matches 44; Conservative 20; Mismatches 34; Indels 21; Gaps 4;
 QY 12 RMISTSELQAHAAADLWISISGDYDVTPLRHHGGEVPLITLAGODATDAFMAYHPP 71
 DB 10 RLVSWMKIREHATPATAMWIVHHKRYVDISKW-DSHGGSV-MITQAGDATDAFAVHPS 67
 QY 72 SVRPLLRPFVGRRLTDYTV---PPAS-----ADFRLAQLSSAGLFE 111
 DB 68 SALKLLEQFVGVDETSAELGEPASDBERARRERINEFLASRYRLKVKVGMGLYD 126

Search completed: January 1, 2004, 06:33:58
 Job time: 12.4316 secs

FILED DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-934-254-5

Query Match 43.6%; Score 258; DB 4; Length 448;
Best Local Similarity 46.8%; Pred. No. 3.8e-23;
Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADLMISISGDVYVTPMLRHHPGGEVPLITLAGODATDAM 66
DB 2 AAQIKKYITSDKLNHDKRGDLMISIQKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAY 61

QY 67 AHPPSVPLRLRRFFVG-RLTDYTPPASADPRRLAQLSAGLPERVG 114
DB 62 AFHPASTWKNLKKFTGYLYLKDYSVSEVKYRKLVFEFSKMGVLVDKKG 110

RESULT 5
US-08-833-610-5
Sequence 5, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-5

Query Match 42.1%; Score 249; DB 2; Length 446;
Best Local Similarity 45.9%; Pred. No. 4.7e-22;
Matches 50; Conservative 21; Mismatches 36; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADLMISISGDVYVTPMLRHHPGGEVPLITLAGODATDAM 66
DB 2 AAQIKKYITSDKLNHDKRGDLMISIQKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAY 61

QY 67 AHPPSVPLRLRRFFVG-RLTDYTPPASADPRRLAQLSAGLPERVG 114
DB 62 AFHPASTWKNLKKFTGYLYLKDYSVSEVKYRKLVFEFSKMGVLVDKKG 110

RESULT 6
US-08-834-033A-15
Sequence 15, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 26
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-15

Query Match 42.1%; Score 249; DB 3; Length 446;
Best Local Similarity 45.9%; Pred. No. 4.7e-22;
Matches 50; Conservative 21; Mismatches 36; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADLMISISGDVYVTPMLRHHPGGEVPLITLAGODATDAM 66
DB 2 AAQIKKYITSDKLNHDKRGDLMISIQKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAY 61

QY 67 AHPPSVPLRLRRFFVG-RLTDYTPPASADPRRLAQLSAGLPERVG 114
DB 62 AFHPASTWKNLKKFTGYLYLKDYSVSEVKYRKLVFEFSKMGVLVDKKG 114

DB 62 AFHASTWKLJDKFTGYLKDYSVSEVSKYRKLVFEPSKMGLYDKG 110

RESULT 7

US-08-833-610-2
Sequence 2, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KUNITZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-2

Query Match 25.1%; Score 148.5; DB 2; Length 446;

Best Local Similarity 40.8%; Pred. No. 8e-10; Matches 31; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 17 KELOAHAAADDLMISIGDYVDTPLRHHGGEVPLITLAGDADTDAFMAVHP-PSVRP 75
DB 12 EELAAHNTKDDLLAARGVYDVKFLSRHGGVDTLLAGAGDVTFVEMVHAFGAADA 71
QY 76 LRRFFVGRLTDTYTP 91
DB 72 IMKXYVGLTVSNELP 87

RESULT 8

US-08-834-033A-5
Sequence 5, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUNITZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,033A

FILING DATE: 11-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-300.USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 446 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-033A-5

Query Match 25.1%; Score 148.5; DB 3; Length 446;

Best Local Similarity 40.8%; Pred. No. 8e-10; Matches 31; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 17 KELOAHAAADDLMISIGDYVDTPLRHHGGEVPLITLAGDADTDAFMAVHP-PSVRP 75
DB 12 EELAAHNTKDDLLAARGVYDVKFLSRHGGVDTLLAGAGDVTFVEMVHAFGAADA 71
QY 76 LRRFFVGRLTDTYTP 91
DB 72 IMKXYVGLTVSNELP 87

RESULT 9

US-09-145-828A-23
Sequence 23, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yong-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kirchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407 US. 01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 446
TYPE: PRT
ORGANISM: Mortierella alpina
US-09-145-828A-23

Query Match 25.1%; Score 148.5; DB 4; Length 446;

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: January 1, 2004, 06:37:05 : Search time 21.7174 Seconds
(without alignments)
1053.214 Million cell updates/sec

Title: US-09-857-524B-17
Perfect score: 592
Sequence: 1 MPAAKDAADVMISTKEIQ.....ADFRLLQLSSAGLFEVVG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274.5	46.4	458	US-10-340-779A-11	Sequence 11, Appl
2	266	44.9	452	US-10-029-756-27	Sequence 27, Appl
3	258	43.6	448	US-10-340-779A-13	Sequence 13, Appl
4	258	43.6	448	US-10-029-756-5	Sequence 5, Appl
5	193.5	32.7	459	US-09-967-477B-8	Sequence 8, Appl
6	161	27.2	453	US-09-769-863-14	Sequence 14, Appl
7	161	27.2	453	US-10-054-534B-14	Sequence 14, Appl
8	161	27.2	453	US-10-431-952-14	Sequence 14, Appl
9	160.5	27.1	509	US-10-120-637A-37	Sequence 37, Appl
10	157.5	26.6	470	US-09-769-863-20	Sequence 20, Appl
11	157.5	26.6	470	US-10-054-534B-20	Sequence 20, Appl
12	157.5	26.6	470	US-10-431-952-20	Sequence 20, Appl
13	153.5	25.9	456	US-09-967-477B-6	Sequence 6, Appl
14	151.5	25.6	519	US-09-967-477B-2	Sequence 2, Appl
15	151	25.5	141	US-10-369-493-5090	Sequence 5090, Ap

16	150.5	25.4	487	15	US-10-168-274-9	Sequence 9, Appl
17	148.5	25.1	446	10	US-09-903-456-30	Sequence 30, Appl
18	148.5	25.1	446	12	US-10-278-391-2	Sequence 2, Appl
19	148.5	25.1	446	12	US-10-156-911-10	Sequence 30, Appl
20	148.5	25.1	446	12	US-10-408-726-27	Sequence 27, Appl
21	148.5	25.1	447	15	US-10-191-513A-10	Sequence 10, Appl
22	146.5	24.7	103	12	US-10-369-493-6503	Sequence 6503, Ap
23	145	24.5	112	12	US-10-369-493-12640	Sequence 12640, A
24	144.5	24.4	446	12	US-10-340-779A-3	Sequence 3, Appl
25	144.5	24.4	446	12	US-10-340-779A-14	Sequence 14, Appl
26	141.5	23.9	129	9	US-09-911-781-5	Sequence 5, Appl
27	141.5	23.9	129	12	US-10-400-902-5	Sequence 5, Appl
28	138	23.3	513	12	US-10-120-637A-16	Sequence 46, Appl
29	136.5	23.1	155	15	US-10-106-698-4650	Sequence 4650, Ap
30	136.5	23.1	169	9	US-09-925-301-902	Sequence 902, Ap
31	135	22.8	360	15	US-10-191-513A-39	Sequence 39, Appl
32	135	22.8	444	15	US-10-262-617-3	Sequence 3, Appl
33	135	22.8	444	15	US-10-191-513A-12	Sequence 12, Appl
34	134	22.6	515	11	US-09-849-199A-18	Sequence 18, Appl
35	134	22.6	515	11	US-09-849-199A-19	Sequence 19, Appl
36	134	22.6	515	11	US-09-849-199A-20	Sequence 20, Appl
37	134	22.6	515	11	US-09-849-199A-21	Sequence 21, Appl
38	134	22.6	515	12	US-10-120-637A-18	Sequence 18, Appl
39	134	22.6	515	12	US-10-120-637A-19	Sequence 19, Appl
40	134	22.6	515	12	US-10-120-637A-20	Sequence 20, Appl
41	134	22.6	515	12	US-10-120-637A-21	Sequence 21, Appl
42	134	22.6	515	12	US-10-120-637A-70	Sequence 29, Appl
43	134	22.6	515	12	US-10-060-793-29	Sequence 31, Appl
44	134	22.6	859	12	US-10-148-907A-31	Sequence 1, Appl
45	131.5	22.2	445	15	US-10-262-617-1	

ALIGNMENTS

RESULT 1
US-10-340-779A-11
; Sequence 11, Application US/10340779A
; Publication No. US20030152963A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Deaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Helianthus annuus
US-10-340-779A-11
Query Match 46.4%; Score 274.5; DB 13; Length 458;
Best Local Similarity 50.0%; Pred. No. 3.2e-24;
Matches 52; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 12 RMISTEQLQAAADLWISIGDYVDYPMKRRHGGCVPLTTAGODATAPMAYHP 71
DB 17 KTTTSKELKKHNNPDLWISLIGKYVNTVMKKHGGGAPLNLNLAGOVDTAFIAHPG 76
QY 72 SVRPLRRFFVG-RLTDYVTPPASADFRLLQLSSAGLFEVVG 114

Db 77 TAWKHLDKLFTGYHLKDQVSDISRDYKRLASEFAKAMFEKKG 120

RESULT 2

US-10-029-756-27

Sequence 27, Application US/10029756

Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029,756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-10-029-756-27

Query Match 44.8%; Score 266; DB 14; Length 452;

Best Local Similarity 49.5%; Pred. No. 3,2e-23;

Matches 52; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 12 RMISTKELQAAADDLWISISGDVDTFPLRHHHGGEVPLITLAGODATDAFMAYHPP 71

DB 7 KYTAEDELRRHNSGDLWISIQGKVDSCSHMAEHPGGEVPLITSLAGODVTDAFIAYHPG 66

QY 72 SVRPLRLRFVVG--RLTDYVPPASADFRLLAQLSAGLFEKVG 114

DB 67 TAWRHLDPFLFTGYHLKDQVSDISRDYKRLASEFAKAMFEKKG 111

RESULT 3

US-10-340-779A-13

Sequence 13, Application US/10340779A

Publication No. US20030152983A1

GENERAL INFORMATION:

APPLICANT: Napier, Johnathan A.

APPLICANT: Michaelson, Louise

APPLICANT: Stobart, Keith

TITLE OF INVENTION: Desaturase

FILE REFERENCE: 005407.00004

CURRENT APPLICATION NUMBER: US/10/340,779A

CURRENT FILING DATE: 2003-03-24

PRIOR APPLICATION NUMBER: US 09/582,034

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: PCT/GB98/03895

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: UK 9814034.6

PRIOR FILING DATE: 1998-06-29

PRIOR APPLICATION NUMBER: UK 9727256.1

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FaesEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 448

TYPE: PRT

ORGANISM: Borago officinalis

US-10-340-779A-13

Query Match 43.6%; Score 258; DB 12; Length 448;

Best Local Similarity 46.8%; Pred. No. 2.9e-22;

Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADDLWISISGDVDTFPLRHHHGGEVPLITLAGODATDAFM 66

DB 2 AAGIKRYTSDLEKNHDKPGDLWISIQKAYDVSDWVKHPPGSPFLKSLAGQEVTDAPV 61

QY 67 AYHPPSVRPLRLRFVVG--RLTDYVPPASADFRLLAQLSAGLFEKVG 114

DB 62 AHPHASTWKNLDFFTGYHLKDQVSDISRDYKRLASEFAKAMFEKKG 110

RESULT 4

US-10-029-756-5

Sequence 5, Application US/10029756

Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029,756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 448 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-029-756-5

Query Match 43.6%; Score 258; DB 14; Length 448;
 Best Local Similarity 46.8%; Pred. No. 2.9e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELOAHAAADDLMISISGVDVTPWLRHHHGGGEVPLITLAGODATDAFMAYHPPSV 73
 DB 2 AAOIKKYIISDEKXNDKXGDLWISIOGKAYDVSDWKHPGSGFPLKSLAGQEVDAFV 61
 QY 67 AVHPPSVRLRRFPVGV-RLTDVTPASADPFRLLAQLSSAGLFEFV 114
 DB 62 AHPASTKXKLDKFFFTGYIKDYSSEVSKDYAKKLVPFSSKXGLYDKG 110

RESULT 5
 US-09-967-477B-8
 ; Sequence 8, Application US/09967477B
 ; Patent No. US20020156254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xiao Qiu
 ; APPLICANT: Haiping Hong
 ; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
 ; FILE REFERENCE: BNZ-001
 ; CURRENT APPLICATION NUMBER: US/09/967,477B
 ; CURRENT FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: 60/236,303
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/297,562
 ; PRIOR FILING DATE: 2001-06-12
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 459
 ; TYPE: PRT
 ; ORGANISM: Thraustochytrium sp.
 ; US-09-967-477B-8

Query Match 32.7%; Score 193.5; DB 10; Length 459;
 Best Local Similarity 37.0%; Pred. No. 1.6e-14;
 Matches 44; Conservative 20; Mismatches 34; Indels 21; Gaps 4;

QY 12 RMISTKELOAHAAADDLMISISGVDVTPWLRHHHGGGEVPLITLAGODATDAFMAYHPPSV 71
 DB 10 RLVSWEIEHKAHPATAMVIVHKKYDIDSKM-DSHGGGV-MITQAGEDATDAFAVFPSSA 67
 QY 72 SVRPLLRFPVGRITDVT-----PPASADPFRLLAQLSSAGLFE 111
 DB 68 SALKLEQYVGVGDVDSKAEIEGEPASDSEBARERERINEFIASVRLKLVKXGMLYD 126

RESULT 6
 US-09-769-863-14
 ; Sequence 14, Application US/09769863
 ; Publication No. US20030157144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradipt
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763 US 01
 ; CURRENT APPLICATION NUMBER: US/09/769,863
 ; CURRENT FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolengia diclina
 ; US-09-769-863-14

Query Match 27.2%; Score 161; DB 12; Length 453;
 Best Local Similarity 34.8%; Pred. No. 1.2e-10;
 Matches 39; Conservative 20; Mismatches 37; Indels 16; Gaps 4;

QY 14 ISTKELQAHAAADDLMISISGVDVTPWLRHHHGGGEVPLITLAGODATDAFMAYHPPSV 73
 DB 10 ISWATIREHNRDAMVIVHKKYDISAF-EDHPG3-VMFTOAGEDATDAFAVFPSSA 67
 QY 74 RPLLRFPVGRITDVT-----VPPASADPFRLLAQLSSAGLFE 111
 DB 68 LKLEQYVGVGDVDSKAEIEGEPASDSEBARERERINEFIASVRLKLVKXGMLYD 119

RESULT 7
 US-10-054-534B-14
 ; Sequence 14, Application US/10054534B
 ; Publication No. US20030167525A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradipt
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer M.
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763 US 01
 ; CURRENT APPLICATION NUMBER: US/10/054,534B
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: US 09/769,863
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolengia diclina
 ; US-10-054-534B-14

Query Match 27.2%; Score 161; DB 12; Length 453;
 Best Local Similarity 34.8%; Pred. No. 1.2e-10;
 Matches 39; Conservative 20; Mismatches 37; Indels 16; Gaps 4;

QY 14 ISTKELQAHAAADDLMISISGVDVTPWLRHHHGGGEVPLITLAGODATDAFMAYHPPSV 73
 DB 10 ISWATIREHNRDAMVIVHKKYDISAF-EDHPG3-VMFTOAGEDATDAFAVFPSSA 67
 QY 74 RPLLRFPVGRITDVT-----VPPASADPFRLLAQLSSAGLFE 111
 DB 68 LKLEQYVGVGDVDSKAEIEGEPASDSEBARERERINEFIASVRLKLVKXGMLYD 119

RESULT 8
 US-10-431-952-14
 ; Sequence 14, Application US/10431952
 ; Publication No. US20030190733A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradipt
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763 US 01
 ; CURRENT APPLICATION NUMBER: US/10/431,952
 ; CURRENT FILING DATE: 2003-05-08
 ; PRIOR APPLICATION NUMBER: US/09/769,863
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453

TYPE: PRT
ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match 27.2%; Score 161; DB 12; Length 453;
Best Local Similarity 34.8%; Pred. No. 1.2e-10;
Matches 39; Conservative 20; Mismatches 37; Indels 16; Gaps 4;

QY 14 ISRKELOAHAAADLMWISGVDVDTFPMLRHHPGGEVPLITLAGODATDAFMAHYHPPSV 73
DB 10 ISMTTTEHRRQDAMVIHHKYDISAF-EDHPGG-VVMFTQGEATDAFVAFHPSA 67
QY 74 RPLRRFFVGRITDYT-----VPPASADF-----RRLAQLSSAGLFE 111
DB 68 LKLEQYVVDVQSTAAVDTSISDEVKSGSDPIASRYRLRLVRLGLYD 119

RESULT 9
US-10-120-637A-37

Sequence 37, Application US/10120637A
Publication No. US20030134400A1

GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Leonard, Amanda E.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 6804 US. P1
CURRENT APPLICATION NUMBER: US/10/120, 637A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 09/849,199
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 509
TYPE: PRT
ORGANISM: Schizochytrium aggregatum
US-10-120-637A-37

Query Match 27.1%; Score 160.5; DB 12; Length 509;
Best Local Similarity 36.0%; Pred. No. 1.6e-10;

Matches 40; Conservative 21; Mismatches 33; Indels 17; Gaps 4;

QY 15 STEKLOAHAAADLMWISGVDVDTFPMLRHHPGGEVPLITLAGODATDAFMAHYHPPSV 74
DB 10 SMAQVRHNTPTDDWCAIHGEVYELTKFARTHPGGDITLLA-AKKEATILFETTH---VR 65
QY 75 PL-----LRFFVGRITDYTVPASADFFRLAQLSSAGLFE 112
DB 66 PISDAVLRKRYRIGKLAAGKDEPANDSTYVSMDSDFYKVLQRVAVRLER 116

RESULT 10
US-09-769-863-20

Sequence 20, Application US/09769863
Publication No. US20030157144A1

GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763 US. O1
CURRENT APPLICATION NUMBER: US/09/769, 863
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 470
TYPE: PRT
ORGANISM: Saprolegnia diclina
US-09-769-863-20

Query Match 26.6%; Score 157.5; DB 12; Length 470;
Best Local Similarity 39.1%; Pred. No. 3.2e-10;
Matches 34; Conservative 12; Mismatches 34; Indels 7; Gaps 2;

QY 2 PAASKDADVRMISTEKLQAHAAADLMWISGVDVDTFPMLRHHPGGEVPLITLAGODA 61
DB 18 PVAGKKA-----FTWQEVQAHNTAASAWIIRKQYDVETEMANKHPGGREMYLLHAGREA 72
QY 62 TDAFMAHYHPPS--VRPLRRFFVGRIT 86
DB 73 TDTFDSYHPPSDKAESILNKYEIGTFT 99

RESULT 11
US-10-054-534B-20

Sequence 20, Application US/10054534B
Publication No. US20030167525A1

GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763 US. P1
CURRENT APPLICATION NUMBER: US/10/054, 534B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769, 863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 470
TYPE: PRT
ORGANISM: Saprolegnia diclina
US-10-054-534B-20

Query Match 26.6%; Score 157.5; DB 12; Length 470;
Best Local Similarity 39.1%; Pred. No. 3.2e-10;
Matches 34; Conservative 12; Mismatches 34; Indels 7; Gaps 2;

QY 2 PAASKDADVRMISTEKLQAHAAADLMWISGVDVDTFPMLRHHPGGEVPLITLAGODA 61
DB 18 PVAGKKA-----FTWQEVQAHNTAASAWIIRKQYDVETEMANKHPGGREMYLLHAGREA 72
QY 62 TDAFMAHYHPPS--VRPLRRFFVGRIT 86
DB 73 TDTFDSYHPPSDKAESILNKYEIGTFT 99

RESULT 12
US-10-431-952-20

Sequence 20, Application US/10431952
Publication No. US20030190733A1

GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763 US. O1
CURRENT APPLICATION NUMBER: US/10/431, 952
CURRENT FILING DATE: 2003-05-08

; PRIOR APPLICATION NUMBER: US/09/769,863
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 470
 ; TYPE: PRF
 ; ORGANISM: *Saprolegnia dictina*
 ; US-10-431-952-20

Query Match 26.6%; Score 157.5; DB 12; Length 470;
 Best Local Similarity 39.1%; Pred. No. 3.2e-10;
 Matches 34; Conservative 12; Mismatches 34; Indels 7; Gaps 2;

QY 2 PASKDAVPMISTELQAHAAADLMISGSDYDVTPLRHHHGGVEPLITLAGODATDAFMAYHPSVR-- 61
 DB 18 PAAKGA---FTWQEVQAHNTAASAWIIRKGVYDVTWANKHGGEMVLLHAGREA 72
 QY 62 TDAFMAVHPS--VRPLRRFVGRLT 86
 DB 73 TDTFDSYHPSDKAESILNKYEIGTFT 99

RESULT 13
 US-09-967-477B-6
 ; Sequence 6, Application US/09967477B
 ; Patent No. US20020156254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xiao Qiu
 ; APPLICANT: Haijing Hong
 ; TITLE OF INVENTION: FAD5, FAD5-2, AND FAD6, NOVEL
 ; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
 ; FILE REFERENCE: BNZ-001
 ; CURRENT APPLICATION NUMBER: US/09/967,477B
 ; CURRENT FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: 60/236,303
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/297,562
 ; PRIOR FILING DATE: 2001-06-12
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 456
 ; TYPE: PRF
 ; ORGANISM: *Thraustochytrium* sp.
 ; US-09-967-477B-6

Query Match 25.9%; Score 153.5; DB 10; Length 456;
 Best Local Similarity 37.3%; Pred. No. 9.4e-10;
 Matches 31; Conservative 15; Mismatches 34; Indels 3; Gaps 2;

QY 17 KELQAHAAADLMISGSDYDVTPLRHHHGGVEPLITLAGODATDAFMAYHPSVR-- 74
 DB 12 QEVAKNTAKSAAVIRGEYDVTWADKHGSEILVHSGRECTDTFYSYHPSNRAD 71
 QY 75 PLRRFVGRLT-DYTVPPASAD 96
 DB 72 KILAKYKIKLVGVGEYFPVFKPD 94

RESULT 14
 US-09-967-477B-2
 ; Sequence 2, Application US/09967477B
 ; Patent No. US20020156254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xiao Qiu
 ; APPLICANT: Haijing Hong
 ; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
 ; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
 ; FILE REFERENCE: BNZ-001
 ; CURRENT APPLICATION NUMBER: US/09/967,477B
 ; CURRENT FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: 60/236,303

; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/297,562
 ; PRIOR FILING DATE: 2001-06-12
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 519
 ; TYPE: PRF
 ; ORGANISM: *Thraustochytrium* sp.
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 462
 ; OTHER INFORMATION: Xaa = Gly
 ; US-09-967-477B-2

Query Match 25.6%; Score 151.5; DB 10; Length 519;
 Best Local Similarity 37.8%; Pred. No. 1.9e-09;
 Matches 37; Conservative 21; Mismatches 37; Indels 3; Gaps 3;

QY 14 ISTKELQAHAAADLMISGSDYDVTPLRHHHGGVEPLITLAGODATDAFMAYHPSV 73
 DB 9 IPPEQVRAHKKPDAMCAIGHVYDVTKPASVHGGDITLLA-AGKATVLYETHVAGV 67
 QY 74 R-PLRRFVGRLTDTYTVPPASADFRRLAQLSSAGLP 110
 DB 68 SDAVLRKRIKLPD-GGGANKEKRTLSGLSSASY 104

RESULT 15
 US-10-369-493-5090
 ; Sequence 5090, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 5090
 ; LENGTH: 141
 ; TYPE: PRF
 ; ORGANISM: *Caenorhabditis elegans*
 ; US-10-369-493-5090

Query Match 25.5%; Score 151; DB 12; Length 141;
 Best Local Similarity 39.1%; Pred. No. 4.2e-10;
 Matches 34; Conservative 14; Mismatches 35; Indels 4; Gaps 2;

QY 9 ADVRMISTKELQAH--AAADLMISGSDYDVTPLRHHHGGVEPLITLAGODATDAF 65
 DB 2 SELRVISLDEVSKEHMBADQSCWIVISGKYDVTFLNEHGGGEVITQLAGKATVGF 61
 QY 66 M-AVHPSVRLRRFVGRLTDTYTP 91
 DB 62 LDVGHSKAIEMANEYLLIGQLPESDVP 88

Search completed: January 1, 2004, 06:58:38
 Job time : 22.7174 secs

